

RESULT 1703
AX320075
LOCUS AX320075 16 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 11 from Patent WO0188116.
ACCESSION AX320075
VERSION AX320075.1 GI:17901576
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Stolka,R., Horwitz,G.A., Zhang,X. and Melmed,S.
TITLE Method of modulating activation of lymphocytes via modulation of pituitary tumor transforming gene, related screening methods
JOURNAL Patent: WO 0188116-A 11 22-NOV-2001;
CEDARS-SINAI MEDICAL CENTER (US)
FEATURES
source Location/Qualifiers
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Anchored primer sequence."
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1767 AAGCTTTTCTTTTCTTG 1782
|||||
Db 1 AAGCTTTTCTTTTCTTG 16
RESULT 1704
AX352386
LOCUS AX352386 16 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 11 from Patent WO0187934.
ACCESSION AX352386
VERSION AX352386.1 GI:18617657
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Horwitz,G.A., Zhang,X., Heaney,A. and Melmed,S.
TITLE Treatment of neoplasia / transformation using pituitary tumor transforming gene carboxy terminal peptides
JOURNAL Patent: WO 0187934-A 11 22-NOV-2001;
CEDARS-SINAI MEDICAL CENTER (US)
FEATURES
source Location/Qualifiers
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Anchored primer sequence."
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1767 AAGCTTTTCTTTTCTTG 1782
|||||
Db 1 AAGCTTTTCTTTTCTTG 16
RESULT 1705
AX391467
LOCUS AX391467 16 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 3 from Patent WO0216632.
ACCESSION AX391467
VERSION AX391467.1 GI:19700077
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Brodin,P. and Thelin,A.
TITLE Pharmaceutical compositions comprising a modulator of adams-1
JOURNAL Patent: WO 0216632-A 3 28-FEB-2002;
Astrazeneca AB (SE)
FEATURES
source Location/Qualifiers
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1767 AAGCTTTTCTTTTCTTG 1782
|||||
Db 1 AAGCTTTTCTTTTCTTG 16
RESULT 1706
AX394754
LOCUS AX394754 16 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 5 from Patent WO0218568.
ACCESSION AX394754
VERSION AX394754.1 GI:21065833
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Brodin,P. and Thelin,A.
TITLE Molecules involved in the regulation of insulin resistance syndrome (irs)
JOURNAL Patent: WO 0218568-A 5 07-MAR-2002;
Astrazeneca AB (SE)
FEATURES
source Location/Qualifiers
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="H-T11-G"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1767 AAGCTTTTCTTTTCTTG 1782
|||||
Db 1 AAGCTTTTCTTTTCTTG 16
RESULT 1707
AX394785
LOCUS AX394785 16 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 9 from Patent WO0218421.
ACCESSION AX394785
VERSION AX394785.1 GI:21065859
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Brodin,P. and Thelin,A.
TITLE Human and mouse e2-protein, nucleic acids coding therefor and uses thereof
JOURNAL Patent: WO 0218421-A 9 07-MAR-2002;
Astrazeneca AB (SE)
FEATURES
source Location/Qualifiers
1. .16

AUTHORS Leffers,H., Jorgensen,M. and skakkeb K,N.E.
TITLE Endogenous gene expression assay
JOURNAL Patent: WO 0134834-A 21 17-MAY-2001;
Rigshospitalet (DK)

FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer sequence"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTT TTTT TTTG 1782
|||||
Db 1 AAGCTTTT TTTT TTTG 16

RESULT 1699
AX235176
LOCUS AX235176 16 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 9 from Patent WO0163282.
ACCESSION AX235176
VERSION AX235176.1 GI:15593767
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
TITLE Analysis of biological targets using a biochip comprising a
fluorescent marker
JOURNAL Patent: WO 0163282-A 9 30-AUG-2001;
COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="sequence synthetic"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2181
|||||
Db 1 TTTT TTTT TTTT TTTT 16

RESULT 1700
AX235176/c
LOCUS AX235176 16 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 9 from Patent WO0163282.
ACCESSION AX235176
VERSION AX235176.1 GI:15593767
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
TITLE Analysis of biological targets using a biochip comprising a
fluorescent marker
JOURNAL Patent: WO 0163282-A 9 30-AUG-2001;
COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

/note="sequence synthetic"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA 2801
|||||
Db 16 AAAAAA AAAAAA 1

RESULT 1701
AX253409
LOCUS AX253409 16 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 21 from Patent WO0171013.
ACCESSION AX253409
VERSION AX253409.1 GI:16073943
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Clendennen,S.K. and Kellogg,J.A.
TITLE Melon promoters for expression of transgenes in plants
JOURNAL Patent: WO 0171013-A 21 27-SEP-2001;
Exelixis Plant Sciences, Inc. (US)
FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTT TTTT TTTG 1782
|||||
Db 1 AAGCTTTT TTTT TTTG 16

RESULT 1702
AX306362
LOCUS AX306362 16 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 11 from Patent WO0187039.
ACCESSION AX306362
VERSION AX306362.1 GI:17645594
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Prezant,T.R., Heaney,A.P. and Melmed,S.
TITLE Treatment of neoplasia / transformation using pituitary tumor
transforming gene 2
JOURNAL Patent: WO 0187039-A 11 22-NOV-2001;
CEDARS-SINAI MEDICAL CENTER (US)
FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Anchored primer sequence."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTT TTTT TTTG 1782
|||||
Db 1 AAGCTTTT TTTT TTTG 16

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTCTTTTCTTTTG 1782
|||||
Db 1 AAGCTTTTCTTTTCTTTTG 16

RESULT 1694
AX039049
LOCUS AX039049.1 GI:11228345
DEFINITION Sequence 15 from patent US 6642438.
ACCESSION AR429377
VERSION AR429377.1 GI:40189570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Clendennen,S.K.; Kellogg,J.A.; Phan,C.B.; Mathews,H.V. and Webb,N.M.
TITLE Melon promoters for expression of transgenes in plants
JOURNAL Patent: US 6642438-A 15 04-NOV-2003;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTCTTTTCTTTTG 1782
|||||
Db 1 AAGCTTTTCTTTTCTTTTG 16

RESULT 1695
AX039049
LOCUS AX039049.1 GI:11228345
DEFINITION Sequence 2 from Patent WO0061594.
ACCESSION AX039049
VERSION AX039049.1 GI:11228345
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Beier,M. and Hoheisel,J.
TITLE Nucleoside derivatives with photo-unstable protective groups
JOURNAL Patent: WO 0061594-A 2 19-OCT-2000;
DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG (DE)

FEATURES Location/Qualifiers
source 1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801
|||||
Db 1 AAAAAAAAAAAAAA 16

RESULT 1696
AX039049/c
LOCUS AX039049

DEFINITION Sequence 2 from Patent WO0061594.
ACCESSION AX039049
VERSION AX039049.1 GI:11228345
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Beier,M. and Hoheisel,J.
TITLE Nucleoside derivatives with photo-unstable protective groups
JOURNAL Patent: WO 0061594-A 2 19-OCT-2000;
DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG (DE)

FEATURES Location/Qualifiers
source 1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTTCTTTT 2181
|||||
Db 16 TTTTCTTTTCTTTTCTTTT 1

RESULT 1697
AX127437
LOCUS AX127437.1 GI:14133900
DEFINITION Sequence 80 from Patent WO0130999.
ACCESSION AX127437
VERSION AX127437.1 GI:14133900
KEYWORDS
SOURCE Bruguiera gymnorrhiza
ORGANISM Bruguiera gymnorrhiza
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Rhizophoraceae; Bruguiera.

REFERENCE 1
AUTHORS Karube,I. and Hanagata,N.
TITLE Salt tolerance genes
JOURNAL Patent: WO 0130999-A 80 03-MAY-2001;
EBARA CORPORATION (JP)

FEATURES Location/Qualifiers
source 1..16
/organism="Bruguiera gymnorrhiza"
/mol_type="unassigned DNA"
/db_xref="taxon:39984"
/note="Artificially Synthesized Primer Sequence"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTCTTTTCTTTTG 1782
|||||
Db 1 AAGCTTTTCTTTTCTTTTG 16

RESULT 1698
AX146679
LOCUS AX146679.1 GI:14285072
DEFINITION Sequence 21 from Patent WO0134834.
ACCESSION AX146679
VERSION AX146679.1 GI:14285072
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1

JOURNAL Patent: US 6486308-A 2 26-NOV-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2181
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 1689
AR257437/c
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6486308.
ACCESSION AR257437
VERSION AR257437.1 GI:27307448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 2 26-NOV-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAA AAAAAA AAAAAA 2801
|||||
Db 16 AAAAAA AAAAAA AAAAAA 1

RESULT 1690
AR266618
LOCUS AR266618 16 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 56 from patent US 6495319.
ACCESSION AR266618
VERSION AR266618.1 GI:29695682
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 56 17-DEC-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTT TTTT TTG 1782
|||||
Db 1 AAGCTTTT TTTT TTG 16

RESULT 1691
AR266645

LOCUS AR266645 16 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 83 from patent US 6495319.
ACCESSION AR266645
VERSION AR266645.1 GI:29695709
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 83 17-DEC-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTT TTTT TTG 1782
|||||
Db 1 AAGCTTTT TTTT TTG 16

RESULT 1692
AR282683
LOCUS AR282683 16 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 4 from patent US 6521750.
ACCESSION AR282683
VERSION AR282683.1 GI:29719309
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Hair,G.A. and Boden,S.D.
TITLE Bone mineralization proteins, DNA, vectors, expression systems
JOURNAL Patent: US 6521750-A 4 18-FEB-2003;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTT TTTT TTG 1782
|||||
Db 1 AAGCTTTT TTTT TTG 16

RESULT 1693
AR369775
LOCUS AR369775 16 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6300127.
ACCESSION AR369775
VERSION AR369775.1 GI:34606215
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Hair,G.A. and Boden,S.D.
TITLE Bone mineralization proteins, DNA, vectors, expression systems
JOURNAL Patent: US 6300127-A 4 09-OCT-2001;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 2 30-JUL-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801
Db 16 AAAAAAAAAAAAAA 1

RESULT 1684
AR222462
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 22 from patent US 6429300.
ACCESSION AR222462
VERSION AR222462.1 GI:23329993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 22 06-AUG-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801
Db 1 AAAAAAAAAAAAAA 16

RESULT 1685
AR222462/c
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 22 from patent US 6429300.
ACCESSION AR222462
VERSION AR222462.1 GI:23329993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 22 06-AUG-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2181

Db 16 TTTTTTTTTTTTTT 1

RESULT 1686
AR227681
LOCUS AR227681 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 6444803.
ACCESSION AR227681
VERSION AR227681.1 GI:27266260
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Hair,G.A. and Boden,S.D.
TITLE Bone mineralization proteins, DNA, vectors, expression systems
JOURNAL Patent: US 6444803-A 4 03-SEP-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTTTTTTT 1782
Db 1 AAGCTTTTTTTTTT 16

RESULT 1687
AR232208
LOCUS AR232208 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6455305.
ACCESSION AR232208
VERSION AR232208.1 GI:27274198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Melmed,S. and Pei,L.
TITLE Pituitary-tumor-transforming-genes, and related products
JOURNAL Patent: US 6455305-A 5 24-SEP-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTTTTTTT 1782
Db 1 AAGCTTTTTTTTTT 16

RESULT 1688
AR257437
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6486308.
ACCESSION AR257437
VERSION AR257437.1 GI:27307448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates

VERSION I38682.1 GI:2084736
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 42 25-MAR-1997;
FEATURES Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 1679
I38682/c
LOCUS I38682 16 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 42 from patent US 5614617.
ACCESSION I38682
VERSION I38682.1 GI:2084736
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 42 25-MAR-1997;
FEATURES Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2801
|||||
Db 16 AAAAAA AAAAAA AAAAAA 1

RESULT 1680
I38700
LOCUS I38700 16 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 60 from patent US 5614617.
ACCESSION I38700
VERSION I38700.1 GI:2084754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 60 25-MAR-1997;
FEATURES Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2181
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 1681
I38700/c
LOCUS I38700 16 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 60 from patent US 5614617.
ACCESSION I38700
VERSION I38700.1 GI:2084754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 60 25-MAR-1997;
FEATURES Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2801
|||||
Db 16 AAAAAA AAAAAA AAAAAA 1

RESULT 1682
AR221692
LOCUS AR221692 16 bp DNA PAT 26-SEP-2002
DEFINITION Sequence 2 from patent US 6426408.
ACCESSION AR221692
VERSION AR221692.1 GI:23328764
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 2 30-JUL-2002;
FEATURES Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 1683
AR221692/c
LOCUS AR221692 16 bp DNA PAT 26-SEP-2002
DEFINITION Sequence 2 from patent US 6426408.
ACCESSION AR221692
VERSION AR221692.1 GI:23328764
KEYWORDS

REFERENCE 1 (bases 1 to 16)
AUTHORS Boden,S.D. and Hair,G.A.
TITLE LIM mineralization protein splice variants
JOURNAL Patent: JP 2002542802-A 3 17-DEC-2002;
EMORY UNIVERSITY
COMMENT OS MMLV
PN JP 2002542802-A/3
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615061
PR 30-APR-1999 US 60/132021
PI SCOTT D BODEN,GREGORY A HAIR
PC C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P19/08,A61P19/10,
PC C07K14/51,
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/ PC
08//
PC A61K35/76,C12N15/00,A61K37/02,C12N5/00
CC LIM mineralization protein splice variants
FH Key Location/Qualifiers
FT source 1..16
FT /organism='MMLV'.
FEATURES
source Location/Qualifiers
1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1767 AAGCTTTT TTTT TTTT TTTT TTTT TTTT 1782
|||||
Db 1 AAGCTTTT TTTT TTTT TTTT TTTT TTTT 16
RESULT 1675
BD268989
LOCUS Banana promoter and melon promoter for expression of transgene in
DEFINITION plant.
ACCESSION BD268989
VERSION BD268989.1 GI:33078757
KEYWORDS JP 2002539779-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and Webb,N.M.
TITLE Banana promoter and melon promoter for expression of transgene in
JOURNAL Patent: JP 2002539779-A 15 26-NOV-2002;
EXBLIXIS PLANT SCIENCES INC
COMMENT OS Artificial Sequence
PN JP 2002539779-A/15
PD 26-NOV-2002
PF 17-MAR-2000 JP 2000606722
PR 19-MAR-1999 US 60/125310
PI STEPHANIE K CLENDENNEN,JILL A KELLOGG,CHAU B PHAN,HELENA V PI
MATHEWS,
PI NANCY M WEBB
PC C12N15/09,A01H1/00,C12N5/10,C12Q1/68//C12N5/10,C12R1:91), PC
C12N15/00,
PC C12N5/00,C12N5/00,C12R1:91)
CC oligonucleotide primer
FH Key Location/Qualifiers
FT source 1..16
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1767 AAGCTTTT TTTT TTTT TTTT TTTT TTTT 1782
|||||
Db 1 AAGCTTTT TTTT TTTT TTTT TTTT TTTT 16
RESULT 1676
I38676
LOCUS Sequence 36 from patent US 5614617.
DEFINITION 16 bp DNA
ACCESSION I38676
VERSION I38676.1 GI:2084730
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 36 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2181
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 16
RESULT 1677
I38676/c
LOCUS Sequence 36 from patent US 5614617.
DEFINITION 16 bp DNA
ACCESSION I38676
VERSION I38676.1 GI:2084730
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 36 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAA AAAAAA AAAAAA 2801
|||||
Db 16 AAAAAA AAAAAA AAAAAA 1
RESULT 1678
I38682
LOCUS Sequence 42 from patent US 5614617.
DEFINITION 16 bp DNA
ACCESSION I38682

ACCESSION AR037355
VERSION AR037355.1 GI:5955211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 5801155-A 2 01-SEP-1998;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAA 2801
|||||
Db 16 AAAAAAAAAAAAAA 1
RESULT 1670
AR104584
LOCUS AR104584 16 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 131 from patent US 6093809.
ACCESSION AR104584
VERSION AR104584.1 GI:12817292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 131 25-JUL-2000;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAA 2801
|||||
Db 1 AAAAAAAAAAAAAA 16
RESULT 1671
AR104584/c
LOCUS AR104584 16 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 131 from patent US 6093809.
ACCESSION AR104584
VERSION AR104584.1 GI:12817292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 131 25-JUL-2000;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAA 2801
|||||
Db 1 AAAAAAAAAAAAAA 16

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTTTTTTTTTTTT 2181
|||||
Db 16 TTTTTTTTTTTTTT 1
RESULT 1672
AR175845
LOCUS AR175845 16 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 131 from patent US 6309867.
ACCESSION AR175845
VERSION AR175845.1 GI:17917144
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 131 30-OCT-2001;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAA 2801
|||||
Db 1 AAAAAAAAAAAAAA 16
RESULT 1673
AR175845/c
LOCUS AR175845 16 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 131 from patent US 6309867.
ACCESSION AR175845
VERSION AR175845.1 GI:17917144
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 131 30-OCT-2001;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTTTTTTTTTTTT 2181
|||||
Db 16 TTTTTTTTTTTTTT 1
RESULT 1674
BD259919
LOCUS BD259919 16 bp DNA linear PAT 17-JUL-2003
DEFINITION LIM mineralization protein splice variants.
ACCESSION BD259919
VERSION BD259919.1 GI:33069689
KEYWORDS JP 2002542802-A/3.
SOURCE unidentified
ORGANISM unidentified
unclassified.

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2801
:|||||
Db 25 BAAAAAAAAAAAAAAAAA 9

RESULT 1656
AR370671/c
LOCUS AR370671 25 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 11 from patent US 6300544.
ACCESSION AR370671
VERSION AR370671.1 GI:34607459
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
AUTHORS Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
TITLE Cytochrome P450 monooxygenases
JOURNAL Patent: US 6300544-A 11 09-OCT-2001;
FEATURES
Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2801
:|||||
Db 25 BAAAAAAAAAAAAAAAAA 9

RESULT 1657
AR431257/c
LOCUS AR431257 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 11 from patent US 6649814.
ACCESSION AR431257
VERSION AR431257.1 GI:40193207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
AUTHORS Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
TITLE Cytochrome P450 monooxygenases
JOURNAL Patent: US 6649814-A 11 18-NOV-2003;
FEATURES
Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2801
:|||||
Db 25 BAAAAAAAAAAAAAAAAA 9

RESULT 1658
BD057791/c
LOCUS BD057791 25 bp DNA linear PAT 27-AUG-2002
DEFINITION Cytochrome P450 Monooxygenases.
ACCESSION BD057791
VERSION BD057791.1 GI:22603397
KEYWORDS JP 2001514515-A/6.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 25)
Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
Cytochrome P450 Monooxygenases
Patent: JP 2001514515-A 6 11-SEP-2001;
NOVARTIS AG,ROYAL VETERINARY AND AGRICULTURE UNIV
PN JP 2001514515-A/6
PD 11-SEP-2001
PF 05-MAR-1998 JP 1998539180
PR 07-MAR-1997 EP 97810132.7,08-DEC-1997 EP 97810954.4 PI
BARBARA ANN HALKIER,SOREN BAK,RACHEL ALICE KAHN,BIRGER PI
LINDBERG MOLLER
PC C12N9/02,C12N15/82//C12N15/53
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2801
:|||||
Db 25 BAAAAAAAAAAAAAAAAA 9

RESULT 1659
AX042981/c
LOCUS AX042981 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 547 from Patent WO0065088.
ACCESSION AX042981
VERSION AX042981.1 GI:11341589
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 547 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="16S rRNA Homozygote Primer Sequence"

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAA 2801
:|||||
Db 21 AGTTCCAAAAAAAAAAAAAAAA 1

RESULT 1660
AX115700
LOCUS AX115700 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 823 from Patent WO0129262.
ACCESSION AX115700
VERSION AX115700.1 GI:14032642
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 1299 05-MAR-2002;
FEATURES
source
1. .24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 266 TCGCGCGGCGCAGCACCTCTAC 286
Db 1 TCGCGCGTGCAGCACGTCAC 21

RESULT 1652
AR260368
LOCUS AR260368 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1299 from patent US 6489455.
ACCESSION AR260368
VERSION AR260368.1 GI:27310879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 1299 03-DEC-2002;
FEATURES
source
1. .24
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 266 TCGCGCGGCGCAGCACCTCTAC 286
Db 1 TCGCGCGTGCAGCACGTCAC 21

RESULT 1653
AX377075
LOCUS AX377075 24 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 33 from Patent WO212557.
ACCESSION AX377075
VERSION AX377075.1 GI:19573369
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Cailloux,F. and Gobron,S.
TITLE Method for detecting known mutations in tube
JOURNAL Patent: WO 0212557-A 33 14-FEB-2002;
FEATURES
source
1. .24
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Amorce pour la detection de mutations responsables de la mucoviscidose."

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.2e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2156 TTTTCTCTCCTTTTCTTTT 2176
Db 2 TTTCTCTCTCTTTCTTTT 22

RESULT 1654
BD064144
LOCUS BD064144 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of the biosynthesis genes for pseudo-oligosaccharides from Streptomyces glaucescens GLA.O and their use.
ACCESSION BD064144
VERSION BD064144.1 GI:22609747
KEYWORDS JP 2001507923-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Decker,H.
TITLE Isolation of the biosynthesis genes for pseudo-oligosaccharides from Streptomyces glaucescens GLA.O and their use
JOURNAL Patent: JP 2001507923-A 2 19-JUN-2001;
COMMENT HOECHST AKTIENGESSELLSCHAFT
PN JP 2001507923-A/2
PD 19-JUN-2001
PF 30-MAY-1997 JP 1998501137
PR 07-JUN-1996 DE 196 22 783.6
PI HEINRICH DECKER
PC C12N15/52,C12N9/00,C07K14/36,C12Q1/68,C12N15/63,C12N1/21, PC C12P19/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT exon 1. .24.
Location/Qualifiers
source
1. .24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 799 GGAGCTGTGGGGGCCGTAAT 819
Db 2 GGWVCTGGYVGGGCCGTAGT 22

RESULT 1655
A85331/c
LOCUS A85331 25 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 11 from Patent WO9840470.
ACCESSION A85331
VERSION A85331.1 GI:6733935
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Halkier,B.A. and Kahn,R.A.
TITLE CYTOCHROME P450 MONOOXYGENASES
JOURNAL Patent: WO 9840470-A 11 17-SEP-1998;
FEATURES
source
1. .25
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;

FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Reverse PCR primer for amplifying a region around the -403 polymorphism (Lui sequence)."

Query Match 0.6%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2261 TGCATATTTATTTCAGATGTT 2281
| | | | | | | | | | | | | | | | | | | | |
Db 1 TGCTTATTCATTACAGATGTT 21

RESULT 1647
AX457060/c
LOCUS AX457060 22 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 21 from Patent WO0231186.
ACCESSION AX457060
VERSION AX457060.1 GI:21715842
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Berlin,K.
TITLE Method for the detection of cytosine methylations
JOURNAL Patent: WO 0231186-A 21 18-APR-2002;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.6%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAAAAAAAAAA 2804
| | | | | | | | | | | | | | | | | | | | |
Db 21 TAATAAAAAAAAAATAAAAAAAAAAAAA 1

RESULT 1648
A93098
LOCUS A93098 24 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 2 from Patent WO9747748.
ACCESSION A93098
VERSION A93098.1 GI:6741496
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Decker,H.
TITLE ISOLATION OF THE BIOSYNTHESIS GENES FOR PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS GLA.O AND THEIR USE
JOURNAL Patent: WO 9747748-A 2 18-DEC-1997;
HOECHST AG (DE); DECKER HEINRICH (DE)
FEATURES
source Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
1..24
exon

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;

Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 799 GGAGCTGGTGGGGCCGTAAT 819
| | | | | | | | | | | | | | | | | | | | |
Db 2 GGWVCTGGYVSGGCCGTAGT 22

RESULT 1649
AR091179
LOCUS AR091179 24 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1299 from patent US 5994076.
ACCESSION AR091179
VERSION AR091179.1 GI:10017934
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 1299 30-NOV-1999;
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QY 266 TCCGCCGGCAGCACCTCTAC 286
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Db 1 TCCGCCGTGCAGCACGTCAC 21

RESULT 1650
AR174054
LOCUS AR174054 24 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6306627.
ACCESSION AR174054
VERSION AR174054.1 GI:17914374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Decker,H.
TITLE Isolation of the biosynthesis genes for pseudo-oligosaccharides from streptomyces glaucescens GLA.O, and their use
JOURNAL Patent: US 6306627-A 2 23-OCT-2001;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 799 GGAGCTGGTGGGGCCGTAAT 819
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Db 2 GGWVCTGGYVSGGCCGTAGT 22

RESULT 1651
AR198214
LOCUS AR198214 24 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1299 from patent US 6352829.
ACCESSION AR198214
VERSION AR198214.1 GI:20248063
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

JOURNAL Patent: JP 2002531145-A 2 24-SEP-2002;
THE VICTORIA UNIVERSITY OF MANCHESTER
COMMENT OS Artificial Sequence
PN JP 2002531145-A/2
PD 24-SEP-2002
PF 09-DEC-1999 JP 2000586949
PR 10-DEC-1998 GB 9827032.5, 29-SEP-1999 GB 9922984.1 PI
ALI HAJEER, WILLIAM OLLIER
PC C12Q1/68, A61K45/00, A61P11/06, A61P29/00, A61P31/18, A61P43/00//
PC C12N15/09,
PC C12N15/09, C12N15/00, C12N15/00
CC Description of Artificial Sequence: Reverse PCR primer for CC
amplifying a
region around the -403 polymorphism (Lui sequence). FH Key
Location/Qualifiers
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/organism="synthetic construct"
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Query Match 0.6%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2261 TGCATATTATTTCAGATGTT 2281
Db 1 TGCTTATTCATTACAGATGTT 21
RESULT 1643
E28097
LOCUS 21 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for analyzing DNA fragment.
ACCESSION E28097
VERSION E28097.1 GI:13018322
KEYWORDS JP 1999196874-A/8.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)
AUTHORS Hideki, K. and Senshu, U.
TITLE Method for analyzing DNA fragment
JOURNAL Patent: JP 1999196874-A 8 27-JUL-1999;
HITACHI LTD
COMMENT OS Unidentified
PN JP 1999196874-A/8
PD 27-JUL-1999
PF 14-JAN-1998 JP 1998005399
PR
PI HIDEKI KAMIBARA, SENSU UEMATSU
PC C12N15/09, C12Q1/68, G01N27/447, C12N15/00, G01N27/26 CC
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CC Topology: Linear;
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Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2161 TCTCCTTTTCTTTTCTTTTCTTTT 2181
Db 1 TGTGGTTTCTTTTCTTTTCTTTTCTTTT 21

RESULT 1644
AR241776/c
LOCUS 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 64 from patent US 6472154.
ACCESSION AR241776
VERSION AR241776.1 GI:27287588
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 64 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.6%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1938 AGGTAATGGTGGTTTGTG 1958
Db 21 AGGGAATGGTGGTTTGTG 1
RESULT 1645
AR296425
LOCUS 21 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 8160 from patent US 6537751.
ACCESSION AR296425
VERSION AR296425.1 GI:31683709
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 8160 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..21
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Query Match 0.6%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1567 AAAAATCCTTCTCCACCGCAC 1587
Db 1 AATAATCTTCTCCACTGCAC 21
RESULT 1646
AX026215
LOCUS 21 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 2 from Patent WO0034516.
ACCESSION AX026215
VERSION AX026215.1 GI:10187625
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Hajeeer, A. and Ollier, W.
TITLE Detection of rantes gene promotor polymorphisms
JOURNAL Patent: WO 0034516-A 2 15-JUN-2000;
HAJEER ALI (GB); OLLIER WILLIAM (GB); UNIV MANCHESTER (GB)


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    17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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  Db 25 AAAAAAAAAAAAAAAAAAAGAA 8

RESULT 1636
AX692830
LOCUS
  AX692830
  Sequence 5562 from Patent EPI281758.
  25 bp DNA
  linear PAT 31-MAR-2003
DEFINITION
  AX692830
ACCESSION
  AX692830.1 GI:29415793
VERSION
  AX692830.1 GI:29415793
KEYWORDS
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SOURCE
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
  JOURNAL
    Patent: EP 1281758-A 5562 05-FEB-2003;
    Aecomica, Inc. (US)
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RESULT 1637
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  25 bp DNA
  linear PAT 31-MAR-2003
DEFINITION
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ACCESSION
  AX692830.1 GI:29415793
VERSION
  AX692830.1 GI:29415793
KEYWORDS
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SOURCE
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
  JOURNAL
    Patent: EP 1281758-A 5562 05-FEB-2003;
    Aecomica, Inc. (US)
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    /mol_type="unassigned DNA"
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AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 978 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
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1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
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Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803
Db 18 AAGAAAAAAAAAAAAAAAAAAAAA 1
RESULT 1615
AX043581/c
LOCUS AX043581 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 1147 from Patent WO0065088.
ACCESSION AX043581
VERSION AX043581.1 GI:11342189
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 1147 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
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/mol_type="unassigned DNA"
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Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2781 AATTGAAAAAAAAAAAAAAAAA 2798
Db 18 AAGTAAAAAAAAAAAAAAAAAA 1
RESULT 1616
AX042984/c
LOCUS AX042984 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 550 from Patent WO0065088.
ACCESSION AX042984
VERSION AX042984.1 GI:11341592
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 550 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2782 ATTGAAAAAAAAAAAAAAAA 2799
Db 18 ACTGAAAAAAAAAAAAAAAAAA 1
RESULT 1617
AX043693/c
LOCUS AX043693 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 1259 from Patent WO0065088.
ACCESSION AX043693
VERSION AX043693.1 GI:11342308
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 1259 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
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/organism="synthetic construct"
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Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2782 ATTGAAAAAAAAAAAAAAAA 2799
Db 18 ACTGAAAAAAAAAAAAAAAAAA 1
RESULT 1618
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LOCUS AX692829 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5561 from Patent EP1281758.
ACCESSION AX692829
VERSION AX692829.1 GI:29415792
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5561 05-FEB-2003;
Aeomica, Inc. (US)
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Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2784 TGAATAAAAAAAAAAAAAAAAAA 2801
Db 19 TCATAAAAAAAAAAAAAAAAAA 2
RESULT 1619

[illegible]

AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
 TITLE Nucleic acid-protein fusion molecules and libraries
 JOURNAL Patent: US 6281344-A 10 28-AUG-2001;
 FEATURES Location/Qualifiers
 source 1. .24
 /organism="unknown"
 /mol_type="unassigned DNA"

 Query Match 0.6%; Score 16.4; DB 1; Length 24;
 Best Local Similarity 94.4%; Pred. No. 2.1e+03;
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 QY 2785 GAAAAAAAAAAAAAAAAA 2802
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 Db 23 GAAAAAAAAATAAAAA 6

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 BD238389/c
 LOCUS BD238389 24 bp DNA linear PAT 17-JUL-2003
 DEFINITION Sorting of proteins using RNA-protein fused body.
 ACCESSION BD238389
 VERSION BD238389.1 GI:33048159
 KEYWORDS JP 2002536025-A/7.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 1 (bases 1 to 24)
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
 TITLE Sorting of proteins using RNA-protein fused body
 JOURNAL Patent: JP 2002536025-A 7 29-OCT-2002;
 THE GENERAL HOSPITAL CORP
 COMMENT OS Artificial Sequence
 PN JP 2002536025-A/7

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PF 01-FEB-2000 JP 2000598669
PR 09-FEB-1999 US 09/247190
PI JACK W SZOSTAK, RICHARD W ROBERTS, RIHE LIU
PC C12N15/09, C07K7/00, C07K14/00, C12Q1/68, C12N15/00 CC
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Db 23 GAAAAAAAAAAATAAAAA 6

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RESULT 1609

AR257304	AR257304	Sequence 66 from patent US 6486130.	24 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	AR257304					
DEFINITION	Sequence 66 from patent US 6486130.					
ACCESSION	AR257304					
VERSION	AR257304.1	GI:27307146				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 24)					
TITLE	Livey, I., Crowe, B. and Dörner, F.					
	Immunogenic formulation of OSPC antigen vaccines for the prevention					
	and treatment of Lyme disease and recombinant methods for the					
	preparation of such antigens					

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artificial sequences.
1 (bases 1 to 23)
Hartwich,G. and Heller,A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 24 02-OCT-2002;
FRIZ BIOCHEM GMBH
COMMENT OS Artificial Sequence
PN JP 2002532386-A/24
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
G01N27/30,
PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
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CC Method of electrochemically detecting nucleic acid FH Key
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QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 6 AAAAAAAAAAAAAAAAAA 23
RESULT 1602
BD245242
LOCUS BD245242 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245242
VERSION BD245242.1 GI:33055012
KEYWORDS JP 2002532386-A/28.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hartwich,G. and Heller,A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 28 02-OCT-2002;
FRIZ BIOCHEM GMBH
COMMENT OS Artificial Sequence
PN JP 2002532386-A/28
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
G01N27/30,
PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
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CC Method of electrochemically detecting nucleic acid FH Key
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QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 6 AAAAAAAAAAAAAAAAAA 23
RESULT 1603
AX052992
LOCUS AX052992 23 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 8 from Patent WO0071749.
ACCESSION AX052992
VERSION AX052992.1 GI:12227094
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
Pignot,M.
TITLE Detection system for analyzing molecular interactions, production
and utilization thereof
JOURNAL Patent: WO 0071749-A 8 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES
Location/Qualifiers
source 1..23
/organism="synthetic construct"
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 TTTT TTTT TTTT TTTT TTTT TAG 18
RESULT 1604
AX052993
LOCUS AX052993 23 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 9 from Patent WO0071749.
ACCESSION AX052993
VERSION AX052993.1 GI:12227095
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
Pignot,M.
TITLE Detection system for analyzing molecular interactions, production
and utilization thereof
JOURNAL Patent: WO 0071749-A 9 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
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Query Match 0.6%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2170 TTTT TTTT TTTT TTTT TTTT TTA 2187
Db 1 TTTT TTTT TTTT TTTT TTTT TTA 18
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QY 2533 ATACAGGGTATTAGAAT 2550
Db 3 ATACAGGGTATTAGAAT 20

RESULT 1597
AR003288 AR003288 22 bp DNA linear PAT 04-DEC-1998
LOCUS Sequence 10 from patent US 5744300.
DEFINITION AR003288
ACCESSION AR003288
VERSION AR003288.1 GI:3964547
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and West,M.David.
TITLE Methods and reagents for the identification and regulation of senescence-related genes
JOURNAL Patent: US 5744300-A 10 28-APR-1998;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 AAGCTTTTGTGAA 1784
Db 5 AAGCTTTTGTGAA 22

RESULT 1598
I30199
LOCUS I30199 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 28 from patent US 5580726.
ACCESSION I30199
VERSION I30199.1 GI:1820990
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
TITLE Method and Kit for enhanced differential display
JOURNAL Patent: US 5580726-A 28 03-DEC-1996;
FEATURES Location/Qualifiers
source 1..22
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/mol_type="unassigned DNA"

Query Match 0.6%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 AAGCTTTTGTGAA 1784
Db 5 AAGCTTTTGTGAA 22

RESULT 1599
BD206201
LOCUS BD206201 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Process for producing polypeptide in mold variant cell.
ACCESSION BD206201
VERSION BD206201.1 GI:33015971
KEYWORDS JP 2002515252-A/14.
SOURCE Aspergillus oryzae
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 22)
Wahleithner,J. and Christensen,T.
Process for producing polypeptide in mold variant cell
Patent: JP 2002515252-A 14 28-MAY-2002;
NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
OS Aspergillus oryzae
PN JP 2002515252-A/14
PD 28-MAY-2002
PF 14-MAY-1999 JP 2000549742
PR 15-MAY-1998 US 09/079601,15-MAY-1998 US 09/079344 PI
JILL WAHLEITHNER,TOVE CHRISTENSEN
PC C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/30,
PC C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
PC (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
Process for producing polypeptide in mold variant cell. FH Key
Location/Qualifiers
FT source 1..22
/organism='Aspergillus oryzae'.
FT Location/Qualifiers
source 1..22
/organism="Aspergillus oryzae"
/mol_type="genomic DNA"
/db_xref="taxon:5062"

Query Match 0.6%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 AAGCTTTTGTGAA 1784
Db 5 AAGCTTTTGTGAA 22

RESULT 1600
AR123791
LOCUS AR123791 23 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6171803.
ACCESSION AR123791
VERSION AR123791.1 GI:14109152
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kinet,J.Pierre.
TITLE Isolation, characterization, and use of the human .beta. subunit of the high affinity receptor for immunoglobulin E
JOURNAL Patent: US 6171803-A 7 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2803
Db 4 AAACACAAAAAAAAAAAA 21

RESULT 1601
BD245238
LOCUS BD245238 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245238
VERSION BD245238.1 GI:33055008
KEYWORDS JP 2002532386-A/24.
SOURCE synthetic construct
ORGANISM synthetic construct

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1588
AX085251/c
LOCUS AX085251 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 5 from Patent WO0112855.
ACCESSION AX085251
VERSION AX085251.1 GI:13275309
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 5 22-FEB-2001;
YALE UNIVERSITY (US)

FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2802
Db 18 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 1589
AX085252
LOCUS AX085252 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 6 from Patent WO0112855.
ACCESSION AX085252
VERSION AX085252.1 GI:13275310
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 6 22-FEB-2001;
YALE UNIVERSITY (US)

FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 1 TTTTTTTTTTTTTTTTGT 18

RESULT 1590
AX085252/c
LOCUS AX085252 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 6 from Patent WO0112855.
ACCESSION AX085252
VERSION AX085252.1 GI:13275310

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 6 22-FEB-2001;
YALE UNIVERSITY (US)

FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1591
E59328
LOCUS E59328 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION E59328
VERSION E59328.1 GI:18622505
KEYWORDS JP 2000342265-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose,K. and Yoshida,T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 9 12-DEC-2000;
TOGOSEI CHEM IND CO LTD

COMMENT
OS Artificial Sequence
PN JP 2000342265-A/9
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999154974
PR
PI KUNIHICO HIROSE,TADAO YOSHIDA
PC C12N15/09,B01D15/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2803
Db 2 AAAAAAAAAAGAAAAAAAAA 19

RESULT 1592
AR231312
LOCUS AR231312 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 49 from patent US 6451968.
ACCESSION AR231312
VERSION AR231312.1 GI:27272243
KEYWORDS

<hr/>					
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 18)				
TITLE	Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.				
JOURNAL	Binary encoded sequence tags				
FEATURES	Patent: US 6383754-A 5 07-MAY-2002;				
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source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.6%; Score 16.4; DB 1; Length 18;				
Best Local Similarity	94.4%; Pred. No.1e+03;				
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	2785 GAAAAAAAAAAAAAAA 2802				
Db	18 GCAAAAAAAAAAAAAAAA 1				
<hr/>					
RESULT 1586					
AR208426					
LOCUS	AR208426	18 bp	DNA	linear	PAT 20-JUN-2002
DEFINITION	Sequence 6 from patent US 6383754.				
ACCESSION	AR208426				
VERSION	AR208426.1 GI:21509577				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 18)				
TITLE	Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.				
JOURNAL	Binary encoded sequence tags				
FEATURES	Patent: US 6383754-A 6 07-MAY-2002;				
	Location/Qualifiers				
source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.6%; Score 16.4; DB 1; Length 18;				
Best Local Similarity	94.4%; Pred. No.1e+03;				
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	2166 TTTTTTTT				
Db	1 TTTTTTTT				
<hr/>					
RESULT 1587					
AR208426/c					
LOCUS	AR208426	18 bp	DNA	linear	PAT 20-JUN-2002
DEFINITION	Sequence 6 from patent US 6383754.				
ACCESSION	AR208426				
VERSION	AR208426.1 GI:21509577				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 18)				
TITLE	Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.				
JOURNAL	Binary encoded sequence tags				
FEATURES	Patent: US 6383754-A 6 07-MAY-2002;				
	Location/Qualifiers				
source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.6%; Score 16.4; DB 1; Length 18;				
Best Local Similarity	94.4%; Pred. No.1e+03;				
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	2166 TTTTTTTT				
Db	1 TTTTTTTT				
<hr/>					
QUERY MATCH					
BEST LOCAL SIMILARITY	94.4%; PRED. NO. 1E+03;				
MATCHES	17; CONSERVATIVE 0; MISMATCHES 1; INDELS 0; GAPS 0;				

derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

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FEATURES
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    Location/Qualifiers
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        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /cultivar="Wassillewskija"
        /db_xref="taxon:3702"
        /clone="530A11"
        /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
  misc_feature
    1..25
      /note="T-DNA flanking sequence
      right border"

Query Match          0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTTTTTTTTTT 2187
      ||||| ||||| ||||| ||||| |||||
Db 3 CTTTGTGTTGTTTGTCTTTT 25

RESULT 1580
AB068802/c
LOCUS
DEFINITION
  Synthetic construct DNA, forward primer for human STS sts-WI-21093
  at lp36.
ACCESSION
  AB068802
KEYWORDS
  AB068802.1 GI:15129606
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
REFERENCE
  1
  AUTHORS
    Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
    Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
    Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
    and Soeda,E.
  TITLE
    A BAC-based STS-content map spanning a 35-Mb region of human
    chromosome lp35-p36
  JOURNAL
    Genomics 74 (1), 55-70 (2001)
  MEDLINE
    21269192
  PUBMED
    11374902
REFERENCE
  2 (bases 1 to 25)
  AUTHORS
    Horii,A.
  TITLE
    Direct Submission
  JOURNAL
    Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
    Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
    Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
    Tel:81-22-717-8042, Fax:81-22-717-8047)
  Location/Qualifiers
    1..25
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
  misc_feature
    1..25
      /note="forward primer for human STS sts-WI-21093 at lp36
      sts-WI-21093 obtained from clones B127J4, B284O17, B45I3,
      Human BAC library RPCI-11"

Query Match          0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2589 CTATTTAATTGAAACTCTCTGTT 2611
      ||||| ||||| ||||| ||||| |||||
Db 25 CGATTTTATTGAAACCTTCTGTT 3
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```
RESULT 1581
E04206/c
LOCUS
DEFINITION
  single strand DNA sequence of Type C hepatitis virus.
ACCESSION
  E04206
VERSION
  E04206.1 GI:2172416
KEYWORDS
  JP 1993001099-A/34.
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
REFERENCE
  1 (bases 1 to 29)
  AUTHORS
    Morita,K., Hasegawa,M., Yokoo,Y., Sato,M., Sekine,S., Sugimoto,S.,
    Koda,H., Mori,H. and Arima,T.
  TITLE
    FUSED ANTIGENIC POLYPEPTIDE
  JOURNAL
    Patent: JP 1993001099-A 34 08-JAN-1993;
    KYOWA HAKKO KOGYO CO LTD
  COMMENT
    OS Artificial gene
    OC Artificial sequence; Genes.
    PN JP 1993001099-A/34
    PD 08-JAN-1993
    PF 25-JUN-1991 JP 1991153031
    PI MORITA KAZUKI, HASEGAWA MAMORU, YOKOO YOSHIHARU, SATO
    MORIYUKI, PI SEKINE SUSUMU, SUGIMOTO SEIJI, KODA HAJIME, MORI
    HIDEJI, PI ARIMA TERUMASA
    PC C07K7/10,C07K13/00,C12N1/21,C12N15/62,C12N15/70,C12P21/02, PC
    C12Q1/68,
    PC
    G01N33/569,G01N33/576//A61K39/00,C12N15/51,(C12N1/21,C12R1:19), PC
    (C12P21/02,
    PC C12R1:19),C07K99:00;
    CC strandedness: Single;
    CC topology: Linear;
    CC hypothetical: No.
    Location/Qualifiers
      1..29
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        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match          0.6%; Score 16.6; DB 1; Length 29;
Best Local Similarity 82.6%; Pred. No. 2.8e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAATAAAAAA 2801
      ||| ||||| ||||| ||||| |||||
Db 29 AAAAAAGAAAAAAGAAAAA 7

RESULT 1582
AR208427
LOCUS
DEFINITION
  Sequence 7 from patent US 6383754.
ACCESSION
  AR208427
VERSION
  AR208427.1 GI:21509578
KEYWORDS
  Unknown.
SOURCE
  Unknown.
  ORGANISM
    Unclassified.
REFERENCE
  1 (bases 1 to 18)
  AUTHORS
    Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE
    Binary encoded sequence tags
  JOURNAL
    Patent: US 6383754-A 7 07-MAY-2002;
  FEATURES
    Location/Qualifiers
      1..18
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match          0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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PC G01N33/564,G01N33/569,C12N15/00,C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'DNA (synthetic)';
CC /note = 'page 11' Location/Qualifiers
FH key
FT misc_feature 1..25.
 Location/Qualifiers
 1..25
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1951 TTTTGTGTCGCTAAATATTTA 1973
 ||||| ||||| ||||| |||||
Db 1 TTTTGTGAGTCCCTTAGTATTTA 23

RESULT 1577
BD074392
LOCUS
DEFINITION Method of diagnosis and treatment of autoimmune disease such as
 insulin-dependent diabetes mellitus containing retroviral
 superantigen.
ACCESSION BD074392
VERSION BD074392.1 GI:22619995
KEYWORDS JP 2001511363-A/24.
SOURCE unidentified
 ORGANISM unidentified
 unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Conra,B. and Matthew,B.
TITLE Method of diagnosis and treatment of autoimmune disease such as
 insulin-dependent diabetes mellitus containing retroviral
JOURNAL Patent: JP 2001511363-A 24 14-AUG-2001;
 NOVIMMUNE SA
COMMENT OS Unidentified
 PN JP 2001511363-A/24
 PD 14-AUG-2001
 PF 22-JUL-1998 JP 2000504461
 PR 22-JUL-1997 EP 97112482.1,23-JUL-1997 EP 97401773.3 PI
 BERNARD CONRA,BERNARD MATTHEW
 PC C12N15/09,A01K67/027,A61K31/7088,A61K31/7115,A61K39/21,A61P3/
 PC 10,A61P37/00,
 PC C07K7/00,C07K14/08,C12N5/10,C12N7/00,C12P21/02,C12Q1/02,C12Q1/
 PC 68,
 PC G01N33/564,G01N33/569,C12N15/00,C12N5/00
 CC Strandedness: Single;
 CC Topology: Linear;
 CC /desc = 'SYNTHETIC DNA'
 CC /note = 'page 52'
FH key Location/Qualifiers
FT misc_feature 1..25.
 Location/Qualifiers
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 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1951 TTTTGTGTCGCTAAATATTTA 1973
 ||||| ||||| ||||| |||||
Db 1 TTTTGTGAGTCCCTTAGTATTTA 23

RESULT 1578
BD074392
LOCUS
DEFINITION Method of diagnosis and treatment of autoimmune disease such as
 insulin-dependent diabetes mellitus containing retroviral
 superantigen.
ACCESSION BD074392
VERSION BD074392.1 GI:22619995
KEYWORDS JP 2001511363-A/24.
SOURCE unidentified
 ORGANISM unidentified
 unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Conra,B. and Matthew,B.
TITLE Method of diagnosis and treatment of autoimmune disease such as
 insulin-dependent diabetes mellitus containing retroviral
JOURNAL Patent: JP 2001511363-A 24 14-AUG-2001;
 NOVIMMUNE SA
COMMENT OS Unidentified
 PN JP 2001511363-A/24
 PD 14-AUG-2001
 PF 22-JUL-1998 JP 2000504461
 PR 22-JUL-1997 EP 97112482.1,23-JUL-1997 EP 97401773.3 PI
 BERNARD CONRA,BERNARD MATTHEW
 PC C12N15/09,A01K67/027,A61K31/7088,A61K31/7115,A61K39/21,A61P3/
 PC 10,A61P37/00,
 PC C07K7/00,C07K14/08,C12N5/10,C12N7/00,C12P21/02,C12Q1/02,C12Q1/
 PC 68,
 PC G01N33/564,G01N33/569,C12N15/00,C12N5/00
 CC Strandedness: Single;
 CC Topology: Linear;
 CC /desc = 'SYNTHETIC DNA'
 CC /note = 'page 52'
FH key Location/Qualifiers
FT misc_feature 1..25.
 Location/Qualifiers
 1..25
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

BD088021/c
LOCUS
DEFINITION A method of arraying genome clone.
ACCESSION BD088021
VERSION BD088021.1 GI:22633631
KEYWORDS JP 2001321190-A/265.
SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 265 20-NOV-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
 GENOTECHS
COMMENT OS Artificial Sequence
 PN JP 2001321190-A/265
 PD 20-NOV-2001
 PF 12-MAR-2001 JP 2001068285
 PI EIICHI SOEDA
 PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
 C12N15/00,
 PC C12N15/00
 CC Description of Artificial Sequence:Synthetic DNA FH Key
 Location/Qualifiers
FT source 1..25
 /organism='Artificial Sequence'.
 FT Location/Qualifiers
 1..25
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2589 CTATTTAATTGAACTCTCTGTT 2611
 ||||| ||||| ||||| |||||
Db 25 CGATTTTATTGAACTTCTGTT 3

RESULT 1579
AJ588309
LOCUS
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone
 530A11.
ACCESSION AJ588309
VERSION AJ588309.1 GI:37937933
KEYWORDS right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
 Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
 Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 25)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA

FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPA1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2782 ATTGAAAAA 2804
|||||
24 ATAGAACAACAGAAAAA 2

Db

RESULT 1568
AX043216/c
LOCUS AX043216 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 782 from Patent WO0065088.
ACCESSION AX043216
VERSION AX043216.1 GI:11341824
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 782 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPB1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2801
|||||
23 AGTACTGGAACAAAAA 1

Db

RESULT 1569
AX043257
LOCUS AX043257 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 823 from Patent WO0065088.
ACCESSION AX043257
VERSION AX043257.1 GI:11341865
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 823 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPB1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1771 TTTT TTTTGAACCCCTTCT 1793
|||||
2 TTTT TTTTGAAGGACATCCT 24

Db

RESULT 1570
AX043259/c
LOCUS AX043259 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 825 from Patent WO0065088.
ACCESSION AX043259
VERSION AX043259.1 GI:11341867
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 825 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPB1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2802
|||||
23 GTACTGGAACAAAAA 1

Db

RESULT 1571
AX043286
LOCUS AX043286 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 852 from Patent WO0065088.
ACCESSION AX043286
VERSION AX043286.1 GI:11341894
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 852 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQA1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2173 TTTT TTTTAACTTTGAA 2195
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1 TTTT TTTTTCACATAGAA 23

Db

RESULT 1572
AX043312
LOCUS AX043312 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 878 from Patent WO0065088.
ACCESSION AX043312
VERSION AX043312.1 GI:11341920

RESULT 1558
AR435048
LOCUS AR435048 linear PAT 18-DEC-2003
DEFINITION Sequence 1471 from patent US 6656700.
ACCESSION AR435048
VERSION AR435048.1 GI:40197891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1471 02-DEC-2003;
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1. .25
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 444 CGGCGCCACAGGCAGCCAGCAG 466
Db 2 CGGCCAGCACAGGTAGCCAGCAG 24
RESULT 1559
AR435049
LOCUS AR435049 linear PAT 18-DEC-2003
DEFINITION Sequence 1472 from patent US 6656700.
ACCESSION AR435049
VERSION AR435049.1 GI:40197892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1472 02-DEC-2003;
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source
1. .25
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 444 CGGCGCCACAGGCAGCCAGCAG 466
Db 2 CGGCCAGCACAGGTAGCCAGCAG 24
RESULT 1560
AX000308
LOCUS AX000308 linear PAT 10-MAR-2000
DEFINITION Sequence 1 from Patent WO9905527.
ACCESSION AX000308
VERSION AX000308.1 GI:7240723
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Conrad,B. and Mach,B.
TITLE METHODS FOR DIAGNOSIS AND THERAPY OF AUTOIMMUNE DISEASE, SUCH AS INSULIN DEPENDENT DIABETES MELLITUS, INVOLVING RETROVIRAL SUPERANTIGENS

JOURNAL Patent: WO 9905527-A 1 04-FEB-1999;
MEDIGEN S A (CH); CONRAD BERNARD (CH)
FEATURES
source
1. .25
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1951 TTTTGTGTCGCTAAATATTTA 1973
Db 1 TTTTGTGTCGCTAAATATTTA 23
RESULT 1561
AX000331
LOCUS AX000331 25 bp DNA linear PAT 10-MAR-2000
DEFINITION Sequence 24 from Patent WO9905527.
ACCESSION AX000331
VERSION AX000331.1 GI:7240746
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Conrad,B. and Mach,B.
TITLE METHODS FOR DIAGNOSIS AND THERAPY OF AUTOIMMUNE DISEASE, SUCH AS INSULIN DEPENDENT DIABETES MELLITUS, INVOLVING RETROVIRAL SUPERANTIGENS
JOURNAL Patent: WO 9905527-A 24 04-FEB-1999;
MEDIGEN S A (CH); CONRAD BERNARD (CH)
FEATURES
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1. .25
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Best Local Similarity 82.6%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1951 TTTTGTGTCGCTAAATATTTA 1973
Db 1 TTTTGTGTCGCTAAATATTTA 23
RESULT 1562
AX042593
LOCUS AX042593 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 159 from Patent WO0065088.
ACCESSION AX042593
VERSION AX042593.1 GI:11341201
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 159 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="QDB1 Homozygote Primer Sequence"
Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.1e+03;

Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	1896	CCCTAGATCAACAGATCAACAAT	1918	
Db	2	CTCTAGATCAACACCTCAACATT	24	
FEATURES				
source				
1. .25				
/organism="synthetic construct"				
/mol_type="genomic DNA"				
/db_xref="taxon:32630"				
RESULT 1556				
I42108				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
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1. .25				
/organism="unknown"				
/mol_type="unassigned DNA"				
Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	51	GCGGCGGGGGCGGCGGACGC	73	
Db	3	GCGGCGGGGGCGGCGGCGGC	25	
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source				
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/mol_type="unassigned DNA"				
Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	51	GCGGCGGGGGCGGCGGACGC	73	
Db	3	GCGGCGGGGGCGGCGGCGGC	25	
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/mol_type="unassigned DNA"				
Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	444	CGGCGCCACAGGCGGCGGACG	466	
Db	3	CGGCGGCGGCGGCGGCGGACG	25	
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source				
1. .25				
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/mol_type="genomic DNA"				
Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	444	CGGCGCCACAGGCGGCGGACG	466	
Db	3	CGGCGGCGGCGGCGGCGGACG	25	
FEATURES				
source				
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Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	444	CGGCGCCACAGGCGGCGGACG	466	
Db	3	CGGCGGCGGCGGCGGCGGACG	25	
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source				
1. .25				
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Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	444	CGGCGCCACAGGCGGCGGACG	466	
Db	3	CGGCGGCGGCGGCGGCGGACG	25	
FEATURES				
source				
1. .25				
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Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	444	CGGCGCCACAGGCGGCGGACG	466	
Db	3	CGGCGGCGGCGGCGGCGGACG	25	
FEATURES				
source				
1. .25				
/organism="unknown"				
/mol_type="genomic DNA"				
Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	444	CGGCGCCACAGGCGGCGGACG	466	
Db	3	CGGCGGCGGCGGCGGCGGACG	25	
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source				
1. .25				
/organism="unknown"				
/mol_type="genomic DNA"				
Query Match	0.6%;	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%;	Pred. No. 2.1e+03;		
Matches	19;	Conservative	0;	M

FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQA1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1922 TTTTTCAGTGTAAAGGT 1941
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5 TTTTTCAGTCTTATGGT 24

Db

RESULT 1540
AX043318
LOCUS AX043318 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 884 from Patent WO0065088.
ACCESSION AX043318
VERSION AX043318.1 GI:11341926
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 884 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)

FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQB1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2175 TTTTTCAGTGTAAAGGT 2194
|||||
1 TTTTTCAGTGTAAAGGT 24

Db

RESULT 1541
AX043413/c
LOCUS AX043413 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 979 from Patent WO0065088.
ACCESSION AX043413
VERSION AX043413.1 GI:11342021
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 979 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)

FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DRB345 Heterozygote Primer Sequence"

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2799
|||||
20 GAAGAGAAAAA 1

Db

RESULT 1542
AX744661
LOCUS AX744661 25 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 626 from Patent WO03031621.
ACCESSION AX744661
VERSION AX744661.1 GI:30723328
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
1
REFERENCE 1
AUTHORS Zhang,J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 626 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES Location/Qualifiers
source 1. .25
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2105 GGGGCCCTTCTGGTTTAGG 2124
|||||
6 GGGGACCTTCTGGTTTAGG 25

Db

RESULT 1543
AX744667
LOCUS AX744667 25 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 632 from Patent WO03031621.
ACCESSION AX744667
VERSION AX744667.1 GI:30723334
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
1
REFERENCE 1
AUTHORS Zhang,J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 632 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES Location/Qualifiers
source 1. .25
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GGGGCCCTTCTGGTTTAGG 2125
|||||
1 GGGACCTTCTGGTTTAGG 20

Db

RESULT 1544
I16929
LOCUS I16929 24 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 4 from patent US 5482836.
ACCESSION I16929
VERSION I16929.1 GI:1251837

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2183
Db |||||
22 CCTTTTCTTTTCTTTTCTTTT 3

RESULT 1521
AX803836
LOCUS AX803836 24 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 4 from Patent WO03060160.
ACCESSION AX803836
VERSION AX803836.1 GI:38520971
KEYWORDS
SOURCE Salmo salar (Atlantic salmon)
ORGANISM Salmo salar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE 1
AUTHORS Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
TITLE Verification of food origin based on nucleic acid pattern recognition
JOURNAL Patent: WO 03060160-A 4 24-JUL-2003;
Genomar ASA (NO)
FEATURES
source Location/Qualifiers
1..24
/organism="Salmo salar"
/mol_type="unassigned DNA"
/db_xref="taxon:8030"

Query Match 0.6%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2800
Db |||||
2 AATTGAAAAACAAAAA 21

RESULT 1522
AX692828/c
LOCUS AX692828 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5560 from Patent EP1281758.
ACCESSION AX692828
VERSION AX692828.1 GI:29415791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5560 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGA 2803
Db |||||
20 TCA 1

RESULT 1523
I45922
LOCUS I45922 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 10 from patent US 5639595.
ACCESSION I45922
VERSION I45922.1 GI:2469887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Mirabelli,C.K., Ecker,D.J., Vickers,T.A. and Robertson,D.L.
TITLE Identification of novel drugs and reagents
JOURNAL Patent: US 5639595-A 10 17-JUN-1997;
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTTTCTTTTCTTTTCTTTT 2184
Db |||||
6 CTGTGTTTCTTTTCTTTT 25

RESULT 1524
AR435374
LOCUS AR435374 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1797 from patent US 6656700.
ACCESSION AR435374
VERSION AR435374.1 GI:40198217
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1797 02-DEC-2003;
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source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 AAGCAATTGTTGCTGCTTG 2329
Db |||||
6 AAGCCAGTTGTTGCTGCTTG 25

RESULT 1525
AX042527
LOCUS AX042527 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 93 from Patent WO0065088.
ACCESSION AX042527
VERSION AX042527.1 GI:11341135
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

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ORGANISM      synthetic construct
              artificial sequences.
REFERENCE
AUTHORS      Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
              Pignot,M.
TITLE        Detection system for analyzing molecular interactions, production
              and utilization thereof
JOURNAL      Patent: WO 0071749-A 17 30-NOV-2000;
              Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES
source       Location/Qualifiers
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              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Komponente (b)-4"

Query Match      0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAA..... 2804
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Db 21 GACAAGAAAAA..... 2

RESULT 1519
AX115478
LOCUS      AX115478 23 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 601 from Patent WO0129262.
ACCESSION  AX115478
VERSION    AX115478.1 GI:14032420
KEYWORDS
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Picoult-Newburg,L. and Pohl,M.
TITLE      Genotyping reagents, kits and methods of use thereof
JOURNAL    Patent: WO 0129262-A 601 26-APR-2001;
           Orchid BioSciences, Inc. (US)
FEATURES
source     Location/Qualifiers
              1..23
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Primer"

Query Match      0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGA..... 2803
      ||| ||||| ||||| |||||
Db 1 TGAAGGAAAAA..... 20

RESULT 1520
AX115478/c
LOCUS      AX115478 23 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 601 from Patent WO0129262.
ACCESSION  AX115478
VERSION    AX115478.1 GI:14032420
KEYWORDS
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Picoult-Newburg,L. and Pohl,M.
TITLE      Genotyping reagents, kits and methods of use thereof
JOURNAL    Patent: WO 0129262-A 601 26-APR-2001;
           Orchid BioSciences, Inc. (US)
FEATURES
source     Location/Qualifiers
              1..23

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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 789 CCTGTCAGAGGAGCTGGTG 808
|||||
Db 1 CCTGCCTGAAGGAGCTGGTG 20

RESULT 1513
AR066407
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AR066407
Sequence 31 from patent US 5849995.
AR066407
AR066407.1 GI:5996623
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 22)
Hayden,M., Lin,B. and Nasir,J.
Mouse model for Huntington's Disease and related DNA sequences
Patent: US 5849995-A 31 15-DEC-1998;
Location/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2163 TCCTTTCTTTTATTTT 2182
|||||
Db 1 TCCTTCTTTTATTTT 20

RESULT 1514
HUM0204RA/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

HUM0204RA
A PCR primer for D21S16 locus STS; location 21ql1.2, sequence
tagged site.
D50257
D50257.1 GI:801798
STS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
Tanahashi,H., Ito,T., Hattori,M., Ohira,M., Ohki,M., Tashiro,K. and
Sakaki,Y.
Sixty new STSs (sequence-tagged sites) of human chromosome 21
DNA Res. 1 (2), 85-89 (1994)
96051984
7584032
2 (bases 1 to 22)
Sakaki,Y.
Direct Submission
Submitted (28-APR-1995) Yoshiyuki Sakaki, Institute of Medical
Science, University of Tokyo, Human Genome Center; 4-6-1
Shirokanedai Minato-ku, Tokyo 108, Japan
(E-mail:sakaki@hgc.ims.u-tokyo.ac.jp, Tel:03-5449-5362,
Fax:03-5449-5445)
Submitted (28-Apr-1995) to DDBJ by:
Yoshiyuki Sakaki
Human Genome Center
Institute of Medical Science
University of Tokyo
4-6-1 Shirokanedai Minato-ku
Tokyo, 108
Japan
Phone: 03-5449-5362
Fax : 03-5449-5445.
Location/Qualifiers

FEATURES

source 1..22
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"

Query Match 0.6%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2374 GCGTTGAGTGACAGATTTT 2393
|||||
Db 22 GCTTCAGTGACAGATTTT 3

RESULT 1515
BD245233
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD245233
Method of electrochemically detecting nucleic acid.
BD245233
BD245233.1 GI:33055003
JP 2002532386-A/19.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 23)
Hartwich,G. and Heller,A.
Method of electrochemically detecting nucleic acid
Patent: JP 2002532386-A 19 02-OCT-2002;
FRIZ BIOCHEM GMBH
OS Artificial Sequence
PN JP 2002532386-A/19
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
G01N27/30,
PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
G01N27/46
CC Method of electrochemically detecting nucleic acid FH Key
Location/Qualifiers
FT source 1..23
/organism='Artificial Sequence'.
FT Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTATTTT 2183
|||||
Db 4 CCAATTTTCTTTTATTTT 23

RESULT 1516
BD245237
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD245237
Method of electrochemically detecting nucleic acid.
BD245237
BD245237.1 GI:33055007
JP 2002532386-A/23.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 23)
Hartwich,G. and Heller,A.
Method of electrochemically detecting nucleic acid

TITLE Nucleic acid hairpin probes and uses thereof
JOURNAL Patent: US 6596490-A 16 22-JUL-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2155 TTTTCTCTCCTTTTCTTTT 2174
Db 20 TTTTCTCACATTTTCTTTT 1

RESULT 1509
AR371269/c
LOCUS AR371269 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 5 from patent US 6395474.
ACCESSION AR371269
VERSION AR371269.1 GI:34608201
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 5 28-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2183
Db 20 CCTTTTCTTTTCTTTTCTTTT 1

RESULT 1510
AX067205
LOCUS AX067205 20 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 57 from Patent WO0100669.
ACCESSION AX067205
VERSION AX067205.1 GI:12544870
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barry,C., Bougueleret,L., Chumakov,I. and Cohen-Akenine,A.
TITLE A bap28 gene and protein
JOURNAL Patent: WO 0100669-A 57 04-JAN-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide BAP28polyTcourt"

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2168 TTTTCTTTTCTTTTCTTTTCTTTT 2187
Db 1 TTTTCTTTTCTTTTCTTTTCTTTT 20

RESULT 1511
AX441512/c
LOCUS AX441512 20 bp DNA linear PAT 02-JUL-2002
DEFINITION Sequence 16 from Patent WO0206531.
ACCESSION AX441512
VERSION AX441512.1 GI:21690473
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Dattagupta,N.
TITLE Nucleic acid hairpin probes and uses thereof
JOURNAL Patent: WO 0206531-A 16 24-JAN-2002;
Applied Gene Technologies, Inc. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligo AGT02023"

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2155 TTTTCTCTCCTTTTCTTTTCTTTT 2174
Db 20 TTTTCTCACATTTTCTTTTCTTTT 1

RESULT 1512
BD196314
LOCUS BD196314 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Vertebrate telomerase genes and proteins and uses thereof.
ACCESSION BD196314
VERSION BD196314.1 GI:33006084
KEYWORDS JP 2002514928-A/48.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kilian,A. and Bowtell,D.
TITLE Vertebrate telomerase genes and proteins and uses thereof
JOURNAL Patent: JP 2002514928-A 48 21-MAY-2002;
CAMBIA BIOSYSTEMS LLC,PETER MACCALLUM CANCER INSTITUTE
COMMENT OS Artificial Sequence
PN JP 2002514928-A/48
PD 21-MAY-2002
PF 01-JUL-1998 JP 1999508771
PR 01-JUL-1997 US 60/051410,21-JUL-1997 US 60/053018 PR
21-JUL-1997 US 60/053329,04-AUG-1997 US 60/054642 PR
09-SEP-1997 US 60/058287
PI ANDRZEJ KILIAN,DAVID BOWTELL
PC C12N15/54,C12N9/12,A61K38/45,C07K16/40,C12Q1/68,C12Q1/48, PC
C12N15/11,
PC A61K31/70
CC Description of Artificial Sequence:Synthesized Amplification
Primer Design
CC based on EST Sequence GenBank Accession Number AA281296 FH
Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;

REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3537 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source Location/Qualifiers
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2165 CTTTTTTTTTTTTTTTTTTTAAAC 2189
Db 26 CTTTTTGTGTGATTGTTCAAC 2
RESULT 1495
BD169479/c
LOCUS BD169479 26 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel guanosine triphosphate (GTP)-binding protein-coupled receptor protein, BG7.
ACCESSION BD169479
VERSION BD169479.1 GI:27875291
KEYWORDS WO 0240669-A/30.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 26)
REFERENCE Maruyama,T., Nakamura,T., Itadani,H. and Tanaka,K.
AUTHORS Novel guanosine triphosphate (GTP)-binding protein-coupled receptor protein, BG7
TITLE
JOURNAL BANYU PHARMACEUTICAL CO LTD,TAKAHARU MARUYAMA,TAKAO NAKAMURA,
HIRAKU ITADANI,KENICHI TANAKA
COMMENT OS Artificial Sequence
PN WO 0240669-A/30
PD 23-MAY-2002
PF 30-OCT-2001 WO 2001JP009512
PR 17-NOV-2000 JP 00P 351741,15-FEB-2001 JP 01P 038619 PR
16-MAR-2001 JP 01P 077000
PI TAKAHARU MARUYAMA,TAKAO NAKAMURA,HIRAKU ITADANI,KENICHI TANAKA
PC C12N15/12,C12N1/21,C12N5/10,C07K14/705,C07K16/28,C12P21/02, PC
C12Q1/02,
PC A61K45/00,A61P1/00,A61P7/00,A61P9/00,A61P11/00,A61P13/00, PC
A61P21/00,
PC A61P29/00,A61P43/00,G01N33/15,G01N33/50,G01N33/53 CC
Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
FT source 1. .26
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .26
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 354 CCTACGACGAGCTGGCCTACTCCCA 378
Db 25 CCTACTAGCTGGGCTACTCACA 1
RESULT 1496
AR055108/c

LOCUS AR055108 28 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5837468.
ACCESSION AR055108
VERSION AR055108.1 GI:5980685
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Wang,X., Duvick,J.P. and Briggs,S.P.
TITLE PCR-based cDNA subtractive cloning method
JOURNAL Patent: US 5837468-A 13 17-NOV-1998;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2786 AAAAAAAAAAAAAAAA 2802
Db 27 AAAAAAAAAAAAAAAA 11
RESULT 1497
AR055109/c
LOCUS AR055109 28 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5837468.
ACCESSION AR055109
VERSION AR055109.1 GI:5980686
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Wang,X., Duvick,J.P. and Briggs,S.P.
TITLE PCR-based cDNA subtractive cloning method
JOURNAL Patent: US 5837468-A 14 17-NOV-1998;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2786 AAAAAAAAAAAAAAAA 2802
Db 27 AAAAAAAAAAAAAAAA 11
RESULT 1498
AR068449/c
LOCUS AR068449 28 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5853991.
ACCESSION AR068449
VERSION AR068449.1 GI:6000656
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Wang,X., Duvick,J.P. and Briggs,S.P.
TITLE PCR-based cDNA subtractive cloning method
JOURNAL Patent: US 5853991-A 13 29-DEC-1998;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"

VERSION I18346.1 GI:1598701
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS John,M.
TITLE Genetically engineering cotton plants for altered fiber
JOURNAL Patent: US 5495070-A 1 27-FEB-1996;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180
Db 10 CCTTTTCTTTTCTTTTCTTTT 26
RESULT 1490
I21333
LOCUS I21333 26 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5521078.
ACCESSION I21333
VERSION I21333.1 GI:1601687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS John,M.
TITLE Genetically engineering cotton plants for altered fiber
JOURNAL Patent: US 5521078-A 1 28-MAY-1996;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180
Db 10 CCTTTTCTTTTCTTTTCTTTT 26
RESULT 1490
I21333
LOCUS I21333 26 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5602321.
ACCESSION I35739
VERSION I35739.1 GI:2087590
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS John,M.
TITLE Transgenic cotton plants producing heterologous polyhydroxy(e) butyrate bioplastic
JOURNAL Patent: US 5602321-A 1 11-FEB-1997;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180
Db 10 CCTTTTCTTTTCTTTTCTTTT 26
RESULT 1492
I36757
LOCUS I36757 26 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5608148.
ACCESSION I36757
VERSION I36757.1 GI:2086582
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS John,M.E.
TITLE Transgenic cotton plants producing heterologous peroxidase
JOURNAL Patent: US 5608148-A 1 04-MAR-1997;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180
Db 10 CCTTTTCTTTTCTTTTCTTTT 26
RESULT 1493
I40322
LOCUS I40322 26 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5620882.
ACCESSION I40322
VERSION I40322.1 GI:2082614
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS John,M.
TITLE Genetically engineering cotton plants for altered fiber
JOURNAL Patent: US 5620882-A 1 15-APR-1997;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180
Db 10 CCTTTTCTTTTCTTTTCTTTT 26
RESULT 1494
AX118414/c
LOCUS AX118414 26 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3537 from Patent WO0129262.
ACCESSION AX118414
VERSION AX118414.1 GI:14035365
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="exon No. 2 - 3' end of the exon-intron boundary of
human MLT gene"

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2171 TTTTCTTTTCTTTTCTTTTCTTTA 2187
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Db 1 TTTTCTTTTCTTTTCTTTTCTTTA 17

RESULT 1485
AR034927 AR034927 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5869720.
ACCESSION AR034927
VERSION AR034927.1 GI:5950532
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 26)
AUTHORS John,M.E.
TITLE Transgenic cotton plants producing heterologous peroxidase
JOURNAL Patent: US 5869720-A 1 09-FEB-1999;
FEATURES Location/Qualifiers
source 1. .26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTCTTTTCTTTTCTTTT 2180
|||||
Db 10 CCTTTTCTTTTCTTTTCTTTT 26

RESULT 1486
AR078461/c AR078461 26 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5962664.
ACCESSION AR078461
VERSION AR078461.1 GI:10005207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 26)
AUTHORS Friedhoff,A.J., Basham,D.A. and Miller,J.C.
TITLE Psychosis protecting nucleic acid, peptides, compositions and
method of use
JOURNAL Patent: US 5962664-A 1 05-OCT-1999;
FEATURES Location/Qualifiers
source 1. .26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAATAAAAAA 2801
|||||
Db 17 GAAAAAATAAAAAA 1

RESULT 1487
AR145386 I18346 Sequence 1 from patent US 5495070.
DEFINITION I18346

LOCUS AR145386 26 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6211430.
ACCESSION AR145386
VERSION AR145386.1 GI:15107253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 26)
AUTHORS John,M.E.
TITLE FbLate promoter
JOURNAL Patent: US 6211430-A 10 03-APR-2001;
FEATURES Location/Qualifiers
source 1. .26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTCTTTTCTTTTCTTTT 2180
|||||
Db 10 CCTTTTCTTTTCTTTTCTTTT 26

RESULT 1488
E31574/c E31574 26 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for preparing DNA sample and reagent.
ACCESSION E31574
VERSION E31574.1 GI:13018517
KEYWORDS JP 1999341986-A/10.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 26)
AUTHORS Kazunori,O., Hideki,K., Tim,C.R. and Michal,A.L.
TITLE Method for preparing DNA sample and reagent
JOURNAL Patent: JP 1999341986-A 10 14-DEC-1999;
COMMENT HITACHI LTD,NYCOMED AMERSHAM PLC
OS Unidentified
PN JP 1999341986-A/10
PD 14-DEC-1999
PF 02-JUN-1998 JP 1998152598
PR KAZUNORI OKANO,HIDEKI KAMIBARA,TIM C RICHARDSON,MICHAEL A LIBU
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC Strandedness: Single;
Topologoy: Linear;
FH Key Location/Qualifiers
FT source 1. .26
/organism='Unidentified'.
FT Location/Qualifiers
source 1. .26
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2784 TGAATAAAAAAATA 2800
|||||
Db 22 TGAATAAAAAAATA 6

RESULT 1489
I18346 I18346 26 bp DNA linear PAT 07-OCT-1996
LOCUS I18346
DEFINITION Sequence 1 from patent US 5495070.
ACCESSION I18346

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misc_feature      1. .25
/note="T-DNA flanking sequence
left border"

Query Match      0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2785 GAAAAAAAAAAAAAAAAA 2801
      |||||||
Db      22 GAAAAAAAAAAAAAAAAA 6

RESULT 1480
AR010003/c
LOCUS      AR010003      26 bp      DNA      linear      PAT 04-DEC-1998
DEFINITION      Sequence 15 from patent US 5756684.
ACCESSION      AR010003
VERSION      AR010003.1 GI:3968808
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
Unclassified.
REFERENCE      1 (bases 1 to 26)
AUTHORS      Johnson,E.M. and Bergemann,A.D.
TITLE      Cloning and expression of PUR protein
JOURNAL      Patent: US 5756684-A 15 26-MAY-1998;
FEATURES
      source
      1. .26
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      |||||||
Db      26 AAAAAAAAAAAAAAAAAA 10

RESULT 1481
AR034738/c
LOCUS      AR034738      26 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 15 from patent US 5869622.
ACCESSION      AR034738
VERSION      AR034738.1 GI:5950343
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
Unclassified.
REFERENCE      1 (bases 1 to 26)
AUTHORS      Johnson,E.M. and Bergemann,A.D.
TITLE      Monoclonal antibodies to the pur protein
JOURNAL      Patent: US 5869622-A 15 09-FEB-1999;
FEATURES
      source
      1. .26
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      |||||||
Db      26 AAAAAAAAAAAAAAAAAA 10

RESULT 1482
I24758/c
LOCUS      I24758      26 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION      Sequence 21 from patent US 5545551.
```

```
ACCESSION      I24758
VERSION      I24758.1 GI:1604628
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
Unclassified.
REFERENCE      1 (bases 1 to 26)
AUTHORS      Johnson,E.M. and Bergemann,A.D.
TITLE      Cloning and expression of pur protein
JOURNAL      Patent: US 5545551-A 21 13-AUG-1996;
FEATURES
      source
      1. .26
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      |||||||
Db      26 AAAAAAAAAAAAAAAAAA 10

RESULT 1483
AR050239/c
LOCUS      AR050239      26 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 8 from patent US 5827518.
ACCESSION      AR050239
VERSION      AR050239.1 GI:5972964
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
Unclassified.
REFERENCE      1 (bases 1 to 26)
AUTHORS      Webb,B.Allen. and Cui,L.
TITLE      Viral and insect genes that inhibit the immune system and methods
      of use thereof
JOURNAL      Patent: US 5827518-A 8 27-OCT-1998;
FEATURES
      source
      1. .26
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      |||||||
Db      26 AAAAAAAAAAAAAAAAAA 10

RESULT 1484
AX055876
LOCUS      AX055876      26 bp      DNA      linear      PAT 13-JAN-2001
DEFINITION      Sequence 12 from Patent WO0073500.
ACCESSION      AX055876
VERSION      AX055876.1 GI:12228983
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Baens,M., Marynen,P. and Dierlamm,J.
TITLE      Molecular characterisation of chromosome translocation
      t(11;18)(q21;q21) and its correlation to carcinogenesis
JOURNAL      Patent: WO 0073500-A 12 07-DEC-2000;
      Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
      source
      1. .26
      /organism="Homo sapiens"
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5560 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTT 2181
|||||
Db 2 CTTTTTTTTTTTTTTT 18

RESULT 1477
AX692829
LOCUS AX692829 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5561 from Patent EPI281758.
ACCESSION AX692829
VERSION AX692829.1 GI:29415792
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5561 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTT 2181
|||||
Db 1 CTTTTTTTTTTTTTTT 17

RESULT 1478
BD075857/c
LOCUS BD075857 25 bp DNA linear PAT 27-AUG-2002
DEFINITION Standardized nucleic acid library and method of constructing the same.
ACCESSION BD075857
VERSION BD075857.1 GI:22621460
KEYWORDS JP 2001517460-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 25)
REFERENCE Li,W.B., Jessee,J. and Nissson,P.E.
AUTHORS Standardized nucleic acid library and method of constructing the
TITLE Patent: JP 2001517460-A 2 09-OCT-2001;
JOURNAL LIFE TECHNOLOGIES INC
COMMENT OS Artificial Sequence

PN JP 2001517460-A/2
PD 09-OCT-2001
PF 24-SEP-1998 JP 2000512989
PR 24-SEP-1997 US 60/059817,23-SEP-1998 US 09/159496 PI
WU BO LI,JOEL JESSEE,PAUL E NISSON
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P19/34 PC
,C12Q1/68,C12N15/00,
PC C12N5/00
CC Description of artificial sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1. .25
FT /organism='Artificial Sequence'.
FEATURES
source 1. .25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 CTTTTTTTTTTTTTTT 2180
|||||
Db 17 CTTTTTTTTTTTTTTT 1

RESULT 1479
AJ595474/c
LOCUS AJ595474 25 bp DNA linear PLN 23-OCT-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 417E08.
ACCESSION AJ595474
VERSION AJ595474.1 GI:37945102
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
AUTHORS Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 25)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES
source 1. .25
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="417E08"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2774 TTGTTAGCAATTGAAAAA 2798
Db 1 TTGATCGCATTTGTCAAAAAA 25

RESULT 1472
AX494261

LOCUS AX494261 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 26 from Patent WO02059256.
ACCESSION AX494261
VERSION AX494261.1 GI:23339871
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 02059256-A 26 01-AUG-2002;
MOLECULAR ENGINES LAB (FR)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2774 TTGTTAGCAATTGAAAAA 2798
Db 1 TTGATCGCATTTGTCAAAAAA 25

RESULT 1473
AX494264

LOCUS AX494264 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 29 from Patent WO02059256.
ACCESSION AX494264
VERSION AX494264.1 GI:23339874
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 02059256-A 29 01-AUG-2002;
MOLECULAR ENGINES LAB (FR)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2774 TTGTTAGCAATTGAAAAA 2798
Db 1 TTGATCGCATTTGTCAAAAAA 25

Db 1 TTGATCGCATTTGTCAAAAAA 25

RESULT 1474
AX547804

LOCUS AX547804 25 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 943 from Patent WO02053141.
ACCESSION AX547804
VERSION AX547804.1 GI:25812948
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 943 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2182
Db 9 TTTT TTTT TTTT TTTT TTTT 25

RESULT 1475
AX547804/c

LOCUS AX547804 25 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 943 from Patent WO02053141.
ACCESSION AX547804
VERSION AX547804.1 GI:25812948
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 943 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAA 2802
Db 25 AAAAAA 9

RESULT 1476
AX692828

LOCUS AX692828 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5560 from Patent EP1281758.
ACCESSION AX692828
VERSION AX692828.1 GI:29415791
KEYWORDS
SOURCE Homo sapiens (human)

AUTHORS	Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R., Flanagan, P. and Clary, D.S.
TITLE	Novel human protein kinases and protein kinase-like enzymes

TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 1217 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)

FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HLA-C Heterozygote Primer Sequence"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2174 TTTTCTTTTAACTTTGAAAGT 2198
|||||
Db 1 TTTTCTTTTCAATCTGTGAGT 25
|||||

RESULT 1463
AX043651/c
LOCUS AX043651 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 1217 from Patent WO0065088.
ACCESSION AX043651
VERSION AX043651.1 GI:11342266

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 1217 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)

FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HLA-C Heterozygote Primer Sequence"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAA 2798
|||||
Db 17 ATTGAAAAA 1
|||||

RESULT 1464
AX043680/c
LOCUS AX043680 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 1246 from Patent WO0065088.
ACCESSION AX043680
VERSION AX043680.1 GI:11342295

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 1246 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)

FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HLA-C Heterozygote Primer Sequence"

Query Match 0.6%; Score 17; DB 1; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2773 CTTGTTAGTAATGAAAAA 2797
|||||
Db 25 CTTTCATCGCAGTGAAAAA 1
|||||

RESULT 1465
AX043693
LOCUS AX043693 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 1259 from Patent WO0065088.
ACCESSION AX043693
VERSION AX043693.1 GI:11342308

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 1259 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)

FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HLA-C Heterozygote Primer Sequence"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2173 TTTTCTTTTAACTTTGAAAG 2197
|||||
Db 1 TTTTCTTTTCACTCGGTCAG 25
|||||

RESULT 1466
AX104751
LOCUS AX104751 25 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 943 from Patent WO0122972.
ACCESSION AX104751
VERSION AX104751.1 GI:13920948

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 943 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)

FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTCTTTT 2182
|||||
Db 9 TTTTCTTTT 25
|||||

RESULT 1467
AX104751/c
LOCUS AX104751 25 bp DNA linear PAT 30-APR-2001

LOCUS AX043034 25 bp DNA
 DEFINITION Sequence 600 from Patent WO0065088.
 ACCESSION AX043034
 VERSION AX043034.1 GI:11341642
 KEYWORDS .
 SOURCE synthetic construct

[illegible]

RESULT	1436
AR435380	
LOCUS	AR435380
DEFINITION	Sequence 1803 from patent US 6656700.
ACCESSION	AR435380
VERSION	AR435380.1 GI:40198223
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.

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Query Match      0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 3 TNGNAAAAAAAAAAAAA 21

RESULT 1429
AX496104/c

LOCUS AX496104 23 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1869 from Patent WO02059256.
ACCESSION AX496104
VERSION AX496104.1 GI:23341714
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1
FEATURES
source Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 02059256-A 1869 01-AUG-2002;
MOLECULAR ENGINEES LAB (FR)
Location/Qualifiers
1..23
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTT 2180
|||||
Db 23 CCTTTTCTTTTCTTTT 7

RESULT 1430
I33155

LOCUS I33155 24 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 9 from patent US 5589622.
ACCESSION I33155
VERSION I33155.1 GI:1823946
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS Unclassified.
TITLE 1 (bases 1 to 24)
JOURNAL Gurr,S.J., McPherson,M.J., Atkinson,H.J. and Bowles,D.J.
FEATURES
source Plant parasitic nematode control
Patent: US 5589622-A 9 31-DEC-1996;
Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTTTCTTTTCTTTT 2181
|||||
Db 8 CTTTTTCTTTTCTTTT 24

RESULT 1431
AX043282/c

LOCUS AX043282 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 848 from Patent WO0065088.
ACCESSION AX043282
VERSION AX043282.1 GI:11341890
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

artificial sequences.

REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 848 02-NOV-2000;
FEATURES
source Amersham Pharmacia Biotech AB (SE)
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQAI Heterozygote Primer Sequence"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2776 GTTAGAATTGAAAAA 2800
|||||
Db 25 GGTCAAAATCTAAAAA 1

RESULT 1432
AX043152

LOCUS AX043152 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 718 from Patent WO0065088.
ACCESSION AX043152
VERSION AX043152.1 GI:11341760
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 718 02-NOV-2000;
FEATURES
source Amersham Pharmacia Biotech AB (SE)
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPB1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2173 TTTTTTCTTTTAACTTTGAAAG 2197
|||||
Db 1 TTTTTTCTTTTAAAGTGACCAG 25

RESULT 1433
I56670

LOCUS I56670 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5650279.
ACCESSION I56670
VERSION I56670.1 GI:2477083
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS Unclassified.
TITLE 1 (bases 1 to 25)
JOURNAL Nagpal,S. and Chandraratna,R.A.
FEATURES
source Gene sequence induced in skin by retinoids
Patent: US 5650279-A 1 22-JUL-1997;
Location/Qualifiers
1..25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 25;

DEFINITION						Sequence 15 from patent US 5589375.					
ACCESSION						I32906					
VERSION						I32906.1 GI:1823697					
KEYWORDS											
SOURCE						Unknown.					
ORGANISM						Unknown.					
REFERENCE						Unclassified.					
AUTHORS						1 (bases 1 to 23)					
TITLE						Ullrich,A. and Vogel,W.					
JOURNAL						PTP ID: a novel protein tyrosine phosphatase					
FEATURES						Patent: US 5589375-A 15 31-DEC-1996;					
source						Location/Qualifiers					
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						/mol_type="unassigned DNA"					
Query Match						0.6%; Score 17; DB 1; Length 23;					
Best Local Similarity						100.0%; Pred.No.1.5e+03;					
Matches						17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY						2786 AAAAAAAAAAAAAAAA 2802					
Db						23 AAAAAAAAAAAAAAAA 7					
RESULT 1424											
AR306617/c											
LOCUS						AR306617					
DEFINITION						Sequence 15 from patent US 6548641.					
ACCESSION						AR306617					
VERSION						AR306617.1 GI:31696809					
KEYWORDS											
SOURCE						Unknown.					
ORGANISM						Unknown.					
REFERENCE						Unclassified.					
AUTHORS						1 (bases 1 to 23)					
TITLE						Ullrich,A. and Vogel,W.					
JOURNAL						PTP ID: a novel protein tyrosine phosphatase					
FEATURES						Patent: US 6548641-A 15 15-APR-2003;					
source						Location/Qualifiers					
						1..23					
						/organism="unknown"					
						/mol_type="genomic DNA"					
Query Match						0.6%; Score 17; DB 1; Length 23;					
Best Local Similarity						100.0%; Pred.No.1.5e+03;					
Matches						17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY						2786 AAAAAAAAAAAAAAAA 2802					
Db						23 AAAAAAAAAAAAAAAA 7					
RESULT 1425											
BD105197/c											
LOCUS						BD105197					
DEFINITION						Novel glucosyltransferase gene.					
ACCESSION						BD105197					
VERSION						BD105197.1 GI:22650771					
KEYWORDS						WO 0192509-A/3.					
SOURCE						synthetic construct					
ORGANISM						artificial construct					
REFERENCE						artificial sequences.					
AUTHORS						1 (bases 1 to 23)					
TITLE						Mizutani,M., Sakakibara,K., Tanaka,Y., Kusumi,T. and Ono,E.					
JOURNAL						Novel glucosyltransferase gene					
COMMENT						Patent: WO 0192509-A 3 06-DEC-2001;					
						INTERNATIONAL FLOWER DEVELOPMENTS PROPRIETARY LTD,MASAKO MIZUTANI,					
						KEIKO SAKAKIBARA,YOSHIKAZU TANAKA,TAKAAKI KUSUMI,EICHIRO ONO					
						OS Artificial Sequence					
						PN WO 0192509-A/3					
						PD 06-DEC-2001					
						PF 01-JUN-2001 WO 2001JP004675					

Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182
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Db 4 TTTT TTTT TTTT TTTT TTTT 20

RESULT 1418
BD161924/c
LOCUS
DEFINITION BD161924 20 bp DNA linear PAT 17-JAN-2003
Method for carrying out thermal cycle of PCR using DNA-immobilized substrate.
ACCESSION BD161924
VERSION BD161924.1 GI:27867682
KEYWORDS JP 2002191369-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tanga,M., Okamura,H. and Takahashi,K.
TITLE Method for carrying out thermal cycle of PCR using DNA-immobilized substrate
JOURNAL Patent: JP 2002191369-A 1 09-JUL-2002;
COMMENT TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
OS Artificial Sequence
PN JP 2002191369-A/1
PD 09-JUL-2002
PF 27-DEC-2000 JP 2000399573
PI MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC Method for
carrying out thermal cycle of PCR using DNA- CC
immobilized
CC substrate
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FT Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2802
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Db 20 AAAAAA AAAAAA AAAAAA 4

RESULT 1419
BD244863/c
LOCUS
DEFINITION BD244863 23 bp DNA linear PAT 17-JUL-2003
Oligonucleotide primer capable of making the non-specific double strand formation unstable.
ACCESSION BD244863
VERSION BD244863.1 GI:33054633
KEYWORDS JP 2002532063-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable
JOURNAL Patent: JP 2002532063-A 8 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
OS Artificial Sequence
PN JP 2002532063-A/8
PD 02-OCT-2002

Query Match 0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
CC N = 3-Nitropyroole
CC N = 3-Nitropyroole
FH Key Location/Qualifiers
FT modified_base (8)
FT modified_base (18).
FT Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2804
|||||
Db 23 AAAAAA AAAAAA AAAAAA 5

RESULT 1420
BD244865/c
LOCUS
DEFINITION BD244865 23 bp DNA linear PAT 17-JUL-2003
Oligonucleotide primer capable of making the non-specific double strand formation unstable.
ACCESSION BD244865
VERSION BD244865.1 GI:33054635
KEYWORDS JP 2002532063-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable
JOURNAL Patent: JP 2002532063-A 10 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
OS Artificial Sequence
PN JP 2002532063-A/10
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
CC N - inosine
CC N = inosine
FH Key Location/Qualifiers
FT modified_base (8)
FT modified_base (18).
FT Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2804
|||||
Db 23 AAAAAA AAAAAA AAAAAA 5

RESULT 1421
BD245245/c
LOCUS
DEFINITION BD245245 23 bp DNA linear PAT 17-JUL-2003

REFERENCE 1
AUTHORS Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and Montelius,A.
TITLE Methods and means for manipulating nucleic acid
JOURNAL Patent: WO 03064691-A 18 07-AUG-2003;
Global Genomics AB (SE)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Double-stranded product DNA"

Query Match 0.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAAAAAA 2801
|||||
Db 17 GAAAAA AAAAAAAAAA 1

RESULT 1414
AR030917/c
LOCUS AR030917 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861487.
ACCESSION AR030917
VERSION AR030917.1 GI:5944131
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily., Kovacic,F., Tanaka,Y. and Lester,D.Ruth.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: US 5861487-A 20 19-JAN-1999;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAAAAAA 2802
|||||
Db 17 AAAAAA AAAAAAAAAA 1

RESULT 1415
I28309/c
LOCUS I28309 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 20 from patent US 5569832.
ACCESSION I28309
VERSION I28309.1 GI:1819085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: US 5569832-A 20 29-OCT-1996;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAAAAAA 2802
|||||
Db 17 AAAAAA AAAAAAAAAA 1

RESULT 1416
I47310/c
LOCUS I47310 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5639870.
ACCESSION I47310
VERSION I47310.1 GI:2471275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily. and Tanaka,Y.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: US 5639870-A 11 17-JUN-1997;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAAAAAA 2802
|||||
Db 17 AAAAAA AAAAAAAAAA 1

RESULT 1417
BD161924
LOCUS BD161924 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for carrying out thermal cycle of PCR using DNA-immobilized substrate.
ACCESSION BD161924
VERSION BD161924.1 GI:27867682
KEYWORDS JP 2002191369-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Tanga,M., Okamura,H. and Takahashi,K.
TITLE Method for carrying out thermal cycle of PCR using DNA-immobilized substrate
JOURNAL Patent: JP 2002191369-A 1 09-JUL-2002;
COMMENT TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
OS Artificial Sequence
PN JP 2002191369-A/1
PD 09-JUL-2002
PF 27-DEC-2000 JP 2000399573
PI MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC Method for carrying out thermal cycle of PCR using DNA- CC immobilized
CC substrate
FH Key Location/Qualifiers
FT source 1. .20
/organism='Artificial Sequence'.
FT Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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VERSION      E32458.1  GI:13018694
KEYWORDS     JP 2000037190-A/18.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 18)
AUTHORS     Jun,N., Yusuke,N. and Toshihiro,T.
TITLE       Mammal-derived tissue specific physiologically active protein
JOURNAL     Patent: JP 2000037190-A 18 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS Artificial Sequence
            PN JP 2000037190-A/18
            PD 08-FEB-2000
            PF 23-JUL-1998 JP 1998225228
            PR
            PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC C12N15/00,
            PC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH Key Location/Qualifiers
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            /db_xref="taxon:32630"

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    Best Local Similarity 100.0%; Pred. No. 7.8e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 2784 TGAAGAAAAA 2800
  Db 18 TGAAGAAAAA 2800

RESULT 1410
AX028845 LOCUS AX028845 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION AX028845.1 GI:10189948
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
JOURNAL Patent: WO 9732023-A 29 04-SEP-1997;
        FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
        ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
        Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"

FEATURES
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    Best Local Similarity 100.0%; Pred. No. 7.8e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 2785 GAAAAA 2801
    Db 17 GAAAAA 2801

RESULT 1411
AX028845 LOCUS AX028845 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION AX028845.1 GI:10189948
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
JOURNAL Patent: WO 9732023-A 29 04-SEP-1997;
        FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
        ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
        Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"

FEATURES
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    Query Match 0.6%; Score 17; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 7.8e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 2166 TTTT 2182
    Db 1 TTTT 2182

RESULT 1411
AX028845 LOCUS AX028845 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION AX028845.1 GI:10189948
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
JOURNAL Patent: WO 9732023-A 29 04-SEP-1997;
        FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
        ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
        Location/Qualifiers
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"

FEATURES
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    Query Match 0.6%; Score 17; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 7.8e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 2166 TTTT 2182
    Db 1 TTTT 2182

RESULT 1411
AX028845 LOCUS AX028845 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION AX028845.1 GI:10189948
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
JOURNAL Patent: WO 9732023-A 29 04-SEP-1997;
        FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
        ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
        Location/Qualifiers
        1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"

FEATURES
  source
    Query Match 0.6%; Score 17; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 7.8e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 2786 AAAAAA 2802
    Db 17 AAAAAA 2802

RESULT 1412
AX361600/c LOCUS AX361600 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 18 from Patent WO208461.
ACCESSION AX361600
VERSION AX361600.1 GI:18694219
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
TITLE A method and an algorithm for mrna expression analysis
JOURNAL Patent: WO 0208461-A 18 31-JAN-2002;
        Global Genomics AB (SE)
        Location/Qualifiers
        1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Double-stranded product DNA"

FEATURES
  source
    Query Match 0.6%; Score 17; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 7.8e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 2785 GAAAAA 2801
    Db 17 GAAAAA 2801

RESULT 1413
AX814932/c LOCUS AX814932 18 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 18 from Patent WO3064691.
ACCESSION AX814932
VERSION AX814932.1 GI:39104070
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

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TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: WO 9732023-A 27 04-SEP-1997;
FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 0.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAA 2802
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Db 17 AAAAAAAAAAAAAAAA 1

RESULT 1406
AX028844 LOCUS 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 28 from Patent WO9732023.
ACCESSION AX028844
VERSION AX028844.1 GI:10189947
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Brugliera, F., Holton, T.A. and Michael, M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: WO 9732023-A 28 04-SEP-1997;
FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 0.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1407
BD190553/c LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Secretory proteins and polynucleotides encoding the same.
ACCESSION BD190553
VERSION BD190553.1 GI:33000292
KEYWORDS JP 2002515753-A/12.
SOURCE Rattus
ORGANISM Rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
1 (bases 1 to 18)
AUTHORS Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D., Treacy, M., Spaulding, V. and Agostino, M.J.
TITLE Secretory proteins and polynucleotides encoding the same
JOURNAL Patent: JP 2002515753-A 12 28-MAY-2002;
GENETICS INSTITUTE INC
PD JP 2002515753-A/12
28-MAY-2002

PF 31-OCT-1997 JP 1998521609
PR 01-NOV-1996 US 08/724973
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
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1. .18
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/db_xref="taxon:10114"

Query Match 0.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182
|||||
Db 18 TTTT TTTT TTTT TTTT TTTT 2

RESULT 1408
E32456 LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32456
VERSION E32456.1 GI:13018692
KEYWORDS JP 2000037190-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun, N., Yusuke, N. and Toshihiro, T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 16 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/16
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PI C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91), PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT primer bind (1). .(18).
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2172 TTTT TTTT TTTT TTTT TTTT 2188
|||||
Db 2 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1409
E32458/c LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32458

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QY      1767 AAGCTTTTTTTTTTTGA 1783
SOURCE  |||||
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
        apoptosis and/or viral resistance phenomena and their use as
        medicines
JOURNAL Patent: WO 03040369-A 5433 15-MAY-2003;
FEATURES Molecular Engines Laboratories (PR)
SOURCE Location/Qualifiers
        1. .17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2785 GAAAAAATAAAAAAAAAA 2801
Db      |||||
        17 GAAAAAATAAAAAAAAAA 1

RESULT 1402
AX692525
LOCUS AX692525
DEFINITION Sequence 5257 from Patent EP1281758.
ACCESSION AX692525
VERSION AX692525.1 GI:29415483
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
        mdz12
JOURNAL Patent: EP 1281758-A 5257 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
SOURCE Location/Qualifiers
        1. .17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2165 CTTTTTTTTTTTTTTT 2181
Db      |||||
        1 CTTTTTTTTTTTTTTT 17

RESULT 1403
AX762112
LOCUS AX762112
DEFINITION Sequence 5433 from Patent WO03040369.
ACCESSION AX762112
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VERSION AX762112.1 GI:32256728
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
        apoptosis and/or viral resistance phenomena and their use as
        medicines
JOURNAL Patent: WO 03040369-A 5433 15-MAY-2003;
FEATURES Molecular Engines Laboratories (PR)
SOURCE Location/Qualifiers
        1. .17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2460 GATCCAATTTTATATAT 2476
Db      |||||
        1 GATCCAATTTTATATAT 17

RESULT 1404
AX814938/c
LOCUS AX814938
DEFINITION Sequence 24 from Patent WO03064691.
ACCESSION AX814938
VERSION AX814938.1 GI:39104076
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
        Montelius,A.
TITLE Methods and means for manipulating nucleic acid
JOURNAL Patent: WO 03064691-A 24 07-AUG-2003;
FEATURES Global Genomics AB (SE)
SOURCE Location/Qualifiers
        1. .17
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Description of Artificial Sequence: Double-stranded
        product DNA"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2785 GAAAAAATAAAAAAAAAA 2801
Db      |||||
        17 GAAAAAATAAAAAAAAAA 1

RESULT 1405
AX028843/c
LOCUS AX028843
DEFINITION Sequence 27 from Patent WO9732023.
ACCESSION AX028843
VERSION AX028843.1 GI:10189946
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
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Db 17 TTTTTTTTTTTTTTTTTT 1

RESULT 1396

AR236087

LOCUS AR236087 17 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 5 from patent US 6462184.

ACCESSION AR236087

VERSION AR236087.1 GI:27279786

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Manoharan,M. and Maier,M.A.

TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds

JOURNAL Patent: US 6462184-A 5 08-OCT-2002;

FEATURES Location/Qualifiers

source 1..17

/organism="unknown"

/mol_type="genomic DNA"

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2182

Db 1 TTTTTTTTTTTTTTTTTT 17

RESULT 1397

AR236087/c

LOCUS AR236087 17 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 5 from patent US 6462184.

ACCESSION AR236087

VERSION AR236087.1 GI:27279786

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Manoharan,M. and Maier,M.A.

TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds

JOURNAL Patent: US 6462184-A 5 08-OCT-2002;

FEATURES Location/Qualifiers

source 1..17

/organism="unknown"

/mol_type="genomic DNA"

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2182

Db 1 TTTTTTTTTTTTTTTTTT 17

RESULT 1398

AR23672

LOCUS AR23672 17 bp RNA linear PAT 17-AUG-2003

DEFINITION Sequence 1074 from patent US 6566127.

ACCESSION AR23672

VERSION AR23672.1 GI:33709480

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 1074 20-MAY-2003;

FEATURES Location/Qualifiers

source 1..17

/organism="unknown"

/mol_type="unassigned RNA"

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTTTT 2181

Db 1 CTTTTTTTTTTTTTTTTT 17

RESULT 1399

AR323673/c

LOCUS AR323673 17 bp RNA linear PAT 17-AUG-2003

DEFINITION Sequence 1075 from patent US 6566127.

ACCESSION AR323673

VERSION AR323673.1 GI:33709481

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 1075 20-MAY-2003;

FEATURES Location/Qualifiers

source 1..17

/organism="unknown"

/mol_type="unassigned RNA"

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2801

Db 17 GAAAAAAAAAAAAAAAAA 1

RESULT 1400

AX146682

LOCUS AX146682 17 bp DNA linear PAT 31-MAY-2001

DEFINITION Sequence 24 from Patent WO0134834.

ACCESSION AX146682

VERSION AX146682.1 GI:14285075

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Leffers,H., Jorgensen,M. and skakkeb K,N.E.

TITLE Endogenous gene expression assay

JOURNAL Patent: WO 0134834-A 24 17-MAY-2001;

FEATURES Location/Qualifiers

source 1..17

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Primer sequence"

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2182
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 17

RESULT 1391
AR175846/c
LOCUS AR175846 17 bp DNA PAT 17-DEC-2001
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION AR175846
VERSION AR175846.1 GI:17917145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 132 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2802
Db 17 AAAAAA AAAAAA AAAAAA 1

RESULT 1392
AR187062
LOCUS AR187062 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 2550 from patent US 6346398.
ACCESSION AR187062
VERSION AR187062.1 GI:20233027
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTT TTTT TTTT TTTT TTTT TTTT TTTT 2181
Db 1 CTTT TTTT TTTT TTTT TTTT TTTT TTTT 17

RESULT 1393
AR187063/c
LOCUS AR187063 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 2551 from patent US 6346398.
ACCESSION AR187063
VERSION AR187063.1 GI:20233028
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2551 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAA AAAAAA 2801
Db 17 GAAAAA AAAAAA AAAAAA 1

RESULT 1394
AR222463
LOCUS AR222463 17 bp DNA PAT 26-SEP-2002
DEFINITION Sequence 23 from patent US 6429300.
ACCESSION AR222463
VERSION AR222463.1 GI:23329994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 23 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2802
Db 1 AAAAAA AAAAAA AAAAAA 17

RESULT 1395
AR222463/c
LOCUS AR222463 17 bp DNA PAT 26-SEP-2002
DEFINITION Sequence 23 from patent US 6429300.
ACCESSION AR222463
VERSION AR222463.1 GI:23329994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 23 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2182

/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.6%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1386
AR104585
LOCUS AR104585 17 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION AR104585
VERSION AR104585.1 GI:12817293
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 132 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.6%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1387
AR104585/c
LOCUS AR104585 17 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION AR104585
VERSION AR104585.1 GI:12817293
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 132 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.6%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1388
AR141074
LOCUS AR141074 17 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION AR141074

VERSION AR141074.1 GI:14483570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 5 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.6%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1389
AR141074/c
LOCUS AR141074 17 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION AR141074
VERSION AR141074.1 GI:14483570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 5 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.6%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1390
AR175846
LOCUS AR175846 17 bp DNA PAT 17-DEC-2001
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION AR175846
VERSION AR175846.1 GI:17917145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 132 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.6%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA... 2802
Db 28 BAAAAA... 11

RESULT 1381
AR340907/c
LOCUS AR340907 28 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 9 from patent US 559704.
ACCESSION AR340907
VERSION AR340907.1 GI:33732850
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Duwick, J. and Wang, X.
TITLE Fumonisin detoxification compositions and methods
JOURNAL Patent: US 559704-A 9 03-JUN-2003;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17.2; DB 1; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA... 2802
Db 28 BAAAAA... 11

RESULT 1382
AX029525/c
LOCUS AX029525 28 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 9 from Patent EP0981953.
ACCESSION AX029525
VERSION AX029525.1 GI:10190261
KEYWORDS
SOURCE Exophiala spinifera
ORGANISM Exophiala spinifera
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Chaetothyriomycetes;
Chaetothyriales; Herpotrichiellaceae; mitosporic.
Herpotrichiellaceae; Exophiala.

REFERENCE 1
AUTHORS Duwick, J., Maddox, J.R., Rood, T.A. and Wang, X.
TITLE Transgenic plants transformed with fumonisin detoxifying enzymes
JOURNAL Patent: EP 0981953-A 9 01-MAR-2000;
PIONEER HI BRED INT (US)

FEATURES Location/Qualifiers
source 1..28
/organism="Exophiala spinifera"
/mol_type="unassigned DNA"
/db_xref="taxon:91928"

Query Match 0.6%; Score 17.2; DB 1; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA... 2802
Db 28 BAAAAA... 11

RESULT 1383
I35032/c
LOCUS I35032 35 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 118 from patent US 559704.
ACCESSION I35032

VERSION I35032.1 GI:2088000
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Thompson, J.D. and Draper, K.G.
TITLE ErbB2/neu targeted ribozymes
JOURNAL Patent: US 559704-A 118 04-FEB-1997;
FEATURES Location/Qualifiers
source 1..35
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.2; DB 1; Length 35;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2783 TTGAAAAA... 2804
Db 33 TTAATAAA... 12

RESULT 1384
A28997
LOCUS A28997 17 bp DNA linear PAT 30-JUN-1995
DEFINITION primer sequence 4 from patent EP0522880.
ACCESSION A28997
VERSION A28997.1 GI:1248848
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor

JOURNAL Patent: EP 0522880-A 16 13-JAN-1993;
INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd

FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT... 2182
Db 1 TTTT... 17

RESULT 1385
A28997/c
LOCUS A28997 17 bp DNA linear PAT 30-JUN-1995
DEFINITION primer sequence 4 from patent EP0522880.
ACCESSION A28997
VERSION A28997.1 GI:1248848
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor

JOURNAL Patent: EP 0522880-A 16 13-JAN-1993;
INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd

FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"

FEATURES
source Location/Qualifiers
1. .28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.2; DB 1; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
:|||||
Db 28 BAAAAAAAAAAAAAAAAA 11

RESULT 1376
AR150988/c
LOCUS AR150988 28 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6229071.
ACCESSION AR150988
VERSION AR150988.1 GI:15115579
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Duvick,J., Maddox,J.R., Rood,T.A. and Wang,X.
TITLE Fumonisin detoxification compositions and methods
JOURNAL Patent: US 6229071-A 9 08-MAY-2001;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.2; DB 1; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
:|||||
Db 28 BAAAAAAAAAAAAAAAAA 11

RESULT 1377
AR156058/c
LOCUS AR156058 28 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6239330.
ACCESSION AR156058
VERSION AR156058.1 GI:15124111
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Duvick,J., Maddox,J.R. and Wang,X.
TITLE Fumonisin detoxification compositions and methods
JOURNAL Patent: US 6239330-A 9 29-MAY-2001;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.2; DB 1; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
:|||||
Db 28 BAAAAAAAAAAAAAAAAA 11

RESULT 1378
AR172065/c
LOCUS AR172065 28 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 19 from patent US 6297425.
ACCESSION AR172065
VERSION AR172065.1 GI:17911015
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Scelonge,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6297425-A 19 02-OCT-2001;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.2; DB 1; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
:|||||
Db 28 BAAAAAAAAAAAAAAAAA 11

RESULT 1379
AR173356/c
LOCUS AR173356 28 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 19 from patent US 6303846.
ACCESSION AR173356
VERSION AR173356.1 GI:17912847
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Scelonge,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6303846-A 19 16-OCT-2001;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.2; DB 1; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
:|||||
Db 28 BAAAAAAAAAAAAAAAAA 11

RESULT 1380
I87998/c
LOCUS I87998 28 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 9 from patent US 5716820.
ACCESSION I87998
VERSION I87998.1 GI:3407938
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Duvick,J., Rood,T. and Wang,X.
TITLE Fumonisin detoxification enzymes
JOURNAL Patent: US 5716820-A 9 10-FEB-1998;
FEATURES Location/Qualifiers
source 1. .28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.2; DB 1; Length 28;

FEATURES
source Location/Qualifiers
1. .23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Komponente (b) -3"

Query Match 0.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2800
Db 22 AGCATCCAAAAA 1

RESULT 1363
AX119432/c
LOCUS AX119432 23 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 89 from Patent WO0129251.
ACCESSION AX119432
VERSION AX119432.1 GI:14036351
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nf1 gene
JOURNAL Patent: WO 0129251-A 89 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
source Location/Qualifiers
1. .23
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2750 GATACGCTATAATAAAGTAT 2771
Db 23 GATACGTCATATTACAAGTAT 2

RESULT 1364
AX921569/c
LOCUS AX921569 23 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 562 from Patent WO02068652.
ACCESSION AX921569
VERSION AX921569.1 GI:40215190
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Nov-x proteins and nucleic acids encoding same
TITLE Patent: WO 02068652-A 562 06-SEP-2002;
JOURNAL Location/Qualifiers
FEATURES
source 1. .23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: oligonucleotide primer"

Query Match 0.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 731 GATCAGACAGTCATTCCGAAAG 752
Db 22 GATCCGACAGTCATTCTCAGAG 1

RESULT 1365
BD187389
LOCUS BD187389 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for testing anti-osteoporosis agent.
ACCESSION BD187389
VERSION BD187389.1 GI:32997128
KEYWORDS JP 2003009871-A/6.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Furukawa,H., Matsui,H., Kawaida,R. and Otsuka,T.
TITLE Method for testing anti-osteoporosis agent
JOURNAL Patent: JP 2003009871-A 6 14-JAN-2003;
COMMENT Sankyo Company Limited
OS Artificial Sequence
PN JP 2003009871-A/6
PD 14-JAN-2003
PF 14-JUN-2001 JP 2001180142
PI hidehiko furukawa,hideki matsui,remi kawaida,toshiaki otsuka
CC Description of Artificial Sequence: PCR primer DAPG1 FH Key
Location/Qualifiers
FEATURES
source 1. .23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTT 2183
Db 1 CTCGAGTTT 22

RESULT 1366
BD244864
LOCUS BD244864 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.
ACCESSION BD244864
VERSION BD244864.1 GI:33054634
KEYWORDS JP 2002532063-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 25)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable
JOURNAL Patent: JP 2002532063-A 9 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
OS Artificial Sequence
PN JP 2002532063-A/9
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1. .25
/organism='Artificial Sequence'.
Location/Qualifiers
FEATURES
source 1. .25
/organism="synthetic construct"

Query Match	0.6%;	Score 17.2;	DB 1;	Length 20;
Best Local Similarity	94.4%;	Pred. No. 9.7e+02;		
Matches 17;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY

2170

TTTTTTTTTTTTTTTTTTA

2187

|||||

1

TTTTTTTTTTTTTTTTTV

18

Db

1

TTTTTTTTTTTTTTTTTV

18

RESULT 1354

E08332/c

LOCUS

E08332

Reverse transcription primer.

ACCESSION

E08332

VERSION

E08332.1

GI:2176449

KEYWORDS

JP 1994303997-A/3.

SOURCE

unidentified

ORGANISM

unidentified

unclassified.

1

(bases 1 to 20)

REFERENCE

Takagi, S. and Kamioka, S.

AUTHORS

DETERMINATION OF CDNA

TITLE

Patent: JP 1994303997-A 3 01-NOV-1994;

JOURNAL

NIPPON TELEGR & TELEPH CORP <NTT>

COMMENT

OS

None

OC

Artificial sequences.

PN

JP 1994303997-A/3

PD

01-NOV-1994

PF

16-APR-1993

JP 1993112515

PI

TAKAGI SHIGERU, KAMIOKA SUKEYUKI

PC

C12Q1/68, C12N15/10;

CC

strandedness: Single;

CC

topology: Linear;

CC

hypothetical: No;

CC

anti-sense: Yes;

FH

Key

FH

Location/Qualifiers

FT

source

1. .20

/organism='Artificial sequences'.

FEATURES

source

1. .20

/organism="unidentified"

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/db_xref="taxon:32644"

Query Match	0.6%;	Score 17.2;	DB 1;	Length 20;
Best Local Similarity	94.4%;	Pred. No. 9.7e+02;		
Matches 17;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY

2785

GAAAAAAAAAAAAAAAAA

2802

:

18

BAAAAAAAAAAAAAAAAA

1

Db

18

BAAAAAAAAAAAAAAAAA

1

RESULT 1355

E08333

LOCUS

E08333

Reverse transcription primer.

ACCESSION

E08333

VERSION

E08333.1

GI:2176450

KEYWORDS

JP 1994303997-A/4.

SOURCE

unidentified

ORGANISM

unidentified

unclassified.

1

(bases 1 to 20)

REFERENCE

Takagi, S. and Kamioka, S.

AUTHORS

DETERMINATION OF CDNA

TITLE

Patent: JP 1994303997-A 3 01-NOV-1994;

JOURNAL

NIPPON TELEGR & TELEPH CORP <NTT>

COMMENT

OS

None

OC

Artificial sequences.

PN

JP 1994303997-A/3

PD

01-NOV-1994

PF

16-APR-1993

JP 1993112515

PI

TAKAGI SHIGERU, KAMIOKA SUKEYUKI

PC

C12Q1/68, C12N15/10;

CC

strandedness: Single;

CC

topology: Linear;

CC

hypothetical: No;

CC

anti-sense: Yes;

FH

Key

FH

Location/Qualifiers

FT

source

1. .20

/organism='Artificial sequences'.

FEATURES

source

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/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match	0.6%;	Score 17.2;	DB 1;	Length 20;
Best Local Similarity	94.4%;	Pred. No. 9.7e+02;		
Matches 17;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY

2785

GAAAAAAAAAAAAAAAAA

2802

:

18

BAAAAAAAAAAAAAAAAA

1

Db

18

BAAAAAAAAAAAAAAAAA

1

RESULT 1355

E08333

LOCUS

E08333

Reverse transcription primer.

ACCESSION

E08333

VERSION

E08333.1

GI:2176450

KEYWORDS

JP 1994303997-A/4.

SOURCE

unidentified

ORGANISM

unidentified

unclassified.

1

(bases 1 to 20)

REFERENCE

Takagi, S. and Kamioka, S.

AUTHORS

DETERMINATION OF CDNA

TITLE

Patent: JP 1994303997-A 3 01-NOV-1994;

JOURNAL

NIPPON TELEGR & TELEPH CORP <NTT>

COMMENT

OS

None

OC

Artificial sequences.

PN

JP 1994303997-A/3

PD

01-NOV-1994

PF

16-APR-1993

JP 1993112515

PI

TAKAGI SHIGERU, KAMIOKA SUKEYUKI

PC

C12Q1/68, C12N15/10;

CC

strandedness: Single;

CC

topology: Linear;

CC

hypothetical: No;

CC

anti-sense: Yes;

FH

Key

FH

Location/Qualifiers

FT

source

1. .20

/organism='Artificial sequences'.

FEATURES

source

1. .20

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match	0.6%;	Score 17.2;	DB 1;	Length 20;
Best Local Similarity	94.4%;	Pred. No. 9.7e+02;		
Matches 17;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY

2785

GAAAAAAAAAAAAAAAAA

2802

:

18

BAAAAAAAAAAAAAAAAA

1

Db

18

BAAAAAAAAAAAAAAAAA

1

RESULT 1355

E08333

LOCUS

E08333

Reverse transcription primer.

ACCESSION

E08333

VERSION

E08333.1

GI:2176450

KEYWORDS

JP 1994303997-A/4.

SOURCE

unidentified

ORGANISM

unidentified

unclassified.

1

(bases 1 to 20)

REFERENCE

Takagi, S. and Kamioka, S.

AUTHORS

DETERMINATION OF CDNA

TITLE

Patent: JP 1994303997-A 3 01-NOV-1994;

JOURNAL

NIPPON TELEGR & TELEPH CORP <NTT>

COMMENT

OS

None

OC

Artificial sequences.

PN

JP 1994303997-A/3

PD

01-NOV-1994

PF

16-APR-1993

JP 1993112515

PI

TAKAGI SHIGERU, KAMIOKA SUKEYUKI

PC

C12Q1/68, C12N15/10;

CC

strandedness: Single;

CC

topology: Linear;

CC

hypothetical: No;

CC

anti-sense: Yes;

FH

Key

FH

Location/Qualifiers

FT

source

1. .20

/organism='Artificial sequences'.

FEATURES

source

1. .20

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match	0.6%;	Score 17.2;	DB 1;	Length 20;
Best Local Similarity	94.4%;	Pred. No. 9.7e+02;		
Matches 17;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY

2785

GAAAAAAAAAAAAAAAAA

2802

:

18

BAAAAAAAAAAAAAAAAA

1

Db

18

BAAAAAAAAAAAAAAAAA

1

RESULT 1355

E08333

LOCUS

E08333

Reverse transcription primer.

ACCESSION

E08333

VERSION

E08333.1

GI:2176450

KEYWORDS

JP 1994303997-A/4.

SOURCE

unidentified

ORGANISM

unidentified

unclassified.

1

(bases 1 to 20)

REFERENCE

Takagi, S. and Kamioka, S.

AUTHORS

DETERMINATION OF CDNA

TITLE

Patent: JP 1994303997-A 3 01-NOV-1994;

JOURNAL

NIPPON TELEGR & TELEPH CORP <NTT>

COMMENT

OS

CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAACAAAAA 12
RESULT 1346
BD166032/c
LOCUS
DEFINITION
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166032
VERSION
BD166032.1 GI:27871844
KEYWORDS
JP 2002191372-A/12.
SOURCE
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
JOURNAL
Patent: JP 2002191372-A 12 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/12
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAGAAAAA 12
RESULT 1347
BD166033/c
LOCUS
DEFINITION
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166033
VERSION
BD166033.1 GI:27871845
KEYWORDS
JP 2002191372-A/13.
SOURCE
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
JOURNAL
Patent: JP 2002191372-A 13 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/13
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAGAAAAA 12
RESULT 1348
BD166129/c
LOCUS
DEFINITION
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166129
VERSION
BD166129.1 GI:27871941
KEYWORDS
JP 2002191372-A/109.
SOURCE
unidentified

CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAACAAAA 12

RESULT 1338
BD145026/c
LOCUS
DEFINITION
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
BD145026
BD145026.1 GI:27850784
JP 2002119291-A/7.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 30)
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
Patent: JP 2002119291-A 7 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/7
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53,
PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAACAAAA 12

RESULT 1339
BD145027/c
LOCUS
DEFINITION
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
BD145027
BD145027.1 GI:27850785
JP 2002119291-A/8.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 30)
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
Patent: JP 2002119291-A 8 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/8
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53,
PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAACAAAA 12

RESULT 1340
BD145028/c
LOCUS
DEFINITION
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
BD145028
BD145028.1 GI:27850786
JP 2002119291-A/9.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 30)
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
Patent: JP 2002119291-A 9 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/9
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53,
PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAACAAAA 12

Best Local Similarity 94.7%; Pred. No. 2.4e+03; Mismatches 0; Indels 0; Gaps 0; Matches 18; Conservative 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAACAAAAAAAAA 12

RESULT 1335
BD107500/c
LOCUS BD107500 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107500
VERSION BD107500.1 GI:23202318
KEYWORDS JP 2002000275-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 9 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL

OS Artificial Sequence
PN JP 2002000275-A/9
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base sequence was prepared synthetically on the aim of CC examining the CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAGAAAAAAAAA 12

RESULT 1336
BD107501/c
LOCUS BD107501 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107501
VERSION BD107501.1 GI:23202319
KEYWORDS JP 2002000275-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method

JOURNAL Patent: JP 2002000275-A 10 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL

COMMENT
OS Artificial Sequence
PN JP 2002000275-A/10
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base sequence was prepared synthetically on the aim of CC examining the CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
CC nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAGAAAAAAAAA 12

RESULT 1337
BD145025/c
LOCUS BD145025 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD145025
VERSION BD145025.1 GI:27850783
KEYWORDS JP 2002119291-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 6 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD

COMMENT
OS Artificial Sequence
PN JP 2002119291-A/6
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/PC 53,
PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC hybridization of

JOURNAL Patent: JP 2001286300-A 11 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/11
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAAAAAAAAA 12
RESULT 1330
BD072874/c
LOCUS 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072874
VERSION BD072874.1 GI:22618477
KEYWORDS JP 2001286300-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 12 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/12
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC

labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAAAAAAAAA 12
RESULT 1331
BD107493/c
LOCUS 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107493
VERSION BD107493.1 GI:23202311
KEYWORDS JP 2002000275-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 2 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/2
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAACAAAAA 12

FEATURES
source
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAACAAAAA 12

RESULT 1327
BD072868/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD072868 30 bp DNA linear PAT 27-AUG-2002
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.

BD072868 1 GI:22618471
JP 2001286300-A/6.
synthetic construct
artificial sequences.
1 (bases 1 to 30)

Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method

Patent: JP 2001286300-A 6 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY

OS Artificial Sequence
PN JP 2001286300-A/6
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI

KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC decrease in fluorescence emission of a nucleic acid probe CC

CC BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'

FEATURES
source
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAACAAAAA 12

RESULT 1328
BD072869/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD072869 30 bp DNA linear PAT 27-AUG-2002
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.

BD072869 1 GI:22618472
JP 2001286300-A/7.
synthetic construct
artificial sequences.
1 (bases 1 to 30)

Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method

Patent: JP 2001286300-A 7 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY

OS Artificial Sequence
PN JP 2001286300-A/7
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI

KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC decrease in fluorescence emission of a nucleic acid probe CC

CC BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'

FEATURES
source
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAACAAAAA 12

RESULT 1329
BD072873/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD072873 30 bp DNA linear PAT 27-AUG-2002
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.

BD072873 1 GI:22618476
JP 2001286300-A/11.
synthetic construct
artificial sequences.
1 (bases 1 to 30)

Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method

Patent: JP 2001286300-A 11 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY

OS Artificial Sequence
PN JP 2001286300-A/11
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI

KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC decrease in fluorescence emission of a nucleic acid probe CC

CC BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'

FEATURES
source
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAACAAAAA 12

REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 12 10-DEC-2002;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAAAAAA 12

RESULT 1324
AR264929/c
LOCUS AR264929 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6492121.
ACCESSION AR264929
VERSION AR264929.1 GI:29693316
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 13 10-DEC-2002;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAAAAAA 12

RESULT 1325
BD072866/c
LOCUS BD072866 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD072866
VERSION BD072866.1 GI:22618469
KEYWORDS JP 2001286300-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 4 16-OCT-2001;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
OS Artificial Sequence
COMMENT

PN JP 2001286300-A/4
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, VOICHI KAMAGATA, SHINYA PI KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU, OSAMU KOYAMA, KENTA FURUSHO
PC C12Q1/68, C12M1/00, C12N15/09, G01N31/22, G01N33/53, G01N33/542, PC G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAACAAAAA 12

RESULT 1326
BD072867/c
LOCUS BD072867 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD072867
VERSION BD072867.1 GI:22618470
KEYWORDS JP 2001286300-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 5 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
OS Artificial Sequence
PN JP 2001286300-A/5
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, VOICHI KAMAGATA, SHINYA PI KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU, OSAMU KOYAMA, KENTA FURUSHO
PC C12Q1/68, C12M1/00, C12N15/09, G01N31/22, G01N33/53, G01N33/542, PC G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target CC nucleic
CC acid.

ACCESSION BD107492
VERSION BD107492.1 GI:23202310
KEYWORDS JP 2002000275-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 200200275-A 1 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/1
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
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Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAAAAAAAAACAAAA 12
RESULT 1317
BD145024/c
LOCUS
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145024
VERSION BD145024.1 GI:27850782
KEYWORDS JP 2002119291-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 5 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/5
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC

C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
53,
PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAAAAAAAAACAAAA 12
RESULT 1318
BD166025/c
LOCUS
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166025
VERSION BD166025.1 GI:27871837
KEYWORDS JP 2002191372-A/5.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 5 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/5
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="unidentified"

BD166031/c
LOCUS BD166031 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.
ACCESSION BD166031
VERSION BD166031.1 GI:27871843
KEYWORDS JP 2002191372-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method
JOURNAL Patent: JP 2002191372-A 11 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/11
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
FT /organism='Artificial Sequence'.
FEATURES
source
1..30
Location/Qualifiers
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/db_xref="taxon:32644"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAGAAAAA 12
RESULT 1314
AR264920/c
LOCUS AR264920 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 4 from patent US 6492121.
ACCESSION AR264920
VERSION AR264920.1 GI:29693307
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 4 10-DEC-2002;
FEATURES Location/Qualifiers

source
1..30
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAACAAAA 12
RESULT 1315
BD072865/c
LOCUS BD072865 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD072865
VERSION BD072865.1 GI:22618468
KEYWORDS JP 2001286300-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 3 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/3
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
FT /organism='Artificial Sequence'.
FEATURES
source
1..30
Location/Qualifiers
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/db_xref="taxon:32630"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAACAAAA 12
RESULT 1316
BD107492/c
LOCUS BD107492 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.

PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
53,
-PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
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Db 30 AAAAAAAAAAGAGAAAA 12
RESULT 1311
BD145031/c
LOCUS 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145031
VERSION JP 2002119291-A/12.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
COMMENT OS Artificial Sequence
PN JP 2002119291-A/12
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
53,
PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30

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FEATURES
source Location/Qualifiers
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Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
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Db 30 AAAAAAAAAAGAGAAAA 12
RESULT 1312
BD166030/c
LOCUS 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166030
VERSION BD166030.1 GI:27871842
KEYWORDS JP 2002191372-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL
COMMENT OS Artificial Sequence
PN JP 2002191372-A/10
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
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source Location/Qualifiers
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Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAGAAAA 12
RESULT 1313

labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
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FT Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 30 AAAAAAAAAAAGAAAAA 12
RESULT 1308
BD107498/c
LOCUS
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107498
VERSION BD107498.1 GI:23202316
KEYWORDS JP 2002000275-A/7.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 7 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/7
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
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source
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAAGAAAAA 12
RESULT 1308
BD107498/c
LOCUS
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107498
VERSION BD107498.1 GI:23202316
KEYWORDS JP 2002000275-A/7.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 7 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/7
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
FEATURES
source
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 30 AAAAAAAAAAAGAAAAA 12

RESULT 1309
BD107499/c
LOCUS
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107499
VERSION BD107499.1 GI:23202317
KEYWORDS JP 2002000275-A/8.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 8 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/8
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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source
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAAGAAAAA 12
RESULT 1310
BD145030/c
LOCUS
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145030
VERSION BD145030.1 GI:27850788
KEYWORDS JP 2002119291-A/11.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 11 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/11

VERSION AR264926.1 GI:29693313
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
Patent: US 6492121-A 10 10-DEC-2002;
JOURNAL Location/Qualifiers
FEATURES
source 1..30
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAAAAA 12
RESULT 1305
AR264927/c
LOCUS AR264927 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 11 from patent US 6492121.
ACCESSION AR264927
VERSION AR264927.1 GI:29693314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
Patent: US 6492121-A 11 10-DEC-2002;
JOURNAL Location/Qualifiers
FEATURES
source 1..30
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAAAAA 12
RESULT 1306
BD072871/c
LOCUS BD072871 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072871
VERSION BD072871.1 GI:22618474
KEYWORDS JP 2001286300-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method

JOURNAL Patent: JP 2001286300-A 9 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/9
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the CC
probe with a target
nucleic
acid.
FH Key Location/Qualifiers
FT source 1..30
FT /organism='Artificial Sequence'.
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source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAAAAA 12
RESULT 1307
BD072872/c
LOCUS BD072872 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072872
VERSION BD072872.1 GI:22618475
KEYWORDS JP 2001286300-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
Patent: JP 2001286300-A 10 16-OCT-2001;
JOURNAL JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/10
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC

PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC acid.
FH Key
FT source
FT Location/Qualifiers
FT 1. .30
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAGAAA 12

RESULT 1302
BD145029/c 30 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145029
VERSION BD145029.1 GI:27850787
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,
Yamada, K. and Yokomaku, T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
COMMENT OS Artificial Sequence
PN JP 2002119291-A/10
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N1/28, G01N33/ PC
53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key
FT source
FT Location/Qualifiers
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Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAGAAA 12

RESULT 1302
BD145029/c 30 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145029
VERSION BD145029.1 GI:27850787
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,
Yamada, K. and Yokomaku, T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
COMMENT OS Artificial Sequence
PN JP 2002119291-A/10
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N1/28, G01N33/ PC
53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key
FT source
FT Location/Qualifiers
FT 1. .30
/organism="synthetic construct"

/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAGAAA 12

RESULT 1303
BD166029/c 30 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166029
VERSION BD166029.1 GI:27871841
KEYWORDS JP 2002191372-A/9.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,
Yamada, K. and Yokomaku, T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 9 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/9
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12M1/00, C12Q1/68, G01N33/58//G01N33/53, G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key
FT source
FT Location/Qualifiers
FT 1. .30
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 30 AAAAAAAAAAGAGAAA 12

RESULT 1304
AR264926/c 30 bp DNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 10 from patent US 6492121.
ACCESSION AR264926

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Query Match          0.6%; Score 17.4; DB 1; Length 28;
Best Local Similarity 94.7%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2803
Db 9 GCAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1298
AR068458
LOCUS
DEFINITION
Sequence 22 from patent US 5853991.
ACCESSION
AR068458
VERSION
AR068458.1 GI:6000665
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 28)
AUTHORS
Wang,X., Duvick,J.P. and Briggs,S.P.
TITLE
PCR-based cDNA subtractive cloning method
JOURNAL
Patent: US 5853991-A 22 29-DEC-1998;
FEATURES
Location/Qualifiers
source
1..28
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Query Match          0.6%; Score 17.4; DB 1; Length 28;
Best Local Similarity 94.7%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2803
Db 9 GCAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1299
AR264925/c
LOCUS
DEFINITION
Sequence 9 from patent US 6492121.
ACCESSION
AR264925
VERSION
AR264925.1 GI:29693312
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE
Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL
Patent: US 6492121-A 9 10-DEC-2002;
FEATURES
Location/Qualifiers
source
1..30
/organism="unknown"
/mol_type="genomic DNA"

Query Match          0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAAAAAAAAAGAAA 12

RESULT 1300
BD072870/c
LOCUS
DEFINITION
Method for assaying nucleic acid, nucleic acid probe used therefor,
PAT 27-AUG-2002
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and method for analyzing data obtained by that method.
BD072870
VERSION
BD072870.1 GI:22618473
KEYWORDS
JP 2001286300-A/8.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2001286300-A 8 16-OCT-2001;
COMMENT
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
OS Artificial Sequence
PN JP 2001286300-A/8
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the CC
probe with a target
nucleic
acid.
FH Key
FT source
FT Location/Qualifiers
1..30
/organism='Artificial Sequence'.
Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match          0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 30 AAAAAAAAAAAAAAAAAAGAAA 12

RESULT 1301
BD107497/c
LOCUS
DEFINITION
Novel quantitative polymorphism analysis method.
ACCESSION
BD107497
VERSION
BD107497.1 GI:23202315
KEYWORDS
JP 2002000275-A/6.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE
Novel quantitative polymorphism analysis method
JOURNAL
Patent: JP 2002000275-A 6 08-JAN-2002;
COMMENT
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
OS Artificial Sequence
PN JP 2002000275-A/6
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
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/mol_type="unassigned DNA"  
/db xref="taxon:9606"
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Best Local Similarity 94.7%;      Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels
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QY 2786 AAAAAAAAAAAAAAAAAA 2804
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 Db 25 AAAAAAAAAAAAAAAAAA 7

RESULT	1294
AX692822	
LOCUS	AX692822
DEFINITION	Sequence 5554 from Patent EP1281758.
ACCESSION	AX692822
VERSION	AX692822.1 GI:29415785
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria. Primates: Catarrhini; Hominidae; Homo.

1 Shannon, M., Gu, Y. and Nguyen, C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
Patent: EP 1281758-A 5554 05-FEB-2003;
Aeomica, Inc. (US)

Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels

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Dd	6	TTCTTTTTTTTTTTTTTTTTTT	24

RESULT	1295
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LOCUS	AX692822
DEFINITION	Sequence 5554 from Patent EP1281758.
ACCESSION	AX692822
VERSION	AX692822.1 GI:29415785
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mollusca; Mollusca; Bivalvia; Brachyodonta; Catarrhini; Hominidae; Homo.
	linear PAT 31-MAR-2003

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REFERENCE
AUTHORS      Shannon,M., Gu, Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL       Patent: EP 1281758-A 5554 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

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Query Match	0.6%;	Score 17.4;	DB 1;	Length 25;
Best Local Similarity	94.7%;	Pred. No. 1.6e+03;		
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				Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 24 AAAAAAAAAAAAAAAAAAGAA 6

RESULT 1296					
BD006733/c					
LOCUS	BD006733	25 bp	linear	PAT 31-JAN-2002	
DEFINITION	Novel polypeptide.				
ACCESSION	BD006733				
VERSION	BD006733.1 GI:18635104				
KEYWORDS	JP 2001029090-A/36.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 25)				
AUTHORS	Ito, Y., Mogi, S., Tanaka, H., Okubo, S. and Ogi, K.				
TITLE	Novel polypeptide				
JOURNAL	Patent: JP 2001029090-A 36 06-FEB-2001; TAKEDA CHEMICAL INDUSTRIES LTD				
COMMENT	OS Artificial Sequence				
	PN JP 2001029090-A/36				
	PD 06-FEB-2001				
	PF 19-MAY-2000 JP 2000147530				

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Query Match          0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 454 AGCAGCCAGCAGCAGGCC 472
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nb 25 AAGCAGCCAGCAGCAGGCC 7

RESULT	1297
AR055117	
LOCUS	AR055117
DEFINITION	Sequence 22 from patent US 5837468.
ACCESSION	AR055117
VERSION	AR055117.1 GI:5980694
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown. Unclassified.
	DNA
	linear
	PAT 29-SEP-1999

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REFERENCE
1 (bases 1 to 207)
AUTHORS
Wang, X., Duvick, J.P. and Briggs, S.P.
TITLE
PCR-based cDNA substructure cloning method
JOURNAL
Patent: US 5837468-A 22 17-NOV-1998;
FEATURES
Location/Qualifiers
1..28
source
/organism="unknown"
/mol type="unassigned DNA"

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REFERENCE
1
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2699 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source
location/Qualifiers
1..25
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY 2166 TTTTTCCTTTTTCCTTTTTCCTTTT 2184
Db 19 TTTTTCCTTTTTCCTTTTTCCTTTT 1
RESULT 1292
AX692821
LOCUS
DEFINITION Sequence 5553 from Patent EP1281758.
ACCESSION AX692821
VERSION AX692821.1 GI:29415784
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5553 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
location/Qualifiers
1..25
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/mol_type="unassigned DNA"
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Query Match 0.6%; Score 17.4; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2163 TCCCTTTTTCCTTTTTCCTTTTTCCTTTT 2181
Db 7 TCCCTTTTTCCTTTTTCCTTTTTCCTTTT 25
RESULT 1293
AX692821/c
LOCUS
DEFINITION Sequence 5553 from Patent EP1281758.
ACCESSION AX692821
VERSION AX692821.1 GI:29415784
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5553 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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location/Qualifiers
1..25
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/db_xref="taxon:32630"
/note="Primer"

Query Match          0.6%;   Score 17.4;   DB 1;   Length 25;
Best Local Similarity 94.7%;   Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2786 AAAAAAAAAAAAAAAAAAAAA 2804
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Db   25 AAAAAAAAACAAAAAAAAAAAAA 7

RESULT 1287
AX042590          25 bp   DNA          linear          PAT 23-NOV-2000
LOCUS
DEFINITION
Sequence 156 from Patent WO0065088.
ACCESSION AX042590
VERSION AX042590.1 GI:11341198
KEYWORDS
SOURCE
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 156 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="DQAL Homozygote primer sequence"

Query Match          0.6%;   Score 17.4;   DB 1;   Length 25;
Best Local Similarity 94.7%;   Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2174 TTTTTTTTTTTTTTAACTTT 2192
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Db   1 TTTTTTTTTTTTTTAACTCT 19

RESULT 1288
AX043064/c
LOCUS
DEFINITION
Sequence 630 from Patent WO0065088.
ACCESSION AX043064
VERSION AX043064.1 GI:11341672
KEYWORDS
SOURCE
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 630 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="16S rRNA Homozygote Primer Sequence"

Query Match          0.6%;   Score 17.4;   DB 1;   Length 25;
Best Local Similarity 94.7%;   Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2782 ATTGAAAAAAAAAAAAAAAAA 2800
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Db   19 ACTGAAAAAAAAAAAAAAAAA 1

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[illegible]

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RESULT 879
LOCUS AR118155/c
DEFINITION AR118155 21 bp DNA
ACCESSION Sequence 23 From patent US 6140489.
VERSION AR118155
KEYWORDS AR118155.1 GI:14099061
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
TITLE Brenner, S.
JOURNAL Compositions for sorting polynucleotides
        Patent: US 6140489-A 23 31-OCT-2000;
        location/Qualifiers
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"

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	Query Match	0.7%;	Score 19;	DB 1;	length 21;
	Best Local Similarity	100.0%;	Pred. No. 5.4e+02;		
Matches	19; Conservative	0;	Mismatches	0;	Gaps 0;
QY	2786 AAAAAAAAAAAAAAAAAAAAAA	2804			
Ddb	21 AAAAAAAAAAAAAAAAAAAAAA	3			

RESULT	880				
LOCUS	184433				
DEFINITION	184433	21 bp	DNA	linear	PAT 04-APR-1998
ACCESSION	184433	Sequence 23 from patent US 5695934.			
VERSION	184433.1	GI:3021953			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1	(bases 1 to 21)			
AUTHORS	Brenner, S.				
TITLE	Massively parallel sequencing of sorted polynucleotides				
JOURNAL	Patent: US 5695934-A 23 09-DEC-1997;				
FEATURES	location/Qualifiers				
	1..21				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
source					

Query Match	0.7%;	Score 19;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 5.4e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2166	TTTTTTTTTTTTTTTTTTTT	2184	
Db	3	TTTTTTTTTTTTTTTTTTTT	21	

RESULT	881		
	184433/c		
LOCUS	184433	21 bp	DNA
DEFINITION	Sequence	23 from patent	US 5695934.
ACCESSION	184433		
VERSION	184433.1	GI:3021953	
KEYWORDS	.		
SOURCE	Unknown.		
			PAT 04-APR-1998
		linear	

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ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Brenner, S.
TITLE          Massively parallel sequencing of sorted polynucleotides
JOURNAL        Patent: US 5695934-A 23 09-DEC-1997;
FEATURES
source         1..21
               /organism="unknown"
               /mol_type="unassigned DNA"

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Query Match	0.7%;	Score 19;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 5.4e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2786	AAAAAAAAAAAAAAAAAAAAA	2804	
Db	21	AAAAAAAAAAAAAAAAAAAAA	3	

RESULT	882		
AX825107			
LOCUS	AX825107	21 bp	DNA
DEFINITION	Sequence 5 from Patent WO03072818.		linear
ACCESSION	AX825107		
VERSION	AX825107.1	GI:39750836	
KEYWORDS			
SOURCE			
ORGANISM			
	synthetic construct		
	synthetic construct		
	artificial sequences.		

REFERENCE	1
AUTHORS	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE	Method for sorting single-stranded nucleic acids
JOURNAL	Patent: WO 03072818-A 5 04-SEP-2003;
DEGUSSEA	Bioactives GmbH (DE)
FEATURES	Location/Qualifiers
SOURCE	1. .21

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"
misc_binding
1/bound_moiety="Biotin"
modified_base
3/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base
6/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base
9/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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/mod_base=OTHER
modified_base
18/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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	Query Match	0.7%;	Score 19;	DB 1;	length 21;	
	Best Local Similarity	100.0%;	Pred. NO. 5.4e+02;			
Matches	19; Conservative	0;	Mismatches	0;	Gaps	0;
OY	2169 TTTTTTTTTTTTTTTTAA 2187					
Dd	1 TTTTTTTTTTTTTTTTAA 19					

RESULT 883

AX825108	LOCUS	AX825108	21 bp	DNA	linear	PAT 11-DEC-2003
	DEFINITION	Sequence 6 from Patent WO03072818.				
	ACCESSION	AX825108				
	VERSION	AX825108.1	GI:39750837			
	KEYWORDS					
	SOURCE	synthetic construct				
	ORGANISM	synthetic construct				
	REFERENCE	artificial sequences.				
	AUTHORS	1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.				
	TITLE	Method for sorting single-stranded nucleic acids				
	JOURNAL	Patent: WO 03072818-A 6 04-SEP-2003;				
		Degussa Bioactives GmbH (DE)				
FEATURES	source	Location/Qualifiers				
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		/organism="synthetic construct"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:32630"				
		/note="Beschreibung der kuenstlichen				
		Sequenz:Capture-Oligonukleotid"				
		1				
	misc_binding	/bound_moiety="Biotin"				
		3				
	modified_base	/note="LNA-T (Locked Nucleic Acid) "				
		6				
	modified_base	/mod_base=OTHER				
		/note="LNA-T (Locked Nucleic Acid) "				
		9				
	modified_base	/mod_base=OTHER				
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		12				
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	modified_base	/mod_base=OTHER				
		/note="LNA-T (Locked Nucleic Acid) "				
		18				
	modified_base	/mod_base=OTHER				

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modified_base	3	/note="LNA-T (Locked Nucleic Acid) "
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modified_base	12	/note="LNA-T (Locked Nucleic Acid) "
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modified_base	15	/note="LNA-T (Locked Nucleic Acid) "
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modified_base	18	/note="LNA-T (Locked Nucleic Acid) "
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Query Match	0.7%;	Score 19;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 5.4e+02;		
Matches	19; Conservative	0; Mismatches	0; Indels	0; Gaps

Oy	2169	TTTTTTT	TTTTTTT	TATTA	2187
Db	1	TTTTTTT	TTTTTTT	TTT	19

RESULT 885
AX825112 LOCUS AX825112 Sequence 10 from Patent WO03072818.
ACCESSION AX825112
VERSION AX825112.1 GI:39750841
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 10 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"
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 /bound_moiety="Biotin"
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 /note="LNA-T (Locked Nucleic Acid) "
 /mod_base=OTHER
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9
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 /mod_base=OTHER
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 /mod_base=OTHER
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 /note="LNA-T (Locked Nucleic Acid) "
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18
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 /mod_base=OTHER


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modified_base 12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803
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19 GAAAAAAAAAAAAAAAAA 1

RESULT 889
AX825142/c
LOCUS AX825142 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 40 from Patent WO03072818.
ACCESSION AX825142
VERSION AX825142.1 GI:39750871
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 40 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 6
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modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803
|||||
19 GAAAAAAAAAAAAAAAAA 1

RESULT 890
AX825144/c
LOCUS AX825144 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 40 from Patent WO03072818.
ACCESSION AX825144
VERSION AX825144.1 GI:39750871
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 40 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
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Sequenz: Capture-Oligonukleotid"
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/bound_moiety="Biotin"
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modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
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/note="LNA-T (Locked Nucleic Acid) "
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LOCUS AX825144 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 42 from Patent WO03072818.
ACCESSION AX825144
VERSION AX825144.1 GI:39750873
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 42 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
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/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803
|||||
19 GAAAAAAAAAAAAAAAAA 1

RESULT 891
AX825145/c
LOCUS AX825145 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 43 from Patent WO03072818.
ACCESSION AX825145
VERSION AX825145.1 GI:39750874
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 43 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
1..21
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Sequenz: Capture-Oligonukleotid"
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/bound_moiety="Biotin"
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/mod_base=OTHER
modified_base 18
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Query Match      0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0;
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Dy 2785 GAAAAAAAAAAAAAAA 2803

Db 19 GAAAAAAAAAAAAAAA 1

RESULT 892
AX825146/c 21 bp DNA linear PAT 11-DEC-2003

LOCUS AX825146 Sequence 44 from Patent WO03072818.

DEFINITION AX825146

ACCESSION AX825146

VERSION AX825146.1 GI:39750875

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 Boenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 44 04 SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
 location/Qualifiers

FEATURES
source

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modified_base
modified_base
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modified_base
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modified_base
modified_base

/bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

1 .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid)"
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6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0;

Best Local Similarity 100.0%; Pred. No. 5.4e+02; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2785 GAAAAAAAAAAAAAAAAAAAAA 2803
Db	19 GAAAAAAAAAAAAAAAAAAAAA 1
RESULT 893	
LOCUS	AX825148/c 21 bp DNA PAT 11-DEC-2003
DEFINITION	Sequence 46 from Patent WO03072818.
ACCESSION	AX825148
VERSION	AX825148.1 GI:39750877
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
	artificial sequences.
REFERENCE	1
AUTHORS	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE	Method for sorting single-stranded nucleic acids
JOURNAL	Patent: WO 03072818-A 46 04-SEP-2003; Degussa Biactives GmbH (DE) Location/Qualifiers
FEATURES	1. 21
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misc_binding	1 /bound_moiety="Biotin"
modified_base	3 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base	6 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base	9 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base	12 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base	15 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base	18 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
Query Match	0.7%; Score 19; DB 1; Length 21;
Best Local Similarity	100.0%; Pred. No. 5.4e+02;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2785 GAAAAAAAAAAAAAAAAAAAAA 2803
Db	19 GAAAAAAAAAAAAAAAAAAAAA 1
RESULT 894	
LOCUS	AX825149/c 21 bp DNA PAT 11-DEC-2003
DEFINITION	Sequence 47 from Patent WO03072818.
ACCESSION	AX825149
VERSION	AX825149.1 GI:39750878
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
	artificial sequences.
REFERENCE	1
AUTHORS	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE	Method for sorting single-stranded nucleic acids

JOURNAL Patent: WO 03072818-A 47 04-SEP-2003;
 Degussa Bioactives GmbH (DE)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:32630"
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"
 misc_binding 1
 /bound_moiety="Biotin"
 modified_base 3
 /note="LNA-T (Locked Nucleic Acid) "
 modified_base 6
 /mod_base=OTHER
 modified_base 9
 /note="LNA-T (Locked Nucleic Acid) "
 /mod_base=OTHER
 modified_base 12
 /note="LNA-T (Locked Nucleic Acid) "
 /mod_base=OTHER
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 modified_base 19
 /note="LNA-T (Locked Nucleic Acid) "
 /mod_base=OTHER

Query Match 0.7%; Score 19; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803
 Db 19 GAAAAAAAAAAAAAAAAA 1

RESULT 895
 LOCUS AX825156 21 bp DNA linear PAT 11-DEC-2003
 DEFINITION Sequence 54 from Patent WO03072818.
 ACCESSION AX825156
 VERSION AX825156.1 GI:39750885
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
 TITLE Method for sorting single-stranded nucleic acids
 JOURNAL Patent: WO 03072818-A 54 04-SEP-2003;
 Degussa Bioactives GmbH (DE)
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"
 misc_binding 1
 /bound_moiety="Biotin"
 modified_base 3
 /note="LNA-T (Locked Nucleic Acid) "
 modified_base 6
 /mod_base=OTHER
 modified_base 9
 /note="LNA-T (Locked Nucleic Acid) "
 /mod_base=OTHER
 modified_base 12
 /note="LNA-T (Locked Nucleic Acid) "
 /mod_base=OTHER

/note="LNA-T (Locked Nucleic Acid) "
 /mod_base=OTHER
 modified_base 15
 /note="LNA-T (Locked Nucleic Acid) "
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Query Match 0.7%; Score 19; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
 Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 896
 LOCUS AX825156/c 21 bp DNA linear PAT 11-DEC-2003
 DEFINITION Sequence 54 from Patent WO03072818.
 ACCESSION AX825156
 VERSION AX825156.1 GI:39750885
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
 TITLE Method for sorting single-stranded nucleic acids
 JOURNAL Patent: WO 03072818-A 54 04-SEP-2003;
 Degussa Bioactives GmbH (DE)
 FEATURES Location/Qualifiers
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 /bound_moiety="Biotin"
 modified_base 3
 /note="LNA-T (Locked Nucleic Acid) "
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QY 2786 AAAAAAAAAAAAAAAAAA 2804
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 897
 LOCUS AX825157 21 bp DNA linear PAT 11-DEC-2003

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DEFINITION Sequence 55 from Patent WO03072818.
ACCESSION AX825157
VERSION AX825157.1 GI:39750886
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 55 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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/db_xref="taxon:32630"
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 898
AX825157 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825157/c
DEFINITION Sequence 55 from Patent WO03072818.
ACCESSION AX825157
VERSION AX825157.1 GI:39750886
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 55 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
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QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19
RESULT 899
AR164336 22 bp DNA linear PAT 17-OCT-2001
LOCUS AR164336
DEFINITION Sequence 19 from patent US 6271369.
ACCESSION AR164336
VERSION AR164336.1 GI:16235464
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 19 07-AUG-2001;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19
RESULT 900
I31828 22 bp DNA linear PAT 06-FEB-1997
LOCUS I31828
DEFINITION Sequence 19 from patent US 5583032.
ACCESSION I31828
VERSION I31828.1 GI:1822619
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 19 10-DEC-1996;
FEATURES
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 901

LOCUS

I69425 169425 22 bp DNA linear PAT 04-FEB-1998

DEFINITION Sequence 19 from patent US 5677289.

ACCESSION I69425

VERSION I69425.1 GI:2831547

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 22)

AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.

TITLE Method of cleaving specific strands of RNA and medical treatments thereby

JOURNAL Patent: US 5677289-A 19 14-OCT-1997;

FEATURES Location/Qualifiers

source

1..22

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Query Match

0.7%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 902

LOCUS

BD244857 23 bp DNA linear PAT 17-JUL-2003

DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.

ACCESSION BD244857

VERSION BD244857.1 GI:33054627

KEYWORDS JP 2002532063-A/2.

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1 (bases 1 to 23)

AUTHORS Pelletier,J. and Das,M.

TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable

JOURNAL Patent: JP 2002532063-A 2 02-OCT-2002;

COMMENT MCGILL UNIVERSITY

OS Artificial Sequence

PN JP 2002532063-A/2

PD 02-OCT-2002

PF 06-OCT-1999 JP 2000574722

PR 07-OCT-1998 CA 2246623

PI JERRY PELLETIER,MANJULA DAS

PC C12N15/09,C12Q1/68,C12N15/00

CC Description of Artificial Sequence: synthetic oligonucleotide

FH Key Location/Qualifiers

FT source 1..23

Location/Qualifiers

1..23

Location/Qualifiers

1..23

Location/Qualifiers

1..23

Location/Qualifiers

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Location/Qualifiers

1..23

Location/Qualifiers

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Location/Qualifiers

1..23

Query Match

0.7%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 23 AAAAAAAAAAAAAAAAAA 5

RESULT 903

LOCUS

BD244863 23 bp DNA linear PAT 17-JUL-2003

DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.

ACCESSION BD244863

VERSION BD244863.1 GI:33054633

KEYWORDS JP 2002532063-A/8.

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1 (bases 1 to 23)

AUTHORS Pelletier,J. and Das,M.

TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable

JOURNAL Patent: JP 2002532063-A 8 02-OCT-2002;

COMMENT MCGILL UNIVERSITY

OS Artificial Sequence

PN JP 2002532063-A/8

PD 02-OCT-2002

PF 06-OCT-1999 JP 2000574722

PR 07-OCT-1998 CA 2246623

PI JERRY PELLETIER,MANJULA DAS

PC C12N15/09,C12Q1/68,C12N15/00

CC Description of Artificial Sequence: synthetic oligonucleotide

CC N = 3-Nitropyroole

CC N = 3-Nitropyroole

FH Key Location/Qualifiers

FT modified base (8)

FT modified base (18).

FT Location/Qualifiers

1..23

Location/Qualifiers

1..23

Location/Qualifiers

1..23

Location/Qualifiers

1..23

Location/Qualifiers

1..23

Location/Qualifiers

1..23

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Location/Qualifiers

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Location/Qualifiers

1..23

Location/Qualifiers

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PN      JP 2002532063-A/10
PD      02-OCT-2002
PF      06-OCT-1999 JP 2000574722
PR      07-OCT-1998 CA 2246623
PI      JERRY PELETER, MANJULA DAS
PC      C12N15/09, C12Q1/68, C12N15/00
CC      Description of Artificial Sequence: synthetic oligonucleotide
CC      N - inosine
CC      N = inosine
FH      Key Location/Qualifiers
FT      modified_base (8)
FT      modified_base (18).
FT      Location/Qualifiers
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        /mol_type="genomic DNA"
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Best Local Similarity	90.5%;	Pred. No. 7e+02;		
Matches 19;	Conservative	0;	Mismatches	2; Indels

QY	2166	TTTTTTTTTTTTTTTTTTTT	21866
Db	1	TTTTTTTTTTTTTTTTTTTT	21

RESULT	905		
I79497			
LOCUS	I79497	23 bp	DNA
DEFINITION	Sequence 4 from patent US 5707807.		linear
ACCESSION	I79497		PAT 10-JUN-1998
VERSION	I79497.1	GI:3207787	

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SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Kato, K.
TITLE        Molecular indexing for expressed gene analysis
JOURNAL      Patent: US 5707807-A 4 13-JAN-1998;
FEATURES     Location/Qualifiers
              1..23
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Query Match      0.7%;   Score 19;   DB 1;   Length 23;
Best Local Similarity 100.0%;   Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT	906
BD133515	
LOCUS	
DEFINITION	BD133515 23 bp DNA linear PAT 18-SEP-2002
	Method for testing remedy or preventive for osteoporosis or
	articular rheumatism.
ACCESSION	BD133515
VERSION	BD133515.1 GI:23228460
KEYWORDS	JP 2002051782-A/6.
SOURCE	synthetic construct
ORGANISM	synthetic construct
	artificial sequences.
REFERENCE	1 (bases 1 to 23)
AUTHORS	Okutsu,J., Kawaida,R., Otsuka,T. and Takahashi,W.
TITLE	Method for testing remedy or preventive for osteoporosis or
JOURNAL	articular rheumatism
	Patent: JP 2002051782-A 6 19-FEB-2002;
	SANKYO CO LTD
COMMENT	OS Artificial Sequence

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PN      JP 2002051782-A/6
PD      19-FEB-2002
PF      09-AUG-2000 JP 2000241413
PI      JUNICHI OKUTSU, REMI KAWAIDA, TOSHIAKI OTSUKA, WATARU TAKAHASHI
PC      C12N15/09, C07K14/47, C07K16/18, C12Q1/02, C12Q1/66, C12Q1/68, PC
        G01N33/15,
PC      G01N33/50, G01N33/50, G01N33/53//C12P21/08, C12N15/00 CC
Description of Artificial Sequence: PCR primer for molecular CC
Indexing
FH      Key      Location/Qualifiers
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FT      Location/Qualifiers
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FEATURES
source

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Query Match	0.7%;	Score 19;	DB 1;	Length 23;
Best Local Similarity	100.0%;	Pred. No. 7e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY		2163	TCCCTTTT TTTTTT TT	2181
Dd		4	TCCCTTTT TTTTTT TT	22

RESULT	907
AR431310/c	
LOCUS	AR431310
DEFINITION	Sequence 4 from patent US 6651008.
ACCESSION	AR431310
VERSION	AR431310.1 GI:40193278
	24 bp DNA linear PAT 18-DEC-2003

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SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 24)
AUTHORS         Vaisberg, E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
TITLE           database system including computer code for predictive cellular
                bioinformatics
JOURNAL         Patent: US 6651008-A 4 18-NOV-2003;
FEATURES        Location/Qualifiers
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Query Match      0.7%;   Score 19;   DB 1;   Length 24;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2786	AAAAAAAAAAAAAAAAAAAAA	2804
Db	24	AAAAAAAAAAAAAAAAAAAAA	6

RESULT	908
AX817782	
LOCUS	
DEFINITION	AX817782 24 bp DNA
ACCESSION	Sequence 18 from Patent WO02067861.
VERSION	AX817782
KEYWORDS	AX817782.1 GI:39722977
SOURCE	.
ORGANISM	synthetic construct
	synthetic construct
	artificial sequences.
REFERENCE	1
AUTHORS	.
TITLE	Oncolytic adenoviral vectors
JOURNAL	Patent: WO 02067861-A 18 06-SEP-2002;
FEATURES	Location/Qualifiers
source	1..24
	/organism="synthetic construct"


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                                polya_site
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Best Local Similarity 100.0%; Score 19; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
    |||
    3 AAAAAAAAAAAAAAAAAA 21

RESULT 909
LOCUS AX838369 24 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 8 from Patent WO02068627.
ACCESSION AX838369
VERSION AX838369.1 GI:39922050
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS
TITILE Vector constructs
JOURNAL Patent: WO 02068627-A 8 06-SEP-2002;
FEATURES
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            /note="Viral vector sequence"
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            polya_site
            3..24

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Best Local Similarity 100.0%; Score 19; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
    |||
    3 AAAAAAAAAAAAAAAAAA 21

RESULT 910
LOCUS E13209 24 bp DNA linear PAT 27-APR-1998
DEFINITION DNA probe.
ACCESSION E13209
VERSION E13209.1 GI:3252014
KEYWORDS JP 1997149799-A/1.
SOURCE unidentifed
ORGANISM unidentifed
REFERENCE 1 (bases 1 to 24)
AUTHORS Kanbara,H., Okano,K. and Uematsu,K.
TITILE ANALYSIS OR DETECTION OF NUCLEIC ACID AND ANALYSER OR INSPECTION
JOURNAL DEVICE OF NUCLEIC ACID
Patent: JP 1997149799-A 1 10-JUN-1997;
HITACHI LTD
OS None
OC Artificial sequences.
PN JP 1997149799-A/1
PD 10-JUN-1997
PF 30-NOV-1995 JP 1995311949
PI KANBARA HIDEKI, OKANO KAZUNOBU, UEMATSU KAZUMUNE PC
C12Q1/68,C07H21/04,C12M1/00,C12N15/09,C12Q1/44,C12Q1/48, PC
G01N27/447,
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PC G01N27/447,G01N33/50;
CC strandedness: Single;
CC topology: linear;
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            /db_xref="taxon:32644"

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Best Local Similarity 100.0%; Score 19; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
    |||
    1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 911
LOCUS AX394507 25 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 52 from Patent WO0218638.
ACCESSION AX394507
VERSION AX394507.1 GI:21065645
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
TITILE Detection of cyp2d6 polymorphisms
JOURNAL Patent: WO 0218638-A 52 07-MAR-2002;
FEATURES
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Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
    |||
    3 AAAAAAAAAAAAAAAAAA 21

RESULT 912
LOCUS AX394514 25 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 59 from Patent WO0218638.
ACCESSION AX394514
VERSION AX394514.1 GI:21065652
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
TITILE Detection of cyp2d6 polymorphisms
JOURNAL Patent: WO 0218638-A 59 07-MAR-2002;
FEATURES
    Location/Qualifiers
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            /mol_type="unassigned DNA"
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Matches 19;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	2786	AAAAAAAAAAAAAAAAAAAA	2804
Db	28	AAAAAAAAAAAAAAAAAAAA	10
RESULT 920			
LOCUS	AR371171	28 bp	DNA
DEFINITION	Sequence 10 from patent US 6395306.	linear	PAT 12-SEP-2003
ACCESSION	AR371171		
VERSION	AR371171.1	GI:34608085	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 28)		
TITLE	Cui, X. and Lu, Y.		
JOURNAL	Bee venom protein and gene encoding same		
FEATURES	Patent: US 6395306-A 10 28-MAY-2002;		
source	Location/Qualifiers		
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	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	0.7%;	Score 19;	DB 1; Length 28;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;	
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	2165	CTTTTCTTTTCTTTTCTTTT	2183
Db	10	CTTTTCTTTTCTTTTCTTTT	28
RESULT 921			
LOCUS	BD015304	28 bp	DNA
DEFINITION	BD015304		
Primer single-stranded DNA, process for preparing double-stranded			
cDNA by using the same and process for amplifying one side			
single-stranded DNA.			
ACCESSION	BD015304		
VERSION	BD015304.1	GI:22556442	
KEYWORDS	JP 2001204472-A/5.		
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	1 (bases 1 to 28)		
TITLE	Nakamura, T.		
JOURNAL	Primer single-stranded DNA, process for preparing double-stranded		
Patent: JP 2001204472-A 5 31-JUL-2001;			
SUMITOMO ELECTRIC INDUSTRIES LTD			
OS	Artificial Sequence		
PN	JP 2001204472-A/5		
PD	31-JUL-2001		
PF	21-JAN-2000 JP 2000012535		
PI	TAKEISHI NAKAMURA		
PC	C12N15/09, C12P19/34, G01N33/50//C12Q1/68, C12N15/00 CC		PCR
primer			
FH	Key	Location/Qualifiers.	
source	Location/Qualifiers		
	1. 28		
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	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
Query Match	0.7%;	Score 19;	DB 1; Length 28;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;	

	Matches	19;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	2165	CTTTTTTTTTTTTTTTTT	TTTTT	2183						
Db	10	CTTTTTTTTTTTTTTTTT	TTTTT	28						

RESULT 922
I65795/c

LOCUS	I65795	13 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence from patent US 5668295.				
ACCESSION	I65795				
VERSION	I65795.1	GI:2482365			
KEYWORDS	.				

SOURCE	ORGANISM
Unknown.	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 29)
TITLE	Wahab,S.Z. and Malik,V.S. Protein involved in nicotine synthesis, DNA encoding, and use of

TITLE	JOURNAL	FEATURES	source
Protein involved in nicotine synthesis, DNA encoding, and use of sense and antisense DNAs corresponding thereto to affect nicotine content in transgenic tobacco cells and plants	Patent: US 5668295-A 13 16-SEP-1997;	Location/Qualifiers	1. .29

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/organism="unknown"
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Query Match      0.7%; Score 19; DB 1; length 29;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2786 AAAAAAAAAAAAAAAAAA 2804
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Db      29 AAAAAAAAAAAAAAAAAA 11
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RESULT 923			
AR268128			
LOCUS	AR268128	29 bp	DNA
DEFINITION	Sequence 5 from patent US 6498025.	1 linear	PAT 10-APR-2003

VERSION	AR268128.1	GI:29698371
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	

REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 29)
TITLE	Miller, J.E.
JOURNAL	Methods and compositions for cDNA synthesis
	Patent: US 6498025-A 5 24-DEC-2002;

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FEATURES      Location/Qualifiers
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                  /organism="unknown"
                  /mol_type="genomic DNA"

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Query Match	0.7%;	Score 19;	DB 1;	Length 29;
Best Local Similarity	100.0%;	Pred. No. 1.3e+03;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2786	AAAAAAAAAAAAAAAA	2804
Db	1	AAAAAAAAAAAAAAAA	19

RESULT 924					
AX079109/c					
LOCUS	AX079109	30 bp	DNA	linear	PAT 22-FEB-2001
DEFINITION	Sequence 7 from Patent WO0106226.				

ACCESSION	AX079109
VERSION	AX079109.1
KEYWORDS	GI:13158683
SOURCE	synthetic construct

ORGANISM synthetic construct
artificial sequences.

REFERENCE	1
AUTHORS	Mueller, O.
TITLE	Methods for determining the proliferation activity of cells
JOURNAL	Patent: WO 0106226-A 7 25-JAN-2001;

Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
Location/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Oligonucleotide"
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Query Match	0.7%;	Score 19;	DB 1;	Length 30;
Best Local Similarity	100.0%;	Pred. No. 1.4e+03;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY 2786 AAAAAAAAAAAAAAAAAA 2804
    ||||| ||||| |||||
Db 28 AAAAAAAAAAAAAAAAAA 10
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RESULT	925		
AX196237			
LOCUS	AX196237	30 bp	DNA
DEFINITION	Sequence 68 from Patent WO0151665.	linear	PAT 28-AUG-2001

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AX196237 AX196237.1	GI.15386440
	synthetic construct	
	synthetic construct	
	artificial sequences.	

REFERENCE	AUTHORS	TITLE
1	Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A. and Li, Z.	Nanoparticles having oligonucleotides attached thereto and uses therefor

JOURNAL	Patent: WO 0151665-A 68 19-JUL-2001;
FEATURES	Nanosphere, Inc. (US)
source	Location/Qualifiers
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/organism="synthetic construct"  
/mol_type="unassigned DNA"  
/db_xref="taxon:32630"  
/note="random synthetic sequence"
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Query Match	0.7%;	Score 19;	DB 1;	Length 30;
Best Local Similarity	100.0%;	Pred. No. 1.4e+03;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	2786	AAAAAAAAAAAAAAAAAA	2809
Db	1	AAAAAAAAAAAAAAAAAA	19

RESULT	926		
AX440138			
LOCUS	AX440138	30 bp	DNA
DEFINITION	Sequence 68 from Patent WO0173123.		linear
			PAT 28-JUN-2002

KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.

REFERENCE
AUTHORS
1
artificial sequences:
Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J.

TITLE	AUTHORS
Nanoparticles having oligonucleotides attached thereto and uses	Marking, C.R., Weissinger, R.E., Muesel, R.C., and Schmitt, J.C.
	Elghamian, R., Taton, T.A., Park, S.-J., and Li, Z.

JOURNAL Patent: WO 0173123-A 68 04-OCT-2001;

Nanosphere, Inc. (US)

FEATURES
source

Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 0.7%; Score 19; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
1 AAAAAAAAAAAAAAAAAA 19

RESULT 927

AX465324 30 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 68 from Patent WO0218643.
ACCESSION AX465324
VERSION AX465324.1 GI:21899687
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS 1
Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J.,
Elghanian, R., Taton, T.A., Garimella, V., Li, Z. and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0218643-A 68 07-MAR-2002;
Nanosphere, Inc. (US)
FEATURES
source
Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 0.7%; Score 19; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
1 AAAAAAAAAAAAAAAAAA 19

RESULT 928
AX556137 30 bp DNA linear PAT 27-NOV-2002
LOCUS
DEFINITION Sequence 68 from Patent WO0246472.
ACCESSION AX556137
VERSION AX556137.1 GI:25899519
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS 1
Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J.,
Elghanian, R., Taton, T.A., Garimella, V., Li, Z. and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0246472-A 68 13-JUN-2002;
Nanosphere, Inc. (US)
FEATURES
source
Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 0.7%; Score 19; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
1 AAAAAAAAAAAAAAAAAA 19

RESULT 929

AX079108 30 bp DNA linear PAT 22-FEB-2001
LOCUS
DEFINITION Sequence 6 from Patent WO0106226.
ACCESSION AX079108
VERSION AX079108.1 GI:13158682
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS 1
Mueller, O.
TITLE Methods for determining the proliferation activity of cells
JOURNAL Patent: WO 0106226-A 6 25-JAN-2001;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"

Query Match 0.7%; Score 19; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
7 AAAAAAAAAAAAAAAAAA 25

RESULT 930
AX080522 32 bp DNA linear PAT 26-FEB-2001
LOCUS
DEFINITION Sequence 10 from Patent WO0109291.
ACCESSION AX080522
VERSION AX080522.1 GI:13162176
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS 1
Brownlee, G.G., Fodor, E.S. and Poen, L.S.
TITLE Attenuated influenza virus useful as vaccine
JOURNAL Patent: WO 0109291-A 10 08-FEB-2001;
ISIS INNOVATION LIMITED (GB)
FEATURES
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Location/Qualifiers
1. .32
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/db_xref="taxon:32630"
/note="PRIMER"

Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
32 AAAAAAAAAAAAAAAAAA 14

RESULT 931
I32124/c

LOCUS I32124 32 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 14 from patent US 5585242.
ACCESSION I32124
VERSION I32124.1 GI:1822915
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Bouma,S.R., Khalil,O.S. and Pabich,E.K.
TITLE Method for detection of nucleic acid using total internal
reflectance
JOURNAL Patent: US 5585242-A 14 17-DEC-1996;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 32 AAAAAAAAAAAAAAAAAA 14
RESULT 932
LOCUS AR274390 32 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 51 from patent US 6506564.
ACCESSION AR274390
VERSION AR274390.1 GI:29706836
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6506564-A 51 14-JAN-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19
RESULT 933
LOCUS AR344932 32 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 51 from patent US 6582921.
ACCESSION AR344932
VERSION AR344932.1 GI:33741013
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
thereof
JOURNAL Patent: US 6582921-A 51 24-JUN-2003;

FEATURES
source Location/Qualifiers
1..32
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19
RESULT 934
LOCUS AR382308 32 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 51 from patent US 6610491.
ACCESSION AR382308
VERSION AR382308.1 GI:40090720
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6610491-A 51 26-AUG-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19
RESULT 935
LOCUS AR429649 32 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 51 from patent US 6645721.
ACCESSION AR429649
VERSION AR429649.1 GI:40189945
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6645721-A 51 11-NOV-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

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RESULT 936
AX196220
LOCUS
DEFINITION Sequence 51 from Patent WO0151665.
ACCESSION AX196220
VERSION AX196220.1 GI:15386423
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A. and Li,Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0151665-A 51 19-JUL-2001;
Nanosphere, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match
0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 937
AX440121
LOCUS
DEFINITION Sequence 51 from Patent WO0173123.
ACCESSION AX440121
VERSION AX440121.1 GI:21664932
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0173123-A 51 04-OCT-2001;
Nanosphere, Inc. (US)
FEATURES
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match
0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 938
AX465307
LOCUS
DEFINITION Sequence 51 from Patent WO0218643.
ACCESSION AX465307
VERSION AX465307.1 GI:21899670
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KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0218643-A 51 07-MAR-2002;
Nanosphere, Inc. (US)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match
0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 939
AX556120
LOCUS
DEFINITION Sequence 51 from Patent WO0246472.
ACCESSION AX556120
VERSION AX556120.1 GI:25899502
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0246472-A 51 13-JUN-2002;
Nanosphere, Inc. (US)
FEATURES
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1..32
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match
0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 940
AR174572/c
LOCUS
DEFINITION Sequence 27 from patent US 6307024.
ACCESSION AR174572
VERSION AR174572.1 GI:17914892
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 34)
Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
```

TITLE Hammond,A.K.
JOURNAL Cytokine zalphal1 ligand
Patent: US 6307024-A 27 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 34;
Best Local Similarity 100.0%; Pred.No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
DB 34 AAAAAAAAAAAAAAAAAA 16

RESULT 941
LOCUS BD248965 34 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel cytokine ZALPHA11 ligand.
ACCESSION BD248965
VERSION BD248965.1 GI:33058735
KEYWORDS JP 2002537839-A/26.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 34)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Novel cytokine ZALPHA11 ligand
JOURNAL Patent: JP 2002537839-A 26 12-NOV-2002;
COMMENT ZYMOGENETICS INC

OS Artificial Sequence
PN JP 2002537839-A/26

PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603382
PR 09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR
01-JUL-1999 US 60/142013
PI JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C PI
FOSTER,

PI RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
PI STACEY R DILLON,ANGELA K HAMMOND
PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
PC C07K14/53,
PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02

CC Oligonucleotide primer ZC18698
FH Key Location/Qualifiers
FT source 1..34
/organism='Artificial Sequence'.
location/Qualifiers

1..34
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19; DB 1; Length 34;
Best Local Similarity 100.0%; Pred.No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
DB 34 AAAAAAAAAAAAAAAAAA 16

RESULT 942
LOCUS AR374064 34 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 27 from patent US 6605272.

ACCESSION AR374064
VERSION AR374064.1 GI:40076636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 34)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Methods of using zalphal1 ligand
JOURNAL Patent: US 6605272-A 27 12-AUG-2003;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 34;
Best Local Similarity 100.0%; Pred.No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
DB 34 AAAAAAAAAAAAAAAAAA 16

RESULT 943
LOCUS AX179588 34 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 11 from Patent WO0146422.
ACCESSION AX179588
VERSION AX179588.1 GI:15132019
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Presnell,S.R. and Kindsvogel,W.
TITLE Cytokine zcyto18
JOURNAL Patent: WO 0146422-A 11 28-JUN-2001;
COMMENT ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers
source 1..34
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer ZC18698"

Query Match 0.7%; Score 19; DB 1; Length 34;
Best Local Similarity 100.0%; Pred.No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
DB 34 AAAAAAAAAAAAAAAAAA 16

RESULT 944
LOCUS AR029830 35 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5861244.
ACCESSION AR029830
VERSION AR029830.1 GI:5943044
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 35)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 19 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..35


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/organism="unknown"  
/mol_type="unassigned DNA"
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Query Match	0.7%;	Score 19;	DB 1;	length 35;
Best Local Similarity	100.0%;	Pred. No. 2e+03;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.

QY	2785	GAAAAAAAAAAAAAAAAA	2803
Db	35	GAAAAAAAAAAAAAAAAA	17

RESULT	945			
LOCUS	AX516913/c			
DEFINITION	AX516913	41 bp	DNA	
ACCESSION	AX516913	Sequence 3111 from Patent WO02052044.		linear
VERSION	AX516913.1	GI:23565110		PAT 05-OCT-2002
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE	1	Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
AUTHORS		Detection of genetic polymorphisms
TITLE		Patent: WO 02052044-A 3111 04-JUL-2002;
JOURNAL		Riken (JP)
FEATURES		Location/Qualifiers
source	1..41	
		/organism="Homo sapiens"
		/mol_type="unassigned DNA"
		/db_xref="taxon:9606"

Query Match	0.7%;	Score 19;	DB 1;	Length 41;
Best Local Similarity	100.0%;	Pred. No. 2.4e+03;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2786	AAAAAAAAAAAAAAAAAAAA	2804	
Db	40	AAAAAAAAAAAAAAAAAAAA	22	

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RESULT 946
AX519424/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AX519424
Sequence 5622 from Patent WO02052044.
AX519424
AX519424.1 GI:23569690
41 bp DNA linear PAT 05-OCT-2002
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
Detection of genetic polymorphisms
Patent: WO 02052044-A 5622 04-JUL-2002;
Riken (JP)
location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match	0.7%;	Score 19;	DB 1;	Length 41;
Best Local Similarity	100.0%;	Pred. No. 2.4e+03;		
Matches	19;	Conservative	0;	Mismatches 0;
Indels				Gaps 0;
QY	2786	AAAAAAAAAAAAAAAAAAAA	2804	
Db	40	AAAAAAAAAAAAAAAAAAAA	22	

RESULT	947
BD085544/c	
LOCUS	BD085544
DEFINITION	22 bp RNA linear
ACCESSION	PAT 27-AUG-2002
	Method of comparison and detection of RNA amount and DNA amount.
	BD085544

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
1 (bases 1 to 22)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

INVENTOR
SHIMADA, A.
TITLE
Method of comparison and detection of RNA amount and DNA amount
PATENT
JP 2001333800-A 1 04-DEC-2001;

COMMENT	OS	Homo sapiens (human)
---------	----	----------------------

PN JP 2001333800-A/1

PD 04-DEC-2001

30-MAY-2000 JP 2000160324

PI KAORI SHIMADA
PC C13001 / C00 C13001 F / 00 C010003 (C00 C010001 F / 00

CC Method of comparison and detection of DDT residues in rice

amount of comparison of RNA amount and DNA co

FH	Key	Location/Qualifiers
FT	source	1. .22

FEATURES	Location/Qualifiers
source	1.1.22

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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

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Query Match	0.7%;	Score 18.8;	DB 1;	length 22;
Best Local Similarity	90.9%;	Pred. No. 6.7e+02;		
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QY	2168	TTTTTTTTTTTTTTTTTTTAAAC	2189
Db	22	TTTTTTTTTTTTTTTTTGATC	1

RESULT	948		
BD245230/c			
LOCUS			
BD245230	23 bp	DNA	linear
Method of electrochemically detecting nucleic acid.			PAT 17-JUL-2003

VERSION BD245230.1 GI:33055000
KEYWORDS JP 2002532386-A/16.

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 23)

AUTHORS Hartwich, G. and Heller, A.

JOURNAL Patent: JP 2002532386-A 16 02-OCT-2002;

COMMENT	OS	Artificial Sequence

PN JP 2002532386-A/16

PD	02-OCT-2002
DT	10 NOV 2002

PF	19-NOV-1999	JP	2000583928
DP	23-NOV-1998	DE	108 E3 657

IN 23-NOV-1958 DE 198 33 3
GERHARD HARTWICH ADAM HEITZ

PC C07H21/00, C07H21/02, C07H21/04, C12N15/09, C12O1/68, G01N27/13, B6

GOIN27/30,

PC

G01N27/416, G01N27/48, G01N33/483, G01N33/50, G01N33/566, C12N15/00, PC

GOIN2//46
CC Wetbed -6 3-1-1977

CC	Method of electrochemically detecting nucleic acid	FH	Key
	Location/Onsififers		

FT source 1 23

FT 1. 1.23 /organism='Artificial Semience'

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		/mol_type="genomic DNA"	
		/db_xref="taxon:32630"	
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Best Local Similarity		90.9%;	Pred. No. 7.6e+02;
Matches	20; Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
QY	2169 TTTT	TTTTTTTTTTTTTTTAACT	2190
Db	23 TTTT	TTTTTTTTTTTTTTGGCT	2
RESULT 949			
LOCUS	E12393	23 bp	DNA linear PAT 27-APR-1998
DEFINITION	E12393 Oligonucleotide primer.		
ACCESSION	E12393		
VERSION	E12393.1	GI:3251226	
KEYWORDS	JP 1996322598-A/3.		
SOURCE	unidentified		
ORGANISM	unidentified		
	unclassified.		
REFERENCE	1	(bases 1 to 23)	
AUTHORS	Katou, K.		
TITLE	INDEXING METHOD OF DNA MOLECULE		
JOURNAL	Patent: JP 1996322598-A 3 10-DEC-1996;		
	RES DEV CORP OF JAPAN		
COMMENT	OS	None	
	OC	Artificial sequences.	
	PN	JP 1996322598-A/3	
	PD	10-DEC-1996	
	PF	12-SEP-1995 JP 1995234122	
	PR	28-MAR-1995 JP 95P 69695	
	PI	KATOU KIKUYA	
	PC	C12Q1/68, C07H21/02, C07H21/04, C12N15/09;	
	CC	strandedness: Single;	
	CC	topology: Linear;	
	FH	Key	Location/Qualifiers
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FEATURES		Location/Qualifiers	
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		/mol_type="genomic DNA"	
		/db_xref="taxon:32644"	
Query Match		0.7%;	Score 18.8; DB 1; Length 23;
Best Local Similarity		90.9%;	Pred. No. 7.6e+02;
Matches	20; Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
QY	2162 CTCCT	TTTTTTTTTTTTTTT	2183
Db	1 CTC	CAGT	TTTTTTTTTTTTTTT 22
RESULT 950			
LOCUS	AX043130	25 bp	DNA linear PAT 23-NOV-2000
DEFINITION	Sequence 696 from Patent WO0065088.		
ACCESSION	AX043130		
VERSION	AX043130.1	GI:11341738	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE	1		
AUTHORS	Ulfendahl, P.J. and Wong, K.C.		
TITLE	Primers for identifying typing or classifying nucleic acids		
JOURNAL	Patent: WO 0065088-A 696 02-NOV-2000;		

FEATURES	Amer sham Pharmacia Biotech AB (SE)
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Best Local Similarity	90.9%; Pred. No. 9.6e+02;
Matches	20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	2173 TTTT TTTT TTTT TTTT TTA CTTTGA 2194 Db 1 TTTT TTTT TTTT TTTT GAATTG A 22
RESULT 951	
AX043131	25 bp DNA linear PAT 23-NOV-2000
LOCUS	AX043131
DEFINITION	Sequence 697 from Patent WO0065088.
ACCESSION	AX043131
VERSION	AX043131.1 GI:11341739
KEYWORDS	synthetic construct synthetic construct artificial sequences.
SOURCE	
ORGANISM	
REFERENCE	1 Ulfendahl,P.J. and Wong,K.C. Primers for identifying typing or classifying nucleic acids Patent: WO 0065088-A 697 02-NOV-2000; Amer sham Pharmacia Biotech AB (SE) location/Qualifiers 1..25 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="DPaI Heterozygote Primer Sequence"
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source	
Query Match	0.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity	90.9%; Pred. No. 9.6e+02;
Matches	20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	2173 TTTT TTTT TTTT TTTT TTA CTTTGA 2194 Db 1 TTTT TTTT TTTT TTTT GAATTG A 22
RESULT 952	
E30823/c	26 bp DNA linear PAT 18-JUN-2001
LOCUS	E30823
DEFINITION	Modified antibody Fab fragment.
ACCESSION	E30823
VERSION	E30823.1 GI:13017253
KEYWORDS	JP 1999341980-A/6. unidentified unidentified unclassified.
SOURCE	
ORGANISM	
REFERENCE	1 (bases 1 to 26) Takashi,S., Izumi,I. and Nobuhiko,M. Modified antibody Fab fragment Patent: JP 1999341980-A 6 14-DEC-1999; TOYOBO CO LTD
AUTHORS	
TITLE	
JOURNAL	
COMMENT	OS Unidentified PN JP 1999341980-A/6 PD 14-DEC-1999 PF 02-JUN-1998 JP 1998152956 PR TAKASHI SAZU,IZUMI INOHARA,NOBUHIKO MAEKAWA PI C12N1/21,C07K16/00,C07K17/08,C07K17/14,C12N15/09,G01N33/531, PC G01N33/547// PC C12P21/08,(C12N1/21,C12R1:19),C12N15/00 CC Strandedness: Single;

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CC Topology: Linear;
FH Key Location/Qualifiers
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PT /organism='Unidentified'.
   Location/Qualifiers
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   /organism="unidentified"
   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

FEATURES
   source

Query Match      0.7%; Score 18.8; DB 1; Length 26;
Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2783 TTGAAAAAATATAAAAAA 2804
Db 24 TCGAAAAATATAAAAAA 3

RESULT 953
AX042549 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 115 from Patent WO0065088.
ACCESSION AX042549
VERSION AX042549.1 GI:11341157
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 115 02-NOV-2000;
        Amersham Pharmacia Biotech AB (SE)
FEATURES
   source
   Location/Qualifiers
   1..25
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   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="DPH1 Homozygote primer sequence"

Query Match      0.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2173 TTTTCTTTTCTTAACTTTGAAG 2197
Db 1 TTTTCTTTTCTTAACTTTTCCAG 25

RESULT 954
AX042942 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 508 from Patent WO0065088.
ACCESSION AX042942
VERSION AX042942.1 GI:11341550
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 508 02-NOV-2000;
        Amersham Pharmacia Biotech AB (SE)
FEATURES
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   Location/Qualifiers
   1..25
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="16S rRNA Homozygote Primer Sequence"

Query Match      0.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query Match      0.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Best Local Similarity 84.0%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2167 TTTTCTTTTCTTAACTTTTAACTT 2191
Db 1 TTTTCTTTTCTTAACTTTTAACTT 25

RESULT 955
AX043077/c 25 bp DNA linear PAT 23-NOV-2000
LOCUS AX043077
DEFINITION Sequence 643 from Patent WO0065088.
ACCESSION AX043077
VERSION AX043077.1 GI:11341685
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 643 02-NOV-2000;
        Amersham Pharmacia Biotech AB (SE)
FEATURES
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   Location/Qualifiers
   1..25
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   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="16S rRNA Homozygote Primer Sequence"

Query Match      0.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2775 TGTAGATTTGAAAAA 2799
Db 25 TTTAAGCAGTGA 1

RESULT 956
AX043230 25 bp DNA linear PAT 23-NOV-2000
LOCUS AX043230
DEFINITION Sequence 796 from Patent WO0065088.
ACCESSION AX043230
VERSION AX043230.1 GI:11341838
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 796 02-NOV-2000;
        Amersham Pharmacia Biotech AB (SE)
FEATURES
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   Location/Qualifiers
   1..25
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   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="DPB1 Heterozygote Primer Sequence"

Query Match      0.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2173 TTTTCTTTTCTTAACTTTGAAG 2197
Db 1 TTTTCTTTTCTTAACTTTTCCAG 25

RESULT 957
AR409915 27 bp RNA linear PAT 18-DEC-2003
LOCUS AR409915
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DEFINITION Sequence 28 from patent US 6635422.
ACCESSION AR409915
VERSION AR409915.1 GI:40161050
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
TITLE Methods for isolating and characterizing endogenous mRNA-protein (mRNA) complexes
JOURNAL Patent: US 6635422-A 28 21-OCT-2003;
FEATURES
Source Location/Qualifiers
1. 27
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 18.6; DB 1; Length 27;
Best Local Similarity 84.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2152 TGATTGTTTCTCCTTTTCTTTT 2176
DB 3 TTAATTCTCTCTTTTCTTTTCTT 27

RESULT 958
LOCUS AX052989 29 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 5 from Patent WO0071749.
ACCESSION AX052989
VERSION AX052989.1 GI:12227091
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and Pignot,M.
TITLE Detection system for analyzing molecular interactions, production and utilization thereof
JOURNAL Patent: WO 0071749-A 5 30-NOV-2000;
FEATURES
Source Aventis Research & Technology GmbH & Co. KG. (DE)
Location/Qualifiers
1. 29
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Beschreibung der kunstlichen Sequenz:Puromycin-Linker"

Query Match 0.7%; Score 18.6; DB 1; Length 29;
Best Local Similarity 80.8%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAAAAAA 2804
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 959
LOCUS AR030917 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861487.
ACCESSION AR030917
VERSION AR030917.1 GI:5944131
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily., Kovacic,F., Tanaka,Y. and Lester,D.Ruth.

TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: US 5861487-A 20 19-JAN-1999;
FEATURES
Source Location/Qualifiers
1. 20
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/mol_type="unassigned DNA"

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2170 TTTTCTTTTCTTTTCTTTTAC 2189
DB 1 TTTTCTTTTCTTTTCTTTTAC 20

RESULT 960
LOCUS I28309 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 20 from patent US 5569832.
ACCESSION I28309
VERSION I28309.1 GI:1819085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: US 5569832-A 20 29-OCT-1996;
FEATURES
Source Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2170 TTTTCTTTTCTTTTCTTTTAC 2189
DB 1 TTTTCTTTTCTTTTCTTTTAC 20

RESULT 961
LOCUS I47310 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5639870.
ACCESSION I47310
VERSION I47310.1 GI:2471275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily. and Tanaka,Y.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: US 5639870-A 11 17-JUN-1997;
FEATURES
Source Location/Qualifiers
1. 20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2170 TTTTCTTTTCTTTTCTTTTAC 2189
DB 1 TTTTCTTTTCTTTTCTTTTAC 20

LOCUS	AX825104	21 bp	DNA	linear	PAT 11-DEC-2003
DEFINITION	Sequence 2 from Patent WO03072818.				
ACCESSION	AX825104				
VERSION	AX825104.1	GI:39750833			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.				
TITLE	Method for sorting single-stranded nucleic acids				
JOURNAL	Patent: WO 03072818-A 2 04-SEP-2003;				
	Degussa Bioactives GmbH (DE)				
FEATURES	location/Qualifiers				
source	1..21				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Beschreibung der kuenstlichen				
	Sequenz:Capture-Oligonukleotid"				
misc_binding	1				
	/bound_moiety="Biotin"				
modified_base	3				
	/note="LNA-T (Locked Nucleic Acid) "				
	/mod_base=OTHER				
modified_base	6				
	/note="LNA-T (Locked Nucleic Acid) "				
	/mod_base=OTHER				
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	/mod_base=OTHER				
modified_base	18				
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	/mod_base=OTHER				
Query Match	0.7%; Score 18.4; DB 1; Length 21;				
Best Local Similarity	95.0%; Pred. No. 6.9e+02;				
Matches	19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	2783 TTGAAAAAAAAAAAAAAAAA 2802				
Db	20 TTAATAAAAAAAAAAAAAAAAAA 1				
RESULT 967					
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LOCUS	AX825136	21 bp	DNA	linear	PAT 11-DEC-2003
DEFINITION	Sequence 34 from Patent WO03072818.				
ACCESSION	AX825136				
VERSION	AX825136.1	GI:39750865			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.				
TITLE	Method for sorting single-stranded nucleic acids				
JOURNAL	Patent: WO 03072818-A 34 04-SEP-2003;				
	Degussa Bioactives GmbH (DE)				
FEATURES	location/Qualifiers				
source	1..21				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Beschreibung der kuenstlichen				
	Sequenz:Capture-Oligonukleotid"				
misc_binding	1				

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Query Match      0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity   95.0%; Pred. No. 6.9e+02;  
Matches    19; Conservative    0; Mismatches     1; Indels       0; Gaps        0;
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Qy	2168 TTTT Db	TTTTTTTTTTTTTTTTTA 2187 1 TTTTTTTTTTTTTTTCA 20
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RESULT 968  
AX825138 LOCUS AX825138 21 bp DNA linear PAT 11-DEC-2003  
DEFINITION Sequence 36 from Patent WO03072818.  
ACCESSION AX825138  
VERSION AX825138.1 GI:39750867  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.  
AUTHORS Method for sorting single-stranded nucleic acids  
TITLE Patent: WO 03072818-A 36 04-SEP-2003;  
JOURNAL Degussa Bioactives GmbH (DE)  
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/mol_type="unassigned DNA"  
/db_xref="taxon:32630"  
/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"
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Query Match	0.7%; Score 18.4; DB 1; Length 21; Best Local Similarity 95.0%; Pred. No. 6.9e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy	2168 TTTT Db	TTTTTTTTTTTTTTTTTA 2187 1 TTTTTTTTTTTTTTTCA 20
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RESULT 968  
AX825138 LOCUS AX825138 21 bp DNA linear PAT 11-DEC-2003  
DEFINITION Sequence 36 from Patent WO03072818.  
ACCESSION AX825138  
VERSION AX825138.1 GI:39750867  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.  
AUTHORS Method for sorting single-stranded nucleic acids  
TITLE Patent: WO 03072818-A 36 04-SEP-2003;  
JOURNAL Degussa Bioactives GmbH (DE)
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FEATURES	source
location/Qualifiers	1..21
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/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"	

misc_binding	modified_base	modified_base	modified_base	modified_base	modified_base	modified_base					
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/bound_moiety="Biotin"
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Query Match	0.7%; Score 18.4; DB 1; Length 21;
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 6.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2804
DB 21 GATAAAAAAAAAAAAAAAAA 2

RESULT 972
AX825121/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825121
DEFINITION Sequence 19 from Patent WO03072818.
ACCESSION AX825121
VERSION AX825121.1 GI:39750850
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 19 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
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modified_base 9
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modified_base 18
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Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 6.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAA 2803
DB 20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 973
AX825112/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825112

DEFINITION Sequence 10 from Patent WO03072818.
ACCESSION AX825112
VERSION AX825112.1 GI:39750841
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 10 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 6.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2804
DB 20 GTAAAAAAAAAAAAAAAAA 1

RESULT 974
AX825148 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825148
DEFINITION Sequence 46 from Patent WO03072818.
ACCESSION AX825148
VERSION AX825148.1 GI:39750877
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 46 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"


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    source
    location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Beschreibung der kuenstlichen
    Sequenz: Capture-Oligonukleotid"
    1
    /bound_moiety="Biotin"
    3
    /note="LNA-T (Locked Nucleic Acid) "
    /mod_base=OTHER
    modified_base
    6
    /note="LNA-T (Locked Nucleic Acid) "
    /mod_base=OTHER
    modified_base
    9
    /note="LNA-T (Locked Nucleic Acid) "
    /mod_base=OTHER
    modified_base
    12
    /note="LNA-T (Locked Nucleic Acid) "
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    /note="LNA-T (Locked Nucleic Acid) "
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    modified_base
    18
    /note="LNA-T (Locked Nucleic Acid) "
    /mod_base=OTHER
    modified_base

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Query Match	0.7%;	Score 18.4;	DB 1;	Length 21;
Best Local Similarity	95.0%;	Pred. No. 6.9e+02;		
Matches	19;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY	2784	TGAAAAAAAAAAAAAAAA	2
Db	20	TCAAAAAAAAAAAAAAAA	1

RESULT 978

US			
5122			
AX825122	21 bp	DNA	linear
Sequence	20 from Patent WO03072818.		
NOTATION			
			PAT 11-DEC-2003

DEFINITION	Sequence 20 from Patent WO03072818.
ACCESSION	AX825122
VERSION	AX825122.1
KEYWORDS	GI:39750851
SOURCE	.
ORGANISM	synthetic construct synthetic construct artificial sequences.

REFERENCE	1
AUTHORS	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
TITLE	Method for sorting single-stranded nucleic acids
JOURNAL	Patent: WO 03072818-A 20 04-SEP-2003;

FEATURES	Location/Qualifiers
source	1. .21

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1: organism="synthetic construct"
2: /mol_type="unassigned DNA"
3: /db_xref="taxon:32630"
4: /note="Beschreibung der kuenstlichen
5: Sequenz: Capture-Oligonukleotid"

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misc_binding

modified_base

modified_base

modified base

modified_base

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modified_base      /mod_base=OTHER
15                 /note="INA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base      18
/note="INA-T (Locked Nucleic Acid) "
/mod_base=OTHER

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Query Match	0.7%;	Score 18.4;	DB 1;	Length 21;
Best Local Similarity	95.0%;	Pred. No. 6.9e+02;		
Matches 19;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

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QY      2168 TTTTYYYYTTTTTTTTTTA 2187
          |||||
          |||||
          |||||
          |||||
          ||||| }
Db       1 TTTTTTTTTTTTTTTTTTGGA 20
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RESULT	979
AX825122/c	
Locus	21 bp DNA linear PAT 11-DEC-2003
DEFINITION	
Sequence	20 from Patent WO03072818.
Accession	
AX825122	
Version	
AX825122.1	GI:39750851

SOURCE ORGANISM	synthetic construct synthetic construct artificial sequences.
REFERENCE 1	
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.	
TITLE Method for sorting single-stranded nucleic acids	
JOURNAL Patent: WO 03072818-A 20 04-SEP-2003;	

DEGUSSA BIOACTIVES GMBH (DE)
Location/Qualifiers
FEATURES

Source

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

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misc_binding

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

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Query Match	0.7%;	Score 18.4;	DB 1;	Length 21;
Best Local Similarity	95.0%;	Pred. No. 6.9e+02;		
Matches	19;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

QY	2784	TGAAAAAAAAAAAAAAAAAAAA	2803
Db	20	TCAAAAAAAAAAAAAAAAAAAA	1

RESULT 980		
AX825128/c		
LOCUS	AX825128	
DEFINITION	Sequence 26 from Patent WO03072818.	
	21 bp	DNA
		linear
		PAT 11-DEC-2003

DEFINITION sequence 26 from patent WO030/2018

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ACCESSION      AX825128
VERSION        AX825128.1  GI:39750857
KEYWORDS
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1
AUTHORS        Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE          Method for sorting single-stranded nucleic acids
JOURNAL        Patent: WO 03072818-A 26 04-SEP-2003;
               Degussa Bioactives GmbH (DE)
FEATURES       location/Qualifiers
               1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz:Capture-Oligonukleotid"
misc_binding   1
               /bound_moiety="Biotin"
modified_base  3
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  6
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  9
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modified_base  12
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modified_base  15
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               /mod_base=OTHER
modified_base  18
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               /mod_base=OTHER
modified_base  18
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               /mod_base=OTHER
Query Match    0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 6.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2785 GAAAAAAAAAAAAAAAAAAAA 2804
DB      20 GCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 981
AX825129/c
LOCUS      AX825129      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 27 from Patent WO03072818.
ACCESSION  AX825129
VERSION     AX825129.1  GI:39750858
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
               artificial sequences.
REFERENCE    1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE        Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 27 04-SEP-2003;
               Degussa Bioactives GmbH (DE)
FEATURES     location/Qualifiers
               1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz:Capture-Oligonukleotid"
misc_binding 1
               /bound_moiety="Biotin"
modified_base 3
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
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Query Match    0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 6.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2785 GAAAAAAAAAAAAAAAAAAAA 2804
DB      20 GCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 982
AX825130/c
LOCUS      AX825130      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 28 from Patent WO03072818.
ACCESSION  AX825130
VERSION     AX825130.1  GI:39750859
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
               artificial sequences.
REFERENCE    1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE        Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 28 04-SEP-2003;
               Degussa Bioactives GmbH (DE)
FEATURES     location/Qualifiers
               1..21
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz:Capture-Oligonukleotid"
misc_binding 1
               /bound_moiety="Biotin"
modified_base 3
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 6
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 9
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
Query Match    0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 6.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY	2785	GAIAAAAAAAAAAAAAAAAA	2804	
Db	20	GCIAAAAAAAAAAAAAAAAA	1	
RESULT	983			
LOCUS	AX825132	21 bp	DNA	linear
DEFINITION	Sequence 30 from Patent WO03072818.			
ACCESSION	AX825132			
VERSION	AX825132.1	GI:39750861		
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
	artificial sequences.			
REFERENCE	1			
AUTHORS	Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.			
TITLE	Method for sorting single-stranded nucleic acids			
JOURNAL	Patent: WO 03072818-A 30 04-SEP-2003;			
	Degussa Bioactives GmbH (DE)			
FEATURES	Location/Qualifiers			
source	1..21			
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	/db_xref="taxon:32630"			
	/note="Beschreibung der kuenstlichen			
	Sequenz:Capture-Oligonukleotid"			
misc_binding	1			
	/bound_moiety="Biotin"			
modified_base	3			
	/note="LNA-T (Locked Nucleic Acid) "			
	/mod_base=OTHER			
modified_base	6			
	/note="LNA-T (Locked Nucleic Acid) "			
	/mod_base=OTHER			
modified_base	9			
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modified_base	12			
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	/mod_base=OTHER			
modified_base	18			
	/note="LNA-T (Locked Nucleic Acid) "			
	/mod_base=OTHER			
Query Match	0.7%;	Score 18.4;	DB 1;	Length 21;
Best Local Similarity	95.0%;	Pred. No. 6.9e+02;		
Matches	19;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	2166	TTTTTTTTTTTTTTTTTTT	2185	
Db	1	TTTTTTTTTTTTTTTTTGT	20	
RESULT	984			
LOCUS	AX825133	21 bp	DNA	linear
DEFINITION	Sequence 31 from Patent WO03072818.			
ACCESSION	AX825133			
VERSION	AX825133.1	GI:39750862		
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
	artificial sequences.			
REFERENCE	1			
AUTHORS	Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.			
TITLE	Method for sorting single-stranded nucleic acids			
JOURNAL	Patent: WO 03072818-A 31 04-SEP-2003;			
	Degussa Bioactives GmbH (DE)			

[illegible]

modified_base 15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 6.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804
DB 21 GACAAAAAAAAAAAAAAAAAAA 2

RESULT 986
BD085544
LOCUS BD085544 22 bp RNA linear PAT 27-AUG-2002
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085544
VERSION BD085544.1 GI:22631154
KEYWORDS JP 2001333800-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 22)
Shimada, K.
Method of comparison and detection of RNA amount and DNA amount
Patent: JP 2001333800-A 1 04-DEC-2001;

COMMENT
UNITECH CO LTD
OS Homo sapiens (human)
PN JP 2001333800-A/1
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAO RI SHIMADA
PC C12Q1/68, C12N15/09, G01N33/50, C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC

FEATURES
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FH Key location/Qualifiers
FT source 1..22 /organism='Homo sapiens (human)'.
FT /mol_type='genomic RNA'
/db_xref='taxon:9606'

Query Match 0.7%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2784 TGAATAAAAAAAAAAAAAA 2803
DB 3 TCAAAAAAAAAAAAAAAAAAAA 22

RESULT 987
BD245245 23 bp DNA linear PAT 17-JUL-2003
LOCUS BD245245
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245245
VERSION BD245245.1 GI:33055015
KEYWORDS JP 2002532386-A/31.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hartwich, G. and Heller, A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 31 02-OCT-2002;
FRIZ BIOCHEM GMBH

COMMENT OS Artificial Sequence

PN JP 2002532386-A/31
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1998 DE 198 53 957.6, 29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH, ADAM HELLER
PC C07H21/00, C07H21/02, C07H21/04, C12N15/09, C12Q1/68, G01N27/12, PC
G01N27/30,

PC G01N27/416, G01N27/48, G01N33/483, G01N33/50, G01N33/566, C12N15/00, PC
G01N27/46
CC Method of electrochemically detecting nucleic acid FH Key
location/Qualifiers
FT source 1..23
FT /organism='Artificial Sequence'.
location/Qualifiers
1..23
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2164 CCTTTTCTTTTCTTTTCTTTT 2183
DB 4 CCATTTTCTTTTCTTTTCTTTT 23

RESULT 988
AR136778 26 bp DNA linear PAT 16-JUN-2001
LOCUS AR136778
DEFINITION Sequence 1 from patent US 6162437.
ACCESSION AR136778
VERSION AR136778.1 GI:14478028
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 26)
TITLE Pyun, K.-H., Choi, I., Kang, H.-S., Lee, J.-U. and Kim, Y.-H.
JOURNAL Method for inhibiting interleukin-6 production by administering
extracts from root of Stepania tetrandra
Patent: US 6162437-A 1 19-DEC-2000;
location/Qualifiers
1..26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 18.4; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2164 CCTTTTCTTTTCTTTTCTTTT 2183
DB 7 CGTTTCTTTTCTTTTCTTTTCTTTT 26

RESULT 989
E64577 26 bp DNA linear PAT 31-JAN-2002
LOCUS E64577
DEFINITION Method for obtaining DNA fragment in plant and utilization thereof.
ACCESSION E64577
VERSION E64577.1 GI:18628519
KEYWORDS JP 2000157277-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Hibino, T. and Koshiyama, J.
TITLE Method for obtaining DNA fragment in plant and utilization thereof
JOURNAL Patent: JP 2000157277-A 1 13-JUN-2000;

QY	2166	TTTTTTTTTTTTTTTTTTTT	2184
Db	1	TTTTTTTTTTTTTTTTTTTT	19
RESULT 994			
ARI02020/c			
LOCUS	ARI02020	19 bp	DNA
DEFINITION	Sequence 18 from patent US 6083731.		linear
ACCESSION	ARI02020		PAT 14-FEB-2001
VERSION	ARI02020.1	GI:12812818	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 19)		
AUTHORS	Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.		
TITLE	Recombinant materials and methods for the production of limonene hydroxylases		
JOURNAL	Patent: US 6083731-A 18 04-JUL-2000;		
FEATURES	Location/Qualifiers		
source	1..19		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	0.6%;	Score 18.2;	DB 1;
Best Local Similarity	94.7%;	Pred. No. 5.6e+02;	length 19;
Matches	18;	Conservative 1;	Mismatches 0;
		Indels 0;	Gaps 0;
QY	2785	GAIAAAAAAAAAAAAAAAAA	2803
Db	19	DAAAAAAAAAAAAAAAAAAAAA	1
RESULT 995			
ARI134802			
LOCUS	ARI134802	19 bp	DNA
DEFINITION	Sequence 18 from patent US 6194185.		linear
ACCESSION	ARI134802		PAT 16-MAY-2001
VERSION	ARI134802.1	GI:14123707	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 19)		
AUTHORS	Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.		
TITLE	Recombinant materials and methods for production of limonene hydroxylases		
JOURNAL	Patent: US 6194185-A 18 27-FEB-2001;		
FEATURES	Location/Qualifiers		
source	1..19		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	0.6%;	Score 18.2;	DB 1;
Best Local Similarity	94.7%;	Pred. No. 5.6e+02;	length 19;
Matches	18;	Conservative 1;	Mismatches 0;
		Indels 0;	Gaps 0;
QY	2166	TTTTTTTTTTTTTTTTTTTT	2184
Db	1	TTTTTTTTTTTTTTTTTTTT	19
RESULT 996			
ARI134802/c			
LOCUS	ARI134802	19 bp	DNA
DEFINITION	Sequence 18 from patent US 6194185.		linear
ACCESSION	ARI134802		PAT 16-MAY-2001
VERSION	ARI134802.1	GI:14123707	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 19)		
AUTHORS	Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.		
TITLE	Recombinant materials and methods for production of limonene hydroxylases		
JOURNAL	Patent: US 6194185-A 18 27-FEB-2001;		
FEATURES	Location/Qualifiers		
source	1..19		
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Query Match	0.6%;	Score 18.2;	DB 1;
Best Local Similarity	94.7%;	Pred. No. 5.6e+02;	length 19;
Matches	18;	Conservative 1;	Mismatches 0;
		Indels 0;	Gaps 0;

REFERENCE	1 (bases 1 to 19)				
AUTHORS	Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.				
TITLE	Recombinant materials and methods for production of limonene hydroxylases				
JOURNAL	Patent: US 6194185-A 18 27-FEB-2001;				
FEATURES	Location/Qualifiers				
source	1..19				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.6%;	Score 18.2;	DB 1;	Length 19;	
Best Local Similarity	94.7%;	Pred. No. 5.6e+02;			
Matches	18; Conservative	1;	Mismatches	0;	Indels 0; Gaps 0;
QY	2785	GAIAAAAAAAAAAAAAA	2803		
Db	19	DAIAAAAAAAAAAAAAA	1		
RESULT 997					
E28098					
LOCUS	E28098		20 bp	DNA	linear PAT 18-JUN-2001
DEFINITION	Method for analyzing DNA fragment.				
ACCESSION	E28098				
VERSION	E28098.1	GI:13018323			
KEYWORDS	JP 1999196874-A/9.				
SOURCE	unidentified				
ORGANISM	unidentified				
	unclassified.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Hideki,K. and Senshu,U.				
TITLE	Method for analyzing DNA fragment				
JOURNAL	Patent: JP 1999196874-A 9 27-JUL-1999;				
	HITACHI LTD				
COMMENT	OS Unidentified				
	PN JP 1999196874-A/9				
	PD 27-JUL-1999				
	PF 14-JAN-1998 JP 1998005399				
	PR				
	PI HIDEKI KAMIBARA,SENSHU UEMATSU				
	PC C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC				
	Strandedness: Single;				
	CC Topology: Linear;				
	CH Key	Location/Qualifiers			
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FEATURES					
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	/organism="unidentified"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32644"				
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Best Local Similarity	94.7%;	Pred. No. 6.5e+02;			
Matches	18; Conservative	1;	Mismatches	0;	Indels 0; Gaps 0;
QY	2169	TTTTTTTTTTTTTTT	2187		
Db	1	TTTTTTTTTTTTTTT	19		
RESULT 998					
E28098/c					
LOCUS	E28098		20 bp	DNA	linear PAT 18-JUN-2001
DEFINITION	Method for analyzing DNA fragment.				
ACCESSION	E28098				
VERSION	E28098.1	GI:13018323			
KEYWORDS	JP 1999196874-A/9.				
SOURCE	unidentified				
ORGANISM	unidentified				
	unclassified.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Hideki,K. and Senshu,U.				

TITLE Method for analyzing DNA fragment
JOURNAL Patent: JP 1999196874-A 9 27-JUL-1999;
HITACHI LTD
COMMENT OS Unidentified
PN JP 1999196874-A/9
PD 27-JUL-1999
PF 14-JAN-1998 JP 1998005399
PR
PI HIDEKI KAMIBARA, SENSU UEMATSU
PC C12N15/09, C12Q1/68, G01N27/447, C12N15/00, G01N27/26 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
/organism='Unidentified'.
1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.6%; Score 18.2; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803
DB 19 BAAAAAAAAAAAAAAAAA 1

RESULT 999
AR084981
LOCUS AR084981 23 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 15 from patent US 5981251.
ACCESSION AR084981
VERSION AR084981.1 GI:10011752
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Ullrich, A. and Vogel, W.
TITLE PTP 1D: a novel protein tyrosine phosphatase
JOURNAL Patent: US 5981251-A 15 09-NOV-1999;
FEATURES
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTTCTTTTCTTTT 2184
DB 1 CTCGAGTTTCTTTTCTTTTCTTTT 23

RESULT 1000
ARI00207 23 bp DNA linear PAT 14-FEB-2001
LOCUS ARI00207
DEFINITION Sequence 6 from patent US 6080576.
ACCESSION ARI00207
VERSION ARI00207.1 GI:12810655
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Zambrowicz, B., Friedrich, G. and Sands, A.T.
TITLE Vectors for gene trapping and gene activation
JOURNAL Patent: US 6080576-A 6 27-JUN-2000;
FEATURES
Location/Qualifiers

source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1999 CTAGCTTCTCAGATCAAGTC 2021
DB 1 CCAGAGTCTTCAGATCAAGTC 23

RESULT 1001
ARI23791/c 23 bp DNA linear PAT 16-MAY-2001
LOCUS ARI23791
DEFINITION Sequence 7 from patent US 6171803.
ACCESSION ARI23791
VERSION ARI23791.1 GI:14109152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kinet, J. Pierre.
TITLE Isolation, characterization, and use of the human .beta. subunit of
JOURNAL Patent: US 6171803-A 7 09-JAN-2001;
FEATURES
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2186
DB 23 CATTTTCTTTTCTTTTCTTTTATT 1

RESULT 1002
BD263052 23 bp DNA linear PAT 17-JUL-2003
LOCUS BD263052
DEFINITION Vectors for gene mutagenesis and gene discovery by gene trapping.
ACCESSION BD263052
VERSION BD263052.1 GI:33072820
KEYWORDS JP 2002539764-A/17.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 23)
AUTHORS Zambrowicz, B., Friedrich, G.A., Lilleberg, S. and Sands, A.T.
TITLE Vectors for gene mutagenesis and gene discovery by gene trapping
JOURNAL Patent: JP 2002539764-A 17 26-NOV-2002;
LEXICON GENETICS INC
OS Mus musculus (mouse)
PN JP 2002539764-A/17
PD 26-NOV-2002
PF 19-NOV-1999 JP 2000584047
PR 20-NOV-1998 US 60/109302, 25-MAR-1999 US 09/276533 PI
BRIAN ZAMBROWICZ, GLENN A FRIEDRICH, STAN LILLEBERG, ARTHUR T PI
SANDS
PC C12N15/09, A01K67/027, C12N5/10, C12N7/00// (C12N7/00, C12R1.93),
PC C12N15/00,
PC C12N5/00
CC Vectors for gene mutagenesis and gene discovery by gene CC
FH Key trapping
FT source 1..23
/organism='Mus musculus (mouse)'.

FEATURES
source 1.23
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1999 CTAGCTTCTCAGAGATCAAGTC 2021
Db 1 CCAGAGTCTTCAGAGATCAAGTC 23

RESULT 1003

LOCUS I32906 23 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 15 from patent US 5589375.
ACCESSION I32906
VERSION I32906.1 GI:1823697
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Ullrich,A. and Vogel,W.
TITLE PTP 1D: a novel protein tyrosine phosphatase
JOURNAL Patent: US 5589375-A 15 31-DEC-1996;
FEATURES
source 1.23
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTTCTTTTCTTTT 2184
Db 1 CTCGAGTTTCTTTTCTTTTCTTTT 23

RESULT 1004

LOCUS AR306617 23 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 15 from patent US 6548641.
ACCESSION AR306617
VERSION AR306617.1 GI:31696809
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Ullrich,A. and Vogel,W.
TITLE PTP 1D: a novel protein tyrosine phosphatase
JOURNAL Patent: US 6548641-A 15 15-APR-2003;
FEATURES
source 1.23
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTTCTTTTCTTTT 2184
Db 1 CTCGAGTTTCTTTTCTTTTCTTTT 23

RESULT 1005

BD105197

LOCUS BD105197 23 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel glucosyltransferase gene.
ACCESSION BD105197
VERSION BD105197.1 GI:22650771
KEYWORDS WO 0192509-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS Mizutani,M., Sakakibara,K., Tanaka,Y., Kusumi,T. and Ono,E.
TITLE Novel glucosyltransferase gene
JOURNAL Patent: WO 0192509-A 3 06-DEC-2001;
INTERNATIONAL FLOWER DEVELOPMENTS PROPRIETARY LTD,MASAKO MIZUTANI,
KEIKO SAKAKIBARA,YOSHIKAZU TANAKA,TAKAKI KUSUMI,EIICHIRO ONO
OS Artificial Sequence
PN WO 0192509-A/3
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004675
PR 02-JUN-2000 JP 00P 170436
PI MASAKO MIZUTANI,KEIKO SAKAKIBARA,YOSHIKAZU TANAKA,TAKAKI PI
KUSUMI,
PI EIICHIRO ONO
PC C12N15/09,C12N15/29,C12N15/54,C12N1/15,C12N1/19,C12N1/21 PC
PC C12N5/10,C12N9/10,
PC A01H5/00
CC Primer
FH Key
FT source 1.23
Location/Qualifiers
/organism='Artificial Sequence'.
source 1.23
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTTCTTTTCTTTT 2184
Db 1 CTCGAGTTTCTTTTCTTTTCTTTT 23

RESULT 1006
AX454028/c 25 bp DNA linear PAT 06-JUL-2002
LOCUS AX454028
DEFINITION Sequence 4 from Patent WO0198539.
ACCESSION AX454028
VERSION AX454028.1 GI:21713668
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mitsunashi,M., Kambara,H., Matsunaga,H. and Kawamura,M.
TITLE Gene markers for lung cancer
JOURNAL Patent: WO 0198539-A 4 27-DEC-2001;
Hitachi Chemical Co., Ltd. (JP) ; HITACHI CHEMICAL RESEARCH CENTER,
INC. (US) ; Hitachi, Ltd. (JP)
FEATURES
source 1.25
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="anchor primer P4."

Query Match 0.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAGAAAAAAGAAAAA 2803
:|||||

Db 24 BAAAAAAAAAAAAAAAAAAAA 6

RESULT 1007
AX042942/c

LOCUS AX042942 25 bp DNA PAT 23-NOV-2000
DEFINITION Sequence 508 from Patent WO0065088.
ACCESSION AX042942
VERSION AX042942.1 GI:11341550
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="16S rRNA Homozygote Primer Sequence"

Query Match 0.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2776 GTTAGAATGAAAAAAAAAAAAA 2798
Db 23 GTTAAAACTCAAAAAAAAAAAAA 1

RESULT 1008
I20186 25 bp DNA PAT 07-OCT-1996
LOCUS I20186
DEFINITION Sequence 1 from patent US 5514546.
ACCESSION I20186
VERSION I20186.1 GI:1600541
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2164 CCTTTTCTCTCTCTTTT 2186
Db 1 CCTTTTCTCTCTCTTTT 23

RESULT 1009
AX042923 25 bp DNA PAT 23-NOV-2000
LOCUS AX042923
DEFINITION Sequence 489 from Patent WO0065088.
ACCESSION AX042923
VERSION AX042923.1 GI:11341531
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

REFERENCE 1
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="16S rRNA Homozygote Primer Sequence"

Query Match 0.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2171 TTTTCTTTTAACTTTG 2193
Db 1 TTTTCTTTTAAACGCTG 23

RESULT 1010
AX043281 25 bp DNA PAT 23-NOV-2000
LOCUS AX043281
DEFINITION Sequence 847 from Patent WO0065088.
ACCESSION AX043281
VERSION AX043281.1 GI:11341889
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQAI Heterozygote Primer Sequence"

Query Match 0.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2172 TTTTCTTTTAACTTTGA 2194
Db 1 TTTTCTTTTCTTGAATTGA 23

RESULT 1011
AX115988 25 bp DNA PAT 11-MAY-2001
LOCUS AX115988
DEFINITION Sequence 1111 from Patent WO0129262.
ACCESSION AX115988
VERSION AX115988.1 GI:14032930
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

1 Picoult-Newburg, L. and Pohl, M.
Genotyping reagents, kits and methods of use thereof
Patent: WO 0129262-A 1111 26-APR-2001;
Orchid Biosciences, Inc. (US)
Location/Qualifiers

Query Match 0.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2186
Db 2 CCTAGTTTCTTTTCTTTTCTTTT 24

RESULT 1012

AR172578

LOCUS AR172578 26 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 10 from patent US 6303328.

ACCESSION AR172578

VERSION AR172578.1 GI:17912069

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 26)

TITLE Re,R. and Cook,J.

JOURNAL Inhibition of cellular proliferation in vitro by oligonucleotide
binding to a chromosomal binding site for p53 protein
Patent: US 6303328-A 10 16-OCT-2001;

FEATURES Location/Qualifiers

source 1..26

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2186
Db 2 CCTTTTCTTTTCTTTTCTTTT 24

RESULT 1013

AR430169

LOCUS AR430169 26 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 10 from patent US 6645944.

ACCESSION AR430169

VERSION AR430169.1 GI:40190841

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 26)

TITLE Re,R. and Cook,J.

JOURNAL Inhibition of cellular proliferation by oligonucleotide binding to
a chromosomal binding site for p53 protein
Patent: US 6645944-A 10 11-NOV-2003;

FEATURES Location/Qualifiers

source 1..26

/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2186
Db 2 CCTTTTCTTTTCTTTTCTTTT 24

RESULT 1014

AX391845/c

LOCUS AX391845 28 bp RNA linear PAT 23-MAR-2002

DEFINITION Sequence 10 from Patent WO0216574.

ACCESSION AX391845

VERSION AX391845.1 GI:19700427

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1
synthetic construct
synthetic construct
artificial sequences.

AUTHORS

TITLE Reimholz,R. and Ploeger,F.
Method for identifying peptides that can be specifically cleaved
and the use of peptide sequences of this type

JOURNAL Patent: WO 0216574-A 10 28-FEB-2002;

Xzillion GmbH & CO.KG (DE)

FEATURES Location/Qualifiers

source 1..28

/organism="synthetic construct"

/mol_type="unassigned RNA"

/db_xref="taxon:32630"

/note="Puromycin-Linker-RNA-Teil"

Query Match 0.6%; Score 18.2; DB 1; Length 28;
Best Local Similarity 87.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2167 TTTTCTTTTCTTTTCTTTTCTTTT 2189
Db 28 TTTTCTTTTCTTTTCTTTTCTTTT 6

RESULT 1015

AR055117/c

LOCUS AR055117 28 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 22 from patent US 5837468.

ACCESSION AR055117

VERSION AR055117.1 GI:5980694

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 28)

TITLE Wang,X., Duvick,J.P. and Briggs,S.P.

JOURNAL PCR-based cDNA subtractive cloning method

Patent: US 5837468-A 22 17-NOV-1998;

FEATURES Location/Qualifiers

source 1..28

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 28;
Best Local Similarity 87.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2165 CTTTCTTTTCTTTTCTTTTCTTTT 2187
Db 28 CTTTCTTTTCTTTTCTTTTCTTTT 6

RESULT 1016

AR068458/c

LOCUS AR068458 28 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 22 from patent US 5853991.

ACCESSION AR068458

VERSION AR068458.1 GI:6000665

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 28)

TITLE Wang,X., Duvick,J.P. and Briggs,S.P.

JOURNAL PCR-based cDNA subtractive cloning method

Patent: US 5853991-A 22 29-DEC-1998;

FEATURES Location/Qualifiers

source 1..28

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18.2; DB 1; Length 28;
Best Local Similarity 87.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2165 CTTTTTTTTTTTTTTTTTTT 2187
|||||
28 CTTTTTTTTTTTTTTTGCCTA 6

RESULT 1017
AJ600024/c 28 bp DNA linear PLN 23-OCT-2003
LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone 498E01.
DEFINITION
ACCESSION AJ600024 GI:37949652
VERSION AJ600024.1
KEYWORDS right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., Deroose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 28)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

FEATURES
source
1. .28
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1. .28
/note="T-DNA flanking sequence
right border"

misc_feature
1. .28
/note="T-DNA flanking sequence
right border"

Query Match 0.6%; Score 18.2; DB 1; Length 28;
Best Local Similarity 87.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2164 CTTTTTTTTTTTTTTTTTTT 2186
|||||
23 CTTTTTTGTGTTGTTT 1

RESULT 1018
BD274324/c 29 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION

discovery.
BD274324 GI:33084092
BD274324.1
JP 2002526030-A/291.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 291 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/291
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc_feature (28)..(29).
Location/Qualifiers
1. .29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1. .29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 18.2; DB 1; Length 29;
Best Local Similarity 87.0%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2170 TTTTTTTTTTTTTTTTACTTT 2192
|||||
27 TTTTTTTTTTTTGTGCT 5

RESULT 1019
BD274342/c 29 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION
ACCESSION BD274342
VERSION BD274342.1 GI:33084110
KEYWORDS JP 2002526030-A/309.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 309 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/309
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc_feature (28)..(29).
Location/Qualifiers
1. .29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1. .29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 18.2; DB 1; Length 29;
Best Local Similarity 87.0%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 18 TTTTTTTTTTTTTTTT 1

RESULT 1030

E28535

LOCUS E28535 18 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for labeling oligonucleotide and utilization thereof.

ACCESSION E28535

VERSION E28535.1 GI:13025387

KEYWORDS JP 1999075880-A/2.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 18)

AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.

TITLE Method for labeling oligonucleotide and utilization thereof

JOURNAL Patent: JP 1999075880-A 2 23-MAR-1999;

COMMENT CHEMO SERO THERAPEUT RES INST

OS Unidentified

PN JP 1999075880-A/2

PD 23-MAR-1999

PF 10-JUL-1998 JP 1998195719

PR

PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC

C12N15/09,C12Q1/68,G01N33/58,C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1..18

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source Location/Qualifiers

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Best Local Similarity 100.0%; Pred.No. 5.2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1031

E28535/c

LOCUS E28535 18 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for labeling oligonucleotide and utilization thereof.

ACCESSION E28535

VERSION E28535.1 GI:13025387

KEYWORDS JP 1999075880-A/2.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 18)

AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.

TITLE Method for labeling oligonucleotide and utilization thereof

JOURNAL Patent: JP 1999075880-A 2 23-MAR-1999;

COMMENT CHEMO SERO THERAPEUT RES INST

OS Unidentified

PN JP 1999075880-A/2

PD 23-MAR-1999

PF 10-JUL-1998 JP 1998195719

PR

PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC

C12N15/09,C12Q1/68,G01N33/58,C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1..18

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Location/Qualifiers

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/db_xref="taxon:32644"

Location/Qualifiers

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/organism="unidentified"

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Best Local Similarity 100.0%; Pred.No. 5.2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183

Db 18 TTTTTTTTTTTTTTTT 1

RESULT 1032

E28536

LOCUS E28536 18 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for labeling oligonucleotide and utilization thereof.

ACCESSION E28536

VERSION E28536.1 GI:13025388

KEYWORDS JP 1999075880-A/3.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 18)

AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.

TITLE Method for labeling oligonucleotide and utilization thereof

JOURNAL Patent: JP 1999075880-A 3 23-MAR-1999;

COMMENT CHEMO SERO THERAPEUT RES INST

OS Unidentified

PN JP 1999075880-A/3

PD 23-MAR-1999

PF 10-JUL-1998 JP 1998195719

PR

PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC

C12N15/09,C12Q1/68,G01N33/58,C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1..18

FEATURES

Location/Qualifiers

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Best Local Similarity 100.0%; Pred.No. 5.2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183

Db 1 TTTTTTTTTTTTTTTT 18

RESULT 1033

E28536/c

LOCUS E28536 18 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for labeling oligonucleotide and utilization thereof.

ACCESSION E28536

VERSION E28536.1 GI:13025388

KEYWORDS JP 1999075880-A/3.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 18)

AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.

TITLE Method for labeling oligonucleotide and utilization thereof

JOURNAL Patent: JP 1999075880-A 3 23-MAR-1999;

COMMENT CHEMO SERO THERAPEUT RES INST

OS Unidentified

PN JP 1999075880-A/3

PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719

PR KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
PI C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1.18
FT /organism='Unidentified'.
FT Location/Qualifiers
FT 1.18
FT /organism="unidentified"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32644"

FEATURES
source

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1034

LOCUS 179509 18 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION 179509
VERSION 179509.1 GI:3207799
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 16 13-JAN-1998;
FEATURES
source

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1035

LOCUS 179509 18 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION 179509
VERSION 179509.1 GI:3207799
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 16 13-JAN-1998;
FEATURES
source

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18

Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1036

LOCUS AR208427 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 7 from patent US 6383754.
ACCESSION AR208427
VERSION AR208427.1 GI:21509578
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 7 07-MAY-2002;
FEATURES
source

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2784 TGA AAAAAAAAAAAAAAAAAA 2801
Db 18 TGA AAAAAAAAAAAAAAAAAA 1

RESULT 1037

LOCUS AR215435 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 9 from patent US 6410321.
ACCESSION AR215435
VERSION AR215435.1 GI:23313691
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6410321-A 9 25-JUN-2002;
FEATURES
source

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1038
LOCUS AR215435 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 9 from patent US 6410321.
ACCESSION AR215435
VERSION AR215435.1 GI:23313691
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 18)
TITLE Lin, C.-I.P., Wallace, R.B., Cossman, J. and French, C.
METHOD AND FORMULATION FOR LYOPHILIZING CULTURED HUMAN CELLS TO PRESERVE RNA AND DNA CONTAINED IN CELLS FOR USE IN MOLECULAR BIOLOGY EXPERIMENTS
JOURNAL Patent: US 6410321-A 9 25-JUN-2002;
FEATURES Location/Qualifiers
source 1.18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1039
AR222464 18 bp DNA linear PAT 26-SEP-2002
LOCUS AR222464
DEFINITION Sequence 24 from patent US 6429300.
ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 18)
TITLE Kurz, M., Lohse, P. and Wagner, R.
JOURNAL Peptide acceptor ligation methods
FEATURES Patent: US 6429300-A 24 06-AUG-2002;
source Location/Qualifiers
1.18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1040
AR222464 18 bp DNA linear PAT 26-SEP-2002
LOCUS AR222464
DEFINITION Sequence 24 from patent US 6429300.
ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 18)
TITLE Kurz, M., Lohse, P. and Wagner, R.
JOURNAL Peptide acceptor ligation methods
FEATURES Patent: US 6429300-A 24 06-AUG-2002;
source Location/Qualifiers
1.18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1043
AX004875 18 bp DNA linear PAT 24-AUG-2000
LOCUS AX004875
DEFINITION Sequence 4 from Patent WO910527.
ACCESSION AX004875
VERSION AX004875.1 GI:99282275
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1041
AR412363 18 bp DNA linear PAT 18-DEC-2003
LOCUS AR412363
DEFINITION Sequence 14 from patent US 6639062.
ACCESSION AR412363
VERSION AR412363.1 GI:40167473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 18)
TITLE Manoharan, M., Cook, P.D., Prakash, T.P. and Kawasaki, A.M.
JOURNAL Aminoxy-modified nucleosidic compounds and oligomeric compounds prepared therefrom
FEATURES Patent: US 6639062-A 14 28-OCT-2003;
source Location/Qualifiers
1.18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1042
AR412363 18 bp DNA linear PAT 18-DEC-2003
LOCUS AR412363
DEFINITION Sequence 14 from patent US 6639062.
ACCESSION AR412363
VERSION AR412363.1 GI:40167473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 18)
TITLE Manoharan, M., Cook, P.D., Prakash, T.P. and Kawasaki, A.M.
JOURNAL Aminoxy-modified nucleosidic compounds and oligomeric compounds prepared therefrom
FEATURES Patent: US 6639062-A 14 28-OCT-2003;
source Location/Qualifiers
1.18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1043
AX004875 18 bp DNA linear PAT 24-AUG-2000
LOCUS AX004875
DEFINITION Sequence 4 from Patent WO910527.
ACCESSION AX004875
VERSION AX004875.1 GI:99282275
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

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REFERENCE          1      artificial sequences.
AUTHORS            Bayer,E. and Schweltz,J.
TITLE              Method for isolating anionic organic substances from aqueous
                    systems using cationic polymer nanoparticles
JOURNAL            Patent: WO 9910527-A 4 04-MAR-1999;
                    SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
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source             location/Qualifiers
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Query Match                0.6%; Score 18; DB 1; Length 18;
Best Local Similarity     100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           2166 TTTT TTTT TTTT TTTT TTTT 2183
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Db           1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1044
LOCUS       AX004875/c                      18 bp      DNA      linear      PAT 24-AUG-2000
DEFINITION Sequence 4 from Patent WO9910527.
ACCESSION   AX004875
VERSION     AX004875.1 GI:9928275
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Bayer,E. and Schweltz,J.
TITLE       Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
JOURNAL     Patent: WO 9910527-A 4 04-MAR-1999;
            SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES
source      Location/Qualifiers
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            /organism="synthetic construct"
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            /db_xref="taxon:32630"
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Query Match                0.6%; Score 18; DB 1; Length 18;
Best Local Similarity     100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           2786 AAAAAAAAAAAAAAAAAA 2803
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Db           18 AAAAAAAAAAAAAAAAAA 1

RESULT 1045
LOCUS       AX004879                      18 bp      RNA      linear      PAT 24-AUG-2000
DEFINITION Sequence 8 from Patent WO9910527.
ACCESSION   AX004879
VERSION     AX004879.1 GI:9928279
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Bayer,E. and Schweltz,J.
TITLE       Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
JOURNAL     Patent: WO 9910527-A 8 04-MAR-1999;
            SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES
source      Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="2' methyl-modified oligonucleotide"
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/mod_base=um

modified_base

Query Match          0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT 2183
      |||||
      1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1046
AX004879/c          18 bp      RNA      linear      PAT 24-AUG-2000
LOCUS
DEFINITION Sequence 8 from Patent WO9910527.
ACCESSION AX004879
VERSION AX004879.1 GI:9928279
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.

REFERENCE
AUTHORS     1 Bayer, E. and Schewitz, J.
TITLE       Method for isolating anionic organic substances from aqueous
            systems using cationic polymeric nanoparticles
            Patent: WO 9910527-A 8 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
JOURNAL
FEATURES
source
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            /note="2' methyl-modified oligonucleotide"
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            1. .18
            /mod_base=um

Query Match          0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2803
      |||||
      18 AAAAAAAAAAAAAAAAAA 1

RESULT 1047
AX008117          18 bp      DNA      linear      PAT 06-SEP-2000
LOCUS
DEFINITION Sequence 2 from Patent WO9967378.
ACCESSION AX008117
VERSION AX008117.1 GI:9995742
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.

REFERENCE
AUTHORS     1 Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and
            Borkow, G.
TITLE       Antisense oligonucleotide constructs based on beta -arabino-furanose
            and its analogues
            Patent: WO 9967378-A 2 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
JOURNAL
FEATURES
source
            1. .18
            location/Qualifiers
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            /mol_type="unassigned DNA"

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/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1048
AX008117/c

LOCUS AX008117 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9967378.
ACCESSION AX008117
VERSION AX008117.1 GI:9995742
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 2 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
|||||
Db 18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1049
AX008118

LOCUS AX008118 18 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 3 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)

FEATURES
source Location/Qualifiers
1.18

/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1050
AX008118/c

LOCUS AX008118 18 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 3 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)

FEATURES
source Location/Qualifiers
1.18

/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
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Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1051
AX008122

LOCUS AX008122 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO9967378.
ACCESSION AX008122
VERSION AX008122.1 GI:9995747
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 7 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2166	TTTTTTTTTTTTTTTTTT	2183	
Db	1	TTTTTTTTTTTTTTTTTT	18	

RESULT 1052

LOCUS	AX008122/c	18 bp	DNA	linear	PAT 06-SEP-2000
DEFINITION	Sequence 7 from Patent WO967378.				
ACCESSION	AX008122				
VERSION	AX008122.1	GI:9995747			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1				
AUTHORS	Damba,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.				
TITLE	Antisense oligonucleotide constructs based on beta -arabino-furanose and its analogues				
JOURNAL	Patent: WO 9967378-A 7 29-DEC-1999;				
	DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)				
FEATURES	location/Qualifiers				
source	1..18				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Use as an oligomer"				

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1053					
LOCUS	AX008123	18 bp	DNA	linear	PAT 06-SEP-2000
DEFINITION	Sequence 8 from Patent WO967378.				
ACCESSION	AX008123				
VERSION	AX008123.1	GI:9995748			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1				
AUTHORS	Damba,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.				
TITLE	Antisense oligonucleotide constructs based on beta -arabino-furanose and its analogues				
JOURNAL	Patent: WO 9967378-A 8 29-DEC-1999;				
	DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)				
FEATURES	location/Qualifiers				
source	1..18				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Use as an oligomer"				

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

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RESULT 1054
AX008123/c      18 bp    DNA       linear     PAT 06-SEP-2000
LOCUS           AX008123
DEFINITION      Sequence 8 from Patent WO9967378.
ACCESSION       AX008123
VERSION         AX008123.1   GI:9995748
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE       1
AUTHORS         Damba,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE           Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL         Patent: WO 9967378-A 8 29-DEC-1999; DAMHA MASSAD JOSE (CA); PARNAIK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES        Location/Qualifiers
                1..18
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Oligonucleotide"

Query Match              0.6%; Score 18; DB 1; Length 18;
Best Local Similarity   100.0%; Pred.No.5.2e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY      2166 TTTT'TTTTTTTTTTTTTTTT 2183
Db      18 TTTT'TTTTTTTTTTTTTTTT 1

RESULT 1055
AX028843      18 bp    DNA       linear     PAT 24-NOV-2000
LOCUS         AX028843
DEFINITION    Sequence 27 from Patent WO9732023.
ACCESSION     AX028843
VERSION       AX028843.1   GI:10189946
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
                artifical sequences.
REFERENCE     1
AUTHORS       Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE         Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL       Patent: WO 9732023-A 27 04-SEP-1997; FLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
FEATURES      Location/Qualifiers
                1..18
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Oligonucleotide"

Query Match              0.6%; Score 18; DB 1; Length 18;
Best Local Similarity   100.0%; Pred.No.5.2e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY      2170 TTTT'TTTTTTTTTTTTTTTA 2187
Db      1 TTTT'TTTTTTTTTTTTTTTA 18

RESULT 1056
AX028844/c
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LOCUS AX028844 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 28 from Patent WO9732023.
ACCESSION AX028844
VERSION AX028844.1 GI:10189947
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brugliera, F., Holton, T.A. and Michael, M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: WO 9732023-A 28 04-SEP-1997;
FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
location/Qualifiers
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1057
AX047271 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047271
DEFINITION Sequence 21 from Patent WO0068422.
ACCESSION AX047271
VERSION AX047271.1 GI:11876551
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehlegger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M.,
Gumbiowski, K. and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1058
AX047271 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047271
DEFINITION Sequence 21 from Patent WO0068422.
ACCESSION AX047271
VERSION AX047271.1 GI:11876551
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

REFERENCE 1
AUTHORS Muehlegger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M.,
Gumbiowski, K. and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
location/Qualifiers
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 1 TTTTTTTTTTTTTTTTTT 1

RESULT 1059
AX047273 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047273
DEFINITION Sequence 23 from Patent WO0068422.
ACCESSION AX047273
VERSION AX047273.1 GI:11876553
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehlegger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M.,
Gumbiowski, K. and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1060
AX047273 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047273
DEFINITION Sequence 23 from Patent WO0068422.
ACCESSION AX047273
VERSION AX047273.1 GI:11876553
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehlegger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M.,
Gumbiowski, K. and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;

Roche Diagnostics GmbH (DE)	
Location/Qualifiers	
1. .18	
source	

Query Match	0.6%;	Score 18;	DB 1;	Length 18;
Best Local Similarity	100.0%;	Pred. No. 5.2e+02;		
Matches	18;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
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 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT	1061		
AX085253/c			
LOCUS	AX085253	18 bp	DNA
DEFINITION	Sequence 7	from Patent WO0112855.	linear
ACCESSION	AX085253		
VERSION	AX085253.1	GI:13275311	PAT 09-MAR-2001

REFERENCE	1
AUTHORS	Kaufman, J.C., Roth, M.E., Lizardi, P.M., Feng, L. and Latimer, D.R.
TITLE	Binary encoded sequence tags
JOURNAL	Patent: WO 0112855-A 7 22-FEB-2001;

FEATURES	Location/Qualifiers
source	1..18
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="Primer"

Query Match	0.6%;	Score 18;	DB 1;	Length 18;
Best Local Similarity	100.0%;	Pred. No. 5.2e+02;		
Matches 18; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

	2784	TGAAAAAAAAAAAAA	2801
QY			
Dδ	18	TGAATAAAAAAAAAA	1

AX104721	AX104721	18 bp	DNA	linear	PAT 30-APR-2001
LOCUS	Sequence	913	from Patent WO0122972.		
DEFINITION	AX104721				
ACCESSION	AX104721.1	GI:13920918			
VERSION					

REFERENCE
AUTHORS
TITLE
JOURNAL

1
Krieg, A.M., Schetter, C. and Vollmer, J.C.
Immunostimulatory nucleic acids
Patent: WO 0122972-A 913 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

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FEATURES
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    Location/Qualifiers
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"

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Query Match	0.6%;	Score 18;	DB 1;	Length 18;
Best Local Similarity	100.0%;	Pred. No.	5.2e+02;	
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2166	2183
Db	1	18

RESULT 1063			
AX104721/c	18 bp	DNA	linear
LOCUS			
DEFINITION	Sequence 913 from Patent WO0122972.		
ACCESSION	AX104721		
VERSION	AX104721.1	GI:13920918	

REFERENCE
AUTHORS
TITLE
JOURNAL
1
Krieg, A.M., Schetter, C. and Vollmer, J.C.
Immunostimulatory nucleic acids
Patent: WO 0122972-A 913 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

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FEATURES
source
Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Query Match	0.6%;	Score 18;	DB 1;	Length 18;
Best Local Similarity	100.0%;	Pred. No. 5.2e+02;		
Matches	18;	Conservative	0;	Mismatches 0;
			Indels	Gaps 0;

Qy		2786	AAAAAAAAAAAAAA	2803
Dd		18	AAAAAAAAAAAAAA	1

RESULT	1064				
AXI04747					
LOCUS	AXI04747	18 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence 939 from Patent WO0122972.				
ACCESSION	AXI04747				
VERSION	AXI04747.1	GI:13920944			

REFERENCE
1
Krieg, A.M., Schetter, C. and Vollmer, J.C.
AUTHORS
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: WO 0122972-A 939 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

FEATURES	Location/Qualifiers
source	1. .18
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	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"

Query Match	0.6%;	Score 18;	DB 1;	length 18;
Best Local Similarity	100.0%;	Pred. No. 5.2e+02;		
Matches 18; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

	QY	2166	T T T T T T T T T T T T T T T T T T	2183
			I I I I I I I I I I I I I I I I	
D6		1	T T T T T T T T T T T T T T T T T T	18

RESULT	1065
AX104747/c	
LOCUS	AX104747
DEFINITION	Sequence 939 from Patent WO0122972.
ACCESSION	AX104747
	18 bp DNA linear PAT 30-APR-2001

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VERSION AX104747.1 GI:13920944
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 939 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1066
AX105651
LOCUS AX105651 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
SCIOS Inc. (US)
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            /note="synthetic"
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Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18
RESULT 1067
AX105651/c
LOCUS AX105651 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
SCIOS Inc. (US)
FEATURES
    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="synthetic"
Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1068
AX108642
LOCUS AX108642 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX108642
VERSION AX108642.1 GI:13923875
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
SCIOS INC. (US)
FEATURES
    Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="synthetic"
Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18
RESULT 1069
AX108642/c
LOCUS AX108642 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX108642
VERSION AX108642.1 GI:13923875
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
SCIOS INC. (US)
FEATURES
    Location/Qualifiers
        1..18
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="synthetic"
Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
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VERSION      AX814716.1  GI:39103916
KEYWORDS
SOURCE       synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Damha, M.J. and Parniak, M.A.
TITLE        Oligonucleotides comprising alternating segments and uses thereof
JOURNAL      Patent: WO 03064441-A 1 07-AUG-2003;
              MCGILL UNIVERSITY (CA)
FEATURES
  source      Location/Qualifiers
              1..18
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                /note="Oligonucleotide"

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2803
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 1080
LOCUS      AX814723              18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 8 from Patent WO03064441.
ACCESSION  AX814723
VERSION     AX814723.1  GI:39103922
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Damha, M.J. and Parniak, M.A.
TITLE        Oligonucleotides comprising alternating segments and uses thereof
JOURNAL      Patent: WO 03064441-A 8 07-AUG-2003;
              MCGILL UNIVERSITY (CA)
FEATURES
  source      Location/Qualifiers
              1..18
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

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                /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                2'-O-methyl-D-uridine"

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT 2183
Db      1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1081
LOCUS      AX814723              18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 8 from Patent WO03064441.
ACCESSION  AX814723
VERSION     AX814723.1  GI:39103922
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Damha, M.J. and Parniak, M.A.
TITLE        Oligonucleotides comprising alternating segments and uses thereof
JOURNAL      Patent: WO 03064441-A 9 07-AUG-2003;
              MCGILL UNIVERSITY (CA)
FEATURES
  source      Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

  misc_feature 1..17
                /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                2'-O-methyl-D-uridine"

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT 2183
Db      1 TTTT TTTT TTTT TTTT TTTT 18
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JOURNAL      Patent: WO 03064441-A 8 07-AUG-2003;
              MCGILL UNIVERSITY (CA)
FEATURES
  source      Location/Qualifiers
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                /organism="synthetic construct"
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                /db_xref="taxon:32630"
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  misc_feature 1..17
                /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                2'-O-methyl-D-uridine"

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2803
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 1082
LOCUS      AX814724              18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 9 from Patent WO03064441.
ACCESSION  AX814724
VERSION     AX814724.1  GI:39103923
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Damha, M.J. and Parniak, M.A.
TITLE        Oligonucleotides comprising alternating segments and uses thereof
JOURNAL      Patent: WO 03064441-A 9 07-AUG-2003;
              MCGILL UNIVERSITY (CA)
FEATURES
  source      Location/Qualifiers
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

  misc_feature 1..15
                /note="Residues 1-3, 7-9, and 13-15 are
                2'-O-methyl-D-uridine"

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT 2183
Db      1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1083
LOCUS      AX814724              18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 9 from Patent WO03064441.
ACCESSION  AX814724
VERSION     AX814724.1  GI:39103923
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Damha, M.J. and Parniak, M.A.
TITLE        Oligonucleotides comprising alternating segments and uses thereof
JOURNAL      Patent: WO 03064441-A 9 07-AUG-2003;
              MCGILL UNIVERSITY (CA)
FEATURES
  source      Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

  misc_feature 1..15
                /note="Residues 1-3, 7-9, and 13-15 are
                2'-O-methyl-D-uridine"

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT 2183
Db      1 TTTT TTTT TTTT TTTT TTTT 18
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
1. .15
/note="Residues 1-3, 7-9, and 13-15 are
2'-O-methyl-D-uridine"

misc_feature

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1084

AX814725 18 bp DNA linear PAT 05-DEC-2003
LOCUS AX814725
DEFINITION Sequence 10 from Patent WO03064441.
ACCESSION AX814725
VERSION AX814725.1 GI:39103924
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha, M.J. and Parniak, M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 10 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
1. .18
/note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

misc_feature 1. .18
/note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1085

AX814725/c 18 bp DNA linear PAT 05-DEC-2003
LOCUS AX814725
DEFINITION Sequence 10 from Patent WO03064441.
ACCESSION AX814725
VERSION AX814725.1 GI:39103924
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha, M.J. and Parniak, M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 10 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
1. .18
/note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1086

AX814736 18 bp RNA linear PAT 05-DEC-2003
LOCUS AX814736
DEFINITION Sequence 21 from Patent WO03064441.
ACCESSION AX814736
VERSION AX814736.1 GI:39103935
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha, M.J. and Parniak, M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 21 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Target RNA oligonucleotide"

misc_feature 1. .18
/note="Target RNA oligonucleotide"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1087

AX814736/c 18 bp RNA linear PAT 05-DEC-2003
LOCUS AX814736
DEFINITION Sequence 21 from Patent WO03064441.
ACCESSION AX814736
VERSION AX814736.1 GI:39103935
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha, M.J. and Parniak, M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 21 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Target RNA oligonucleotide"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
|||||
Db 18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1088

BD085545

LOCUS BD085545 18 bp RNA linear PAT 27-AUG-2002
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085545
VERSION BD085545.1 GI:22631155
KEYWORDS JP 2001333800-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 18)
REFERENCE Shimada,K.
AUTHORS Method of comparison and detection of RNA amount and DNA amount
TITLE Patent: JP 2001333800-A 2 04-DEC-2001;
JOURNAL UNITECH CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2001333800-A/2
PD 04-DEC-2001
PF 30-MAY-2000 JP 20000160324
PI KAORI SHIMADA
PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC
amount
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Homo sapiens (human)'.
FEATURES
source 1..18
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1089
LOCUS BD085545 18 bp RNA linear PAT 27-AUG-2002
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085545
VERSION BD085545.1 GI:22631155
KEYWORDS JP 2001333800-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 18)
REFERENCE Shimada,K.
AUTHORS Method of comparison and detection of RNA amount and DNA amount
TITLE Patent: JP 2001333800-A 2 04-DEC-2001;
JOURNAL UNITECH CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2001333800-A/2
PD 04-DEC-2001
PF 30-MAY-2000 JP 20000160324
PI KAORI SHIMADA
PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC
amount
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Homo sapiens (human)'.
FEATURES
source 1..18
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1090
LOCUS BD190553 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Secretory proteins and polynucleotides encoding the same.
ACCESSION BD190553
VERSION BD190553.1 GI:33000292
KEYWORDS JP 2002515753-A/12.
SOURCE Rattus
ORGANISM Rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
1 (bases 1 to 18)
REFERENCE Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
AUTHORS Treacy,M., Spaulding,V. and Agostino,M.J.
TITLE Secretory proteins and polynucleotides encoding the same
JOURNAL Patent: JP 2002515753-A 12 28-MAY-2002;
COMMENT GENETICS INSTITUTE INC
PN JP 2002515753-A/12
PD 28-MAY-2002
PF 31-OCT-1997 JP 1998521609
PR 01-NOV-1996 US 08/724973
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
DAVID MERBERG,
PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC Strandedness:
Double;
CC Topology: linear;
FH Key Location/Qualifiers.
FEATURES
source 1..18
/organism="Rattus"
/mol_type="genomic DNA"
/db_xref="taxon:10114"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2785 GAAAAAAAAAAAAAAAAA 2802
Db 1 GAAAAAAAAAAAAAAAAA 18

RESULT 1091
LOCUS BD222596 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Aminoxy-modified nucleoside compound and oligomer compound
produced therefrom.
ACCESSION BD222596
VERSION BD222596.1 GI:33032366
KEYWORDS JP 2002522447-A/14.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 18)
REFERENCE Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
AUTHORS Aminoxy-modified nucleoside compound and oligomer compound
TITLE produced therefrom
JOURNAL Patent: JP 2002522447-A 14 23-JUL-2002;
COMMENT OS Artificial Sequence
PN JP 2002522447-A/14
PD 23-JUL-2002
PF 09-AUG-1999 JP 2000563675

PR 07-AUG-1998 US 09/130973
PI MUTTHIAH MANOHARAN, PHILIP DAN COOK, THAZHA P PRAKASH, ANDREW M
PI KAWASAKI
PC C07H19/167, C07H19/067, C07H19/10, C07H19/20, C07H21/02, C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence: antisense sequence FH
Key Location/Qualifiers
FT source 1. .18
FT Location/Qualifiers
source /organism="Artificial Sequence".
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1092
BD222596/c
LOCUS BD222596 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Aminoxy-modified nucleoside compound and oligomer compound
produced therefrom.
ACCESSION BD222596
VERSION BD222596.1 GI:33032366
KEYWORDS JP 2002522447-A/14.
SOURCE JP 2002522447-A/14.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Manoharan, M., Cook, P.D., Prakash, T.P. and Kawasaki, A.M.
TITLE Aminoxy-modified nucleoside compound and oligomer compound
JOURNAL produced therefrom
Patent: JP 2002522447-A 14 23-JUL-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002522447-A/14
PD 23-JUL-2002
PF 09-AUG-1999 JP 2000563675
PR 07-AUG-1998 US 09/130973
PI MUTTHIAH MANOHARAN, PHILIP DAN COOK, THAZHA P PRAKASH, ANDREW M
PI KAWASAKI
PC C07H19/167, C07H19/067, C07H19/10, C07H19/20, C07H21/02, C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence: antisense sequence FH
Key Location/Qualifiers
FT source 1. .18
FT Location/Qualifiers
source /organism="Artificial Sequence".
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1093
AR432617/c
LOCUS AR432617 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6653458.

ACCESSION AR432617
VERSION AR432617.1 GI:40195150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 19)
AUTHORS Manoharan, M., Cook, P.D. and Guinosso, C.J.
TITLE Modified oligonucleotides
JOURNAL Patent: US 6653458-A 7 25-NOV-2003;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1094
AR432617/c
LOCUS AR432617 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6653458.
ACCESSION AR432617
VERSION AR432617.1 GI:40195150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 19)
AUTHORS Manoharan, M., Cook, P.D. and Guinosso, C.J.
TITLE Modified oligonucleotides
JOURNAL Patent: US 6653458-A 7 25-NOV-2003;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1095
AR139961/c
LOCUS AR139961 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 33 from patent US 6207417.
ACCESSION AR139961
VERSION AR139961.1 GI:14482457
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Zsebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 33 27-MAR-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e+02;

Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1101

ARI39960

LOCUS ARI39960 20 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 32 from patent US 6207417.

ACCESSION ARI39960

VERSION ARI39960.1 GI:14482456

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.

TITLE DNA encoding stem cell factor

JOURNAL Patent: US 6207417-A 32 27-MAR-2001;

FEATURES

source Location/Qualifiers

1..20

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183

Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1102

ARI39960/c

LOCUS ARI39960 20 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 32 from patent US 6207417.

ACCESSION ARI39960

VERSION ARI39960.1 GI:14482456

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.

TITLE DNA encoding stem cell factor

JOURNAL Patent: US 6207417-A 32 27-MAR-2001;

FEATURES

source Location/Qualifiers

1..20

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1103

ARI40279

LOCUS ARI40279 20 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 32 from patent US 6207454.

ACCESSION ARI40279

VERSION ARI40279.1 GI:14482775

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.

TITLE Method for enhancing the efficiency of gene transfer with stem cell factor (SCF) polypeptide

JOURNAL

FEATURES

source

JOURNAL Patent: US 6207454-A 32 27-MAR-2001;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183

Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1104

ARI40279/c

LOCUS ARI40279 20 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 32 from patent US 6207454.

ACCESSION ARI40279

VERSION ARI40279.1 GI:14482775

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.

TITLE Method for enhancing the efficiency of gene transfer with stem cell factor (SCF) polypeptide

JOURNAL Patent: US 6207454-A 32 27-MAR-2001;

FEATURES

source Location/Qualifiers

1..20

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1105

ARI40557

LOCUS ARI40557 20 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 32 from patent US 6207802.

ACCESSION ARI40557

VERSION ARI40557.1 GI:14483053

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.

TITLE Stem cell factor and compositions

JOURNAL Patent: US 6207802-A 32 27-MAR-2001;

FEATURES

source Location/Qualifiers

1..20

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183

Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1106

ARI40557/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI40557
DEFINITION Sequence 32 from patent US 6207802.
ACCESSION ARI40557
VERSION ARI40557
KEYWORDS ARI40557.1 GI:14483053
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 32 27-MAR-2001;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1107
BD234126 20 bp DNA linear PAT 17-JUL-2003
LOCUS BD234126
DEFINITION Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION BD234126
VERSION BD234126.1 GI:33043896
KEYWORDS JP 2002532072-A/14.
SOURCE JP 2002532072-A/14.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipovsek,D.
TITLE Protein skeleton of antibody mimetics and other binding proteins
JOURNAL Patent: JP 2002532072-A 14 02-OCT-2002;
COMMENT OS Artificial Sequence
PN JP 2002532072-A/14
PD 02-OCT-2002
PF 09-DEC-1999 JP 2000587187
PR 10-DEC-1998 US 60/111737
PI DASA LIPOVSEK
PC C12N15/09,C07K1/04,C07K14/78,C07K16/46,C07K17/00,C07K19/00, PC
C12P21/02,
PC C12N15/00
CC Puromycin linker oligonucleotide
FH Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 1108
BD234126/c 20 bp DNA linear PAT 17-JUL-2003
LOCUS BD234126

DEFINITION Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION BD234126
VERSION BD234126.1 GI:33043896
KEYWORDS JP 2002532072-A/14.
SOURCE JP 2002532072-A/14.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipovsek,D.
TITLE Protein skeleton of antibody mimetics and other binding proteins
JOURNAL Patent: JP 2002532072-A 14 02-OCT-2002;
COMMENT OS Artificial Sequence
PN JP 2002532072-A/14
PD 02-OCT-2002
PF 09-DEC-1999 JP 2000587187
PR 10-DEC-1998 US 60/111737
PI DASA LIPOVSEK
PC C12N15/09,C07K1/04,C07K14/78,C07K16/46,C07K17/00,C07K19/00, PC
C12P21/02,
PC C12N15/00
CC Puromycin linker oligonucleotide
FH Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 18 TTTT TTTT TTTT TTTT TTTT 1
RESULT 1109
AX825109 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825109/c
DEFINITION Sequence 7 from Patent WO03072818.
ACCESSION AX825109
VERSION AX825109.1 GI:39750838
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 7 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 6
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/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

modified_base 12 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 8.1e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1110
AX825115/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825115
DEFINITION Sequence 13 from Patent WO03072818.
ACCESSION AX825115
VERSION AX825115.1 GI:39750844
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 13 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers
source 1. 21

modified_base 3 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 8.1e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1111
AX825118/c

LOCUS AX825118 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 16 from Patent WO03072818.
ACCESSION AX825118
VERSION AX825118.1 GI:39750847
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 16 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers
source 1. 21

misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
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modified_base 15 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) " /mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 8.1e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1112
AX825127 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825127
DEFINITION Sequence 25 from Patent WO03072818.
ACCESSION AX825127
VERSION AX825127.1 GI:39750856
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 25 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers
source 1. 21

misc_binding 1 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

modified_base /bound_moiety="Biotin"
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/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
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Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18
RESULT 1113
LOCUS AX825131 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 29 from Patent WO03072818.
ACCESSION AX825131
VERSION AX825131.1 GI:39750860
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 29 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
1
/bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
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/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
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/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid) "
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modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
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Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1114
LOCUS AX825134 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 32 from Patent WO03072818.
ACCESSION AX825134
VERSION AX825134.1 GI:39750863
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 32 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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/bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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modified_base 15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1115
LOCUS AX825139 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 37 from Patent WO03072818.
ACCESSION AX825139
VERSION AX825139.1 GI:39750868
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids

JOURNAL Patent: WO 03072818-A 37 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18
RESULT 1116
AX825143 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825143
DEFINITION Sequence 41 from Patent WO03072818.
ACCESSION AX825143
VERSION AX825143.1 GI:39750872
KEYWORDS
SOURCE .
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 41 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18
RESULT 1117
AX825107/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825107/c
DEFINITION Sequence 5 from Patent WO03072818.
ACCESSION AX825107
VERSION AX825107.1 GI:39750836
KEYWORDS
SOURCE .
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 5 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 15
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
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Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1118
AX825108/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825108

DEFINITION Sequence 6 from Patent WO03072818.
AX8251108
VERSION AX8251108.1 GI:39750837
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 6 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
modified_base
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/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid) "
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/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1119
AX825110/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 8 from Patent WO03072818.
DEFINITION AX825110
AX825110
ACCESSION AX825110.1 GI:39750839
VERSION AX825110.1
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 8 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1120
AX825116/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 14 from Patent WO03072818.
DEFINITION AX825116
AX825116
ACCESSION AX825116
VERSION AX825116.1 GI:39750845
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 14 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
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modified_base 15
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1121
AX825140

LOCUS AX825140 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 38 from Patent WO03072818.
ACCESSION AX825140
VERSION AX825140.1 GI:39750869
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 38 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES 1..21
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misc_binding
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modified_base
/note="LNA-T (Locked Nucleic Acid) "
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modified_base
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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modified_base
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
12
modified_base
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15
modified_base
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
DB 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1122
AX825141

LOCUS AX825141 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 39 from Patent WO03072818.
ACCESSION AX825141
VERSION AX825141.1 GI:39750870
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 39 04-SEP-2003;

FEATURES Degussa Bioactives GmbH (DE)
source location/Qualifiers
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
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/note="LNA-T (Locked Nucleic Acid) "
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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modified_base
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12
modified_base
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/mod_base=OTHER
18

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
DB 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1123
AX825142

LOCUS AX825142 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 40 from Patent WO03072818.
ACCESSION AX825142
VERSION AX825142.1 GI:39750871
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 40 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

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18

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modified_base
18 /mod_base=OTHER
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Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2166 TTTTTTTTTTTTTTTTTT 2183
|||||
1 TTTTTTTTTTTTTTTTTT 18

RESULT 1124
LOCUS AX825144 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 42 from Patent WO03072818.
ACCESSION AX825144
VERSION AX825144.1 GI:39750873
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 42 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
location/Qualifiers
FEATURES
source
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
1 /bound_moiety="Biotin"
3 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
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6 /note="LNA-T (Locked Nucleic Acid) "
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18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

misc_binding
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9 /note="LNA-T (Locked Nucleic Acid) "
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12 /note="LNA-T (Locked Nucleic Acid) "
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12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

modified_base
3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
|||||
1 TTTTTTTTTTTTTTTTTT 18

Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1125
LOCUS AX825145 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 43 from Patent WO03072818.

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[illegible]

/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1127
AX825128 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825128
DEFINITION Sequence 26 from Patent WO03072818.
ACCESSION AX825128
VERSION AX825128.1 GI:39750857
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 26 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding
1 /bound_moiety="Biotin"
3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1128
AX825129 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825129
DEFINITION Sequence 27 from Patent WO03072818.
ACCESSION AX825129
VERSION AX825129.1 GI:39750858
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 27 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding
1 /bound_moiety="Biotin"
3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1129
AX825130 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825130
DEFINITION Sequence 28 from Patent WO03072818.
ACCESSION AX825130
VERSION AX825130.1 GI:39750859
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 28 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES		Location/Qualifiers	
source		1..21	/organism="synthetic construct"
			/mol_type="unassigned DNA"
			/db_xref="taxon:32630"
			/note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"
misc_binding		1	/bound_moiety="Biotin"
modified_base		3	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER
modified_base		6	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER
modified_base		9	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER
modified_base		12	/note="LNA-T (Locked Nucleic Acid)"
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modified_base		15	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER
modified_base		18	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER
Query Match		0.6%;	Score 18; DB 1; Length 21;
Best Local Similarity		100.0%;	Pred. No. 8.1e+02;
Matches	18;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2166	TTTTTTTTTTTTTTTTTTT	2183
Db	1	TTTTTTTTTTTTTTTTTTT	18
RESULT 1130			
AX825132/c		21 bp	DNA
LOCUS	AX825132	Sequence 30 from Patent WO03072818.	linear
DEFINITION	AX825132		
ACCESSION	AX825132		
VERSION	AX825132.1	GI:39750861	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	1	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.	
TITLE		Method for sorting single-stranded nucleic acids	
JOURNAL		Patent: WO 03072818-A 30 04-SEP-2003;	
		Degussa Bioactives GmbH (DE)	
FEATURES			
source		Location/Qualifiers	
		1..21	/organism="synthetic construct"
			/mol_type="unassigned DNA"
			/db_xref="taxon:32630"
			/note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"
misc_binding		1	/bound_moiety="Biotin"
modified_base		3	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER
modified_base		6	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER
modified_base		9	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER
modified_base		12	/note="LNA-T (Locked Nucleic Acid)"
			/mod_base=OTHER

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modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
18 AAAAAAAAAAAAAAAAAA 1

RESULT 1131
AX825123 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825123
DEFINITION Sequence 21 from Patent WO03072818.
ACCESSION AX825123
VERSION AX825123.1 GI:39750852
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single stranded nucleic acids
JOURNAL Patent: WO 03072818-A 21 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers

FEATURES
source
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
1
/bound_moiety="Biotin"
/misc_binding
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
1 TTTTTTTTTTTTTTTTTT 18

RESULT 1132
AX825123 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825123/c
DEFINITION Sequence 21 from Patent WO03072818.
ACCESSION AX825123

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VERSION	AX825123.1	GI:39750852	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1	artificial sequences.	
AUTHORS	1	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.	
TITLE		Method for sorting single-stranded nucleic acids	
JOURNAL		Patent: WO 03072818-A 21 04-SEP-2003;	
DEGUS		Degussa Bioactives GmbH (DE)	
LOCATION/QUALIFIERS			
1. 21			
/organism="synthetic construct"			
/mol_type="unassigned DNA"			
/db_xref="taxon:32630"			
/note="Beschreibung der kuenstlichen			
Sequenz:Capture-Oligonukleotid"			
1			
/bound_moiety="Biotin"			
3			
/note="LNA-T (Locked Nucleic Acid) "			
/mod_base=OTHER			
6			
/note="LNA-T (Locked Nucleic Acid) "			
/mod_base=OTHER			
9			
/note="LNA-T (Locked Nucleic Acid) "			
/mod_base=OTHER			
12			
/note="LNA-T (Locked Nucleic Acid) "			
/mod_base=OTHER			
15			
/note="LNA-T (Locked Nucleic Acid) "			
/mod_base=OTHER			
18			
/note="LNA-T (Locked Nucleic Acid) "			
/mod_base=OTHER			
Query Match	0.6%;	Score 18;	DB 1; Length 21;
Best Local Similarity	100.0%;	Pred. No. 8.1e+02;	
Matches	18;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2786	AAAAAAAAAAAAAAAAAAAA	2803
Db	18	AAAAAAAAAAAAAAAAAAAA	1
RESULT 1133			
AX825124			
LOCUS	AX825124	21 bp	DNA
DEFINITION	Sequence 22 from Patent WO03072818.		linear
ACCESSION	AX825124		
VERSION	AX825124.1	GI:39750853	
KEYWORDS			
SOURCE			
ORGANISM	synthetic construct		
ARTIFICIAL SEQUENCES			
1			
Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.			
Method for sorting single-stranded nucleic acids			
Patent: WO 03072818-A 22 04-SEP-2003;			
Degussa Bioactives GmbH (DE)			
Location/Qualifiers			
1. 21			
/organism="synthetic construct"			
/mol_type="unassigned DNA"			
/db_xref="taxon:32630"			
/note="Beschreibung der kuenstlichen			
Sequenz:Capture-Oligonukleotid"			
1			
/bound_moiety="Biotin"			
3			
/note="LNA-T (Locked Nucleic Acid) "			

modified_base	/mod_base=OTHER
6	/note="LNA-T (Locked Nucleic Acid) "
modified_base	/mod_base=OTHER
9	/note="LNA-T (Locked Nucleic Acid) "
modified_base	/mod_base=OTHER
12	/note="LNA-T (Locked Nucleic Acid) "
modified_base	/mod_base=OTHER
15	/note="LNA-T (Locked Nucleic Acid) "
modified_base	/mod_base=OTHER
18	/note="LNA-T (Locked Nucleic Acid) "
modified_base	/mod_base=OTHER

Query Match	0.6%;	Score 18;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 8.1e+02;		
Matches	18;	Conservative	0;	Mismatches 0;
Indels			0;	Gaps 0;

Qy	2166	TTTTTTTTTTTTTTTTTT	2183
Db	1	TTTTTTTTTTTTTTTTTT	18

RESULT 1134				
AX825124/c				
LOCUS	AX825124	21 bp	DNA	linear
DEFINITION	Sequence 22 from Patent WO03072818.			PAT 11-DEC-2003
ACCESSION	AX825124			
VERSION	AX825124.1	GI:39750853		
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
	artificial sequences.			
REFERENCE	1			
AUTHORS	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.			
TITLE	Method for sorting single-stranded nucleic acids			
JOURNAL	Patent: WO 03072818-A 22 04-SEP-2003;			
	Degussa Bioactives GmbH (DE)			
FEATURES	Location/Qualifiers			
source	1..21			
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	/mol_type="unassigned DNA"			
	/db_xref="taxon:32630"			
	/note="Beschreibung der kuenstlichen			
	Sequenz: Capture-Oligonukleotid"			
	1			
	/bound_moiety="Biotin"			
	3			
	/note="LNA-T (Locked Nucleic Acid) "			
	/mod_base=OTHER			
	6			
	/note="LNA-T (Locked Nucleic Acid) "			
	/mod_base=OTHER			
	9			
	/note="LNA-T (Locked Nucleic Acid) "			
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	/mod_base=OTHER			
	15			
	/note="LNA-T (Locked Nucleic Acid) "			
	/mod_base=OTHER			
	18			
	/note="LNA-T (Locked Nucleic Acid) "			
	/mod_base=OTHER			

Query Match	0.6%;	Score 18;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 8.1e+02;		
Matches	18;	Conservative	0;	Mismatches 0;
Indels			0;	Gaps 0;

Qy	2166	TTTTTTTTTTTTTTTTTT	2183
Db	1	TTTTTTTTTTTTTTTTTT	18

QY 2786 AAAAAAAAAAAAAAAAAA 2803
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1135
AX825125 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825125
DEFINITION Sequence 23 from Patent WO03072818.
ACCESSION AX825125
VERSION AX825125.1 GI:39750854
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 23 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18
RESULT 1136
AX825125/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825125
DEFINITION Sequence 23 from Patent WO03072818.
ACCESSION AX825125
VERSION AX825125.1 GI:39750854
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 23 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
location/Qualifiers

source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid) "
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1137
AX825126 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825126
DEFINITION Sequence 24 from Patent WO03072818.
ACCESSION AX825126
VERSION AX825126.1 GI:39750855
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 24 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15

modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1138
AX825126/c LOCUS AX825126 21 bp DNA PAT 11-DEC-2003
DEFINITION Sequence 24 from Patent WO03072818.
ACCESSION AX825126
VERSION AX825126.1 GI:39750855
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 24 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
modified_base 3 /bound_moiety="Biotin"
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1139
AR164318 LOCUS AR164318 22 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6271369.
ACCESSION AR164318
VERSION AR164318.1 GI:16235432

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence, P.F., Silverman, R.H., Maitra, R.K. and Lesiak, K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 1 07-AUG-2001;
FEATURES
source 1. 22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 5 TTTT TTTT TTTT TTTT TTTT 22

RESULT 1140
AR164318/c LOCUS AR164318 22 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6271369.
ACCESSION AR164318
VERSION AR164318.1 GI:16235432
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence, P.F., Silverman, R.H., Maitra, R.K. and Lesiak, K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 1 07-AUG-2001;
FEATURES
source 1. 22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 1141
AR164319 LOCUS AR164319 22 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6271369.
ACCESSION AR164319
VERSION AR164319.1 GI:16235434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence, P.F., Silverman, R.H., Maitra, R.K. and Lesiak, K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 2 07-AUG-2001;
FEATURES
source 1. 22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183
|||||
5 TTTT TTTT TTTT TTTT TTTT 22

RESULT 1142

LOCUS AR164319/c 22 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6271369.
ACCESSION AR164319
VERSION AR164319.1 GI:16235434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 2 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..22
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/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 1143

LOCUS I31810 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5583032.
ACCESSION I31810
VERSION I31810.1 GI:1822601
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 1 10-DEC-1996;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183
Db 5 TTTT TTTT TTTT TTTT TTTT 22

RESULT 1144

LOCUS I31810/c 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5583032.
ACCESSION I31810
VERSION I31810.1 GI:1822601
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.

TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 1 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 1145
LOCUS I31811 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5583032.
ACCESSION I31811
VERSION I31811.1 GI:1822602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 2 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..22
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/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183
Db 5 TTTT TTTT TTTT TTTT TTTT 22

RESULT 1146
LOCUS I31811/c 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5583032.
ACCESSION I31811
VERSION I31811.1 GI:1822602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 2 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..22
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/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 1147

169407	LOCUS	169407	22 bp	DNA	linear	PAT 04-FEB-1998
	DEFINITION	Sequence 1 from patent US 5677289.				
	ACCESSION	169407				
	VERSION	169407.1	GI:2831529			
	KEYWORDS					
	SOURCE	Unknown.				
	ORGANISM	Unknown.				
	REFERENCE	Unclassified.				
	AUTHORS	1 (bases 1 to 22)				
	TITLE	Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.				
		Method of cleaving specific strands of RNA and medical treatments thereby				
	JOURNAL	Patent: US 5677289-A 1 14-OCT-1997;				
	FEATURES	Location/Qualifiers				
	source	1. .22				
		/organism="unknown"				
		/mol_type="unassigned DNA"				
	Query Match	0.6%; Score 18; DB 1; Length 22;				
	Best Local Similarity	100.0%; Pred. No. 9.2e+02;				
	Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	2166	TTTTTTTTTTTTTTTTTT	2183			
Db	5	TTTTTTTTTTTTTTTTTT	22			
RESULT 1148						
169407/c	LOCUS	169407	22 bp	DNA	linear	PAT 04-FEB-1998
	DEFINITION	Sequence 1 from patent US 5677289.				
	ACCESSION	169407				
	VERSION	169407.1	GI:2831529			
	KEYWORDS					
	SOURCE	Unknown.				
	ORGANISM	Unknown.				
	REFERENCE	Unclassified.				
	AUTHORS	1 (bases 1 to 22)				
	TITLE	Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.				
		Method of cleaving specific strands of RNA and medical treatments thereby				
	JOURNAL	Patent: US 5677289-A 1 14-OCT-1997;				
	FEATURES	Location/Qualifiers				
	source	1. .22				
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		/mol_type="unassigned DNA"				
	Query Match	0.6%; Score 18; DB 1; Length 22;				
	Best Local Similarity	100.0%; Pred. No. 9.2e+02;				
	Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	2786	AAAAAAAAAAAAAAAAAA	2803			
Db	22	AAAAAAAAAAAAAAAAAA	5			
RESULT 1149						
169408	LOCUS	169408	22 bp	DNA	linear	PAT 04-FEB-1998
	DEFINITION	Sequence 2 from patent US 5677289.				
	ACCESSION	169408				
	VERSION	169408.1	GI:2831530			
	KEYWORDS					
	SOURCE	Unknown.				
	ORGANISM	Unknown.				
	REFERENCE	Unclassified.				
	AUTHORS	1 (bases 1 to 22)				
	TITLE	Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.				
		Method of cleaving specific strands of RNA and medical treatments thereby				
	JOURNAL	Patent: US 5677289-A 2 14-OCT-1997;				
	FEATURES	Location/Qualifiers				

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    /db_xref="taxon:32630"

Query Match
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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 6 AAAAAAAAAAAAAAAAAA 23

RESULT 1152
LOCUS E12391 23 bp DNA linear PAT 27-APR-1998
DEFINITION Oligonucleotide primer.
ACCESSION E12391
VERSION E12391.1 GI:3251224
KEYWORDS JP 1996322598-A/1.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Katou,K.
TITLE INDEXING METHOD OF DNA MOLECULE
JOURNAL Patent: JP 1996322598-A 1 10-DEC-1996;
COMMENT RES DEV CORP OF JAPAN
OS None
OC Artificial sequences.
PN JP 1996322598-A/1
PD 10-DEC-1996
PF 12-SEP-1995 JP 1995234122
PR 28-MAR-1995 JP 95P 69695
PI KATOU KIKUYA
PC C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
CC strandedness: Single;
CC topology: linear;
FH Key Location/Qualifiers
FT source 1. .23
FT location/Qualifiers
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Query Match
    0.6%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTT 2181
Db 5 CCTTTTCTTTTCTTTT 22

RESULT 1153
LOCUS AX394607 23 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 5 from Patent EP1186673.
ACCESSION AX394607
VERSION AX394607.1 GI:21065720
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 5 13-MAR-2002;
Agilent Technologies Inc (US)
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FEATURES
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Query Match
    0.6%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1154
LOCUS AX394607/c 23 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 5 from Patent EP1186673.
ACCESSION AX394607
VERSION AX394607.1 GI:21065720
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 5 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES
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    location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="probes to target sequences"

Query Match
    0.6%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTTCTTT 2183
Db 18 TTTTCTTTTCTTTTCTTT 1

RESULT 1155
LOCUS ARI68453/c 24 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 82 from patent US 6287854.
ACCESSION ARI68453
VERSION ARI68453.1 GI:17904379
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Spurr,N.K., Gray,I.C. and Stewart,L.M.
TITLE Diagnosis of susceptibility to cancer and treatment thereof
JOURNAL Patent: US 6287854-A 82 11-SEP-2001;
FEATURES
    source
    location/Qualifiers
    1. .24
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 24 AAAAAAAAAAAAAAAAAA 7
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RESULT 1156
AX394609
LOCUS AX394609 24 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 7 from Patent EP1186673.
ACCESSION AX394609
VERSION AX394609.1 GI:21065722
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 7 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match 0.6%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1157
AX394609/c
LOCUS AX394609 24 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 7 from Patent EP1186673.
ACCESSION AX394609
VERSION AX394609.1 GI:21065722
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 7 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES
source Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match 0.6%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
Db 18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1158
BD097127
LOCUS BD097127 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Support for immobilizing nucleotide and process for producing the
same.
ACCESSION BD097127
VERSION BD097127.1 GI:22642701
KEYWORDS
SOURCE synthetic construct
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ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
TITLE Support for immobilizing nucleotide and process for producing the
JOURNAL Patent: WO 0155365-A 1 02-AUG-2001;
TOYO KOHAN CO LTD,MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,
KOJIRO TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0155365-A/1
PD 02-AUG-2001
PE 24-JAN-2001 WO 2001JP000443
PR 27-JAN-2000 JP 00P 019301
PI MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,KOJIRO PI
TAKAHASHI
PC C12N15/10,C07H21/04//G01N33/50,C12Q1/68
CC Support for immobilizing nucleotide and process for producing
the same
FH Key location/Qualifiers
FT source 1..24
FEATURES
source Location/Qualifiers
1..24
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Db 6 TTTT TTTT TTTT TTTT TTTT 23
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RESULT 1159
BD097127/c
LOCUS BD097127 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Support for immobilizing nucleotide and process for producing the
same.
ACCESSION BD097127
VERSION BD097127.1 GI:22642701
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
TITLE Support for immobilizing nucleotide and process for producing the
JOURNAL Patent: WO 0155365-A 1 02-AUG-2001;
TOYO KOHAN CO LTD,MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,
KOJIRO TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0155365-A/1
PD 02-AUG-2001
PE 24-JAN-2001 WO 2001JP000443
PR 27-JAN-2000 JP 00P 019301
PI MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,KOJIRO PI
TAKAHASHI
PC C12N15/10,C07H21/04//G01N33/50,C12Q1/68
CC Support for immobilizing nucleotide and process for producing
the same
FH Key location/Qualifiers
FT source 1..24
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 0.6%; Score 18; DB 1; Length 24;
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
DB 23 AAAAAAAAAAAAAAAAAA 6

RESULT 1160

BD161931 24 bp DNA linear PAT 17-JAN-2003

LOCUS BD161931
DEFINITION Method for carrying out thermal cycle of PCR using DNA-immobilized substrate.

ACCESSION BD161931 GI:27867689

VERSION BD161931.1

KEYWORDS JP 2002191369-A/8.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 24)

AUTHORS Tanga,M., Okamura,H. and Takahashi,K.

TITLE Method for carrying out thermal cycle of PCR using DNA-immobilized

JOURNAL Patent: JP 2002191369-A 8 09-JUL-2002;

COMMENT TOYO KOHAN CO LTD,KOJIRO TAKAHASHI

OS Artificial Sequence

PN JP 2002191369-A/8

PD 09-JUL-2002

PF 27-DEC-2000 JP 2000399573

PI MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC

C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC Method for

carrying out thermal cycle of PCR using DNA- CC

immobilized

CC substrate

FH Key Location/Qualifiers

FT source 1..24 /organism='Artificial Sequence'.

FT Location/Qualifiers

1..24

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.6%; Score 18; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183

DB 6 TTTT TTTT TTTT TTTT TTTT 23

RESULT 1161

BD161931 24 bp DNA linear PAT 17-JAN-2003

LOCUS BD161931
DEFINITION Method for carrying out thermal cycle of PCR using DNA-immobilized

substrate.

ACCESSION BD161931

VERSION BD161931.1 GI:27867689

KEYWORDS JP 2002191369-A/8.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 24)

AUTHORS Tanga,M., Okamura,H. and Takahashi,K.

TITLE Method for carrying out thermal cycle of PCR using DNA-immobilized

JOURNAL Patent: JP 2002191369-A 8 09-JUL-2002;

COMMENT TOYO KOHAN CO LTD,KOJIRO TAKAHASHI

OS Artificial Sequence

PN JP 2002191369-A/8

PD 09-JUL-2002

PF 27-DEC-2000 JP 2000399573

PI MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC Method for

carrying out thermal cycle of PCR using DNA- CC

immobilized

CC substrate

FH Key Location/Qualifiers

FT source 1..24 /organism='Artificial Sequence'.

FT Location/Qualifiers

1..24

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.6%; Score 18; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

DB 23 AAAAAAAAAAAAAAAAAA 6

RESULT 1162

AX394611 25 bp DNA linear PAT 18-MAY-2002

LOCUS AX394611
DEFINITION Sequence 9 from Patent EP1186673.

ACCESSION AX394611

VERSION AX394611.1 GI:21065724

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Wobler,P.K. and Delenstarr,G.C.

TITLE Calibration of molecular array data

JOURNAL Patent: EP 1186673-A 9 13-MAR-2002;

Agilent Technologies Inc (US)

FT source Location/Qualifiers

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/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="probes to target sequences"

Query Match 0.6%; Score 18; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1163

AX394611 25 bp DNA linear PAT 18-MAY-2002

LOCUS AX394611
DEFINITION Sequence 9 from Patent EP1186673.

ACCESSION AX394611

VERSION AX394611.1 GI:21065724

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Wobler,P.K. and Delenstarr,G.C.

TITLE Calibration of molecular array data

JOURNAL Patent: EP 1186673-A 9 13-MAR-2002;

Agilent Technologies Inc (US)

FT source Location/Qualifiers

1..25

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match 0.6%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
DB 18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1164

ARI44828/c
LOCUS ARI44828 26 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 59 from patent US 6210942.
ACCESSION ARI44828
VERSION ARI44828.1 GI:15106695
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Unknown.
Unclassified.
1 (bases 1 to 26)
Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
Sarkanen,S. and Ford,J.D.
Recombinant pinorexinol/lariciresinol reductase, recombinant
dirigent protein, and methods of use
Patent: US 6210942-A 59 03-APR-2001;
Location/Qualifiers
1. .26
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/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
DB 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1165

ARI40280/c
LOCUS ARI40280 26 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 59 from patent US 6635459.
ACCESSION ARI40280
VERSION ARI40280.1 GI:40161559
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Unknown.
Unclassified.
1 (bases 1 to 26)
Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
Sarkanen,S. and Ford,J.D.
Nucleotide sequences encoding pinorexinol/lariciresinol reductase
proteins and their methods of use
Patent: US 6635459-A 59 21-OCT-2003;
Location/Qualifiers
1. .26
/organism="unknown"
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Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
DB 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1166

AXI91907/c

LOCUS AXI91907 26 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 59 from Patent WO0149833.
ACCESSION AXI91907
VERSION AXI91907
KEYWORDS AXI91907.1 GI:15210057

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

synthetic construct
synthetic construct
artificial sequences.
1
Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
Ford,J.D. and Sarkanen,S.
Recombinant pinorexinol/lariciresinol reductase, recombinant
dirigent protein, and methods of use
Patent: WO 0149833-A 59 12-JUL-2001;
Washington State University Research Foundation (US) ; REGENTS OF
THE UNIVERSITY OF MINNESOTA (US)
Location/Qualifiers
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
misc_feature 1. .26
/note="cDNA synthesis linker primer"

Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
DB 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1167

BD064385/c
LOCUS BD064385 26 bp DNA linear PAT 27-AUG-2002
DEFINITION Recombinant pinorexinol/lariciresinol reductases,recombinant
dirigent proteins and methods of use.
ACCESSION BD064385
VERSION BD064385.1 GI:22609988
KEYWORDS JP 2001507931-A/26.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unclassified.
1 (bases 1 to 26)
Lewis,N.G., Davin,L.B., Kostova,A.T.D., Fujita,M., Gang,D.R. and
Sarkanen,S.
Recombinant pinorexinol/lariciresinol reductases,recombinant
dirigent proteins and methods of use
Patent: JP 2001507931-A 26 19-JUN-2001;
WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
PN JP 2001507931-A/26
PD 19-JUN-2001
PF 07-NOV-1997 JP 1998521816
PR 08-NOV-1996 US 60/030522,31-JUL-1997 US 60/054380 PI
NORMAN G LEWIS, LAURENCE B DAVIN, ALBENA T DINKOVA KOSTOVA, PI
MASAYUKI FUJITA,
PI DAVID R GANG, SIMO SARKANEN
PC C12N9/02, C12N15/53, C12N15/29
CC Strandedness: Single;
CC Topology: linear;
CC 'cDNA synthesis linker primer'
FH key Location/Qualifiers.

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RESULT 1173
ARI64510
LOCUS ARI64510 26 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6274147.
ACCESSION ARI64510
VERSION ARI64510.1 GI:16237563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Vakharia,V.N. and Yao,K.
TITLE Method for generating nonpathogenic infectious pancreatic necrosis virus (IPNV) from synthetic RNA transcripts
JOURNAL Patent: US 6274147-A 1 14-AUG-2001;
FEATURES
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Location/Qualifiers
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QY 2164 CCTTTTCTTTTCTTTTCTT 2181
Db 9 CCTTTTCTTTTCTTTTCTT 26

RESULT 1174
ARI97618
LOCUS ARI97618 26 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 703 from patent US 6352829.
ACCESSION ARI97618
VERSION ARI97618.1 GI:20247467
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 703 05-MAR-2002;
FEATURES
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Location/Qualifiers
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/mol_type="unassigned DNA"

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Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1093 AGCTGTCATTGGCTAGGACTTTG 1118
Db 1 AGCTGTCACCTAGCCAGGACTTTG 26

RESULT 1175
AR259772
LOCUS AR259772 26 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 703 from patent US 6489455.
ACCESSION AR259772
VERSION AR259772.1 GI:27310283
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.

TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 703 03-DEC-2002;
FEATURES
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Location/Qualifiers
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Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1093 AGCTGTCATTGGCTAGGACTTTG 1118
Db 1 AGCTGTCACCTAGCCAGGACTTTG 26

RESULT 1176
AX394613
LOCUS AX394613 26 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 11 from Patent EP1186673.
ACCESSION AX394613
VERSION AX394613.1 GI:21065726
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 11 13-MAR-2002;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1177
AX394613/c
LOCUS AX394613 26 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 11 from Patent EP1186673.
ACCESSION AX394613
VERSION AX394613.1 GI:21065726
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 11 13-MAR-2002;
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Location/Qualifiers
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/note="probes to target sequences"

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2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183
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18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1178

AX827015 26 bp RNA linear PAT 12-DEC-2003
DEFINITION Sequence 12 from Patent EP1344835.
AX827015
VERSION AX827015.1 GI:39837222
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
Li,D.
TITLE Real-time nucleic acid detection processes and compositions
JOURNAL Patent: EP 1344835-A 12 17-SEP-2003;
Enzo Life Sciences, Inc. (US)
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source Location/Qualifiers
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/note="Description of Artificial Sequence: Primer"

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Best Local Similarity 100.0%; Pred.No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 18

RESULT 1179

AX827015 26 bp RNA linear PAT 12-DEC-2003
LOCUS AX827015/c
DEFINITION Sequence 12 from Patent EP1344835.
AX827015
VERSION AX827015.1 GI:39837222
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
Li,D.
TITLE Real-time nucleic acid detection processes and compositions
JOURNAL Patent: EP 1344835-A 12 17-SEP-2003;
Enzo Life Sciences, Inc. (US)
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Best Local Similarity 100.0%; Pred.No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183
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18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1180
AX839907 26 bp RNA linear PAT 16-DEC-2003
LOCUS AX839907
DEFINITION Sequence 12 from Patent EP1348713.

AX839907 AX839907.1 GI:39978438
VERSION AX839907.1
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stavrianopoulos,J.G. and Rabbani,E.
TITLE Labeling reagents and labeled targets, target labeling
processes and other processes for using same in nucleic acid
determinations and analyses
JOURNAL Patent: EP 1348713-A 12 01-OCT-2003;
Enzo Life Sciences, Inc. (US)
FEATURES
source Location/Qualifiers
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Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 18

RESULT 1181
AX839907 26 bp RNA linear PAT 16-DEC-2003
LOCUS AX839907/c
DEFINITION Sequence 12 from Patent EP1348713.
AX839907
VERSION AX839907.1 GI:39978438
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stavrianopoulos,J.G. and Rabbani,E.
TITLE Labeling reagents and labeled targets, target labeling
processes and other processes for using same in nucleic acid
determinations and analyses
JOURNAL Patent: EP 1348713-A 12 01-OCT-2003;
Enzo Life Sciences, Inc. (US)
FEATURES
source Location/Qualifiers
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/note="Description of Artificial Sequence: Primer"

Query Match 0.6%; Score 18; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1182
ARI42409 27 bp DNA linear PAT 08-AUG-2001
LOCUS ARI42409/c
DEFINITION Sequence 16 from patent US 6174992.
ARI42409
VERSION ARI42409.1 GI:15102709
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 27)

AUTHORS Ni,J., Yu,G.-L. and Gentz,R.
TITLE Human endometrial specific steroid-binding factor I, II and III
JOURNAL Patent: US 6174992-A 16 16-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..27
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Query Match 0.6%; Score 18; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 27 AAAAAAAAAAAAAAAAAA 10

RESULT 1183
AR182555/c

LOCUS AR182555 27 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 16 from patent US 6338948.
ACCESSION AR182555
VERSION AR182555.1 GI:20225762
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Ni,J., Yu,G.-L. and Gentz,R.
TITLE Human endometrial specific steroid-binding factor I, II and III
JOURNAL Patent: US 6338948-A 16 15-JAN-2002;
FEATURES Location/Qualifiers
SOURCE 1..27
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QY 2786 AAAAAAAAAAAAAAAAAA 2803
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RESULT 1184
AR027002/c

LOCUS AR027002 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5856138.
ACCESSION AR027002
VERSION AR027002.1 GI:5937842
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Fukuda,T.
TITLE Human parathyroid hormone muteins and production thereof
JOURNAL Patent: US 5856138-A 14 05-JAN-1999;
FEATURES Location/Qualifiers
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Query Match 0.6%; Score 18; DB 1; Length 27;
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Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1498 AATGAGAAACACAGAAATAAATT 1523
Db 26 AATGGGGCACACAGCAACAAATT 1

RESULT 1185
AX394614 27 bp DNA linear PAT 18-MAY-2002
LOCUS AX394614
DEFINITION Sequence 12 from Patent EP1186673.
ACCESSION AX394614
VERSION AX394614.1 GI:21065727
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 12 13-MAR-2002;
FEATURES Agilent Technologies Inc (US)
SOURCE Location/Qualifiers
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/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match 0.6%; Score 18; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1186
AX394614/c 27 bp DNA linear PAT 18-MAY-2002
LOCUS AX394614
DEFINITION Sequence 12 from Patent EP1186673.
ACCESSION AX394614
VERSION AX394614.1 GI:21065727
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 12 13-MAR-2002;
FEATURES Agilent Technologies Inc (US)
SOURCE Location/Qualifiers
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QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
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RESULT 1187
AR055110/c 28 bp DNA linear PAT 29-SEP-1999
LOCUS AR055110
DEFINITION Sequence 15 from patent US 5837468.
ACCESSION AR055110
VERSION AR055110.1 GI:5980687
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 28)

AUTHORS Wang, X., Duvick, J.P. and Briggs, S.P.
TITLE PCR-based cDNA subtractive cloning method
JOURNAL Patent: US 5837468-A 15 17-NOV-1998;
FEATURES Location/Qualifiers
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2785 GAAAAAAAAAAAAAAAAA 2802
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28 GAAAAAAAAAAAAAAAAA 11

RESULT 1188
AR068451/c 28 bp DNA linear PAT 29-SEP-1999
LOCUS AR068451
DEFINITION Sequence 15 from patent US 5853991.
ACCESSION AR068451
VERSION AR068451.1 GI:6000658
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 28)
AUTHORS Wang, X., Duvick, J.P. and Briggs, S.P.
TITLE PCR-based cDNA subtractive cloning method
JOURNAL Patent: US 5853991-A 15 29-DEC-1998;
FEATURES Location/Qualifiers
source 1..28
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/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
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28 GAAAAAAAAAAAAAAAAA 11

RESULT 1189
AR371171/c 28 bp DNA linear PAT 12-SEP-2003
LOCUS AR371171
DEFINITION Sequence 10 from patent US 6395306.
ACCESSION AR371171
VERSION AR371171.1 GI:34608085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 28)
AUTHORS Cui, X. and Lu, Y.
TITLE Bee venom protein and gene encoding same
JOURNAL Patent: US 6395306-A 10 28-MAY-2002;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
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28 AAAAAAAAAAAAAAAAAA 11

RESULT 1190
BD015304/c 28 bp DNA linear PAT 27-AUG-2002
LOCUS BD015304
DEFINITION Primer single-stranded DNA, process for preparing double-stranded
cDNA by using the same and process for amplifying one side
single-stranded DNA.
ACCESSION BD015304
VERSION BD015304.1 GI:22556442
KEYWORDS JP 2001204472-A/5.
SOURCE JP 2001204472-A/5.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Nakamura, T.
TITLE Primer single-stranded DNA, process for preparing double-stranded
cDNA by using the same and process for amplifying one side
JOURNAL Patent: JP 2001204472-A 5 31-JUL-2001;
SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT OS Artificial Sequence
PN JP 2001204472-A/5
PD 31-JUL-2001
PF 21-JAN-2000 JP 2000012535
PI TAKESHI NAKAMURA
PC C12N15/09, C12P19/34, G01N33/50//C12Q1/68, C12N15/00 CC PCR
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FH Key
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Query Match 0.6%; Score 18; DB 1; Length 28;
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QY 2786 AAAAAAAAAAAAAAAAAA 2803
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28 AAAAAAAAAAAAAAAAAA 11

RESULT 1191
AX394616 28 bp DNA linear PAT 18-MAY-2002
LOCUS AX394616
DEFINITION Sequence 14 from Patent Epl186673.
ACCESSION AX394616
VERSION AX394616.1 GI:21065729
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Wobler, P.K. and Delenstarr, G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 14 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES Location/Qualifiers
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QY 2786 AAAAAAAAAAAAAAAAAA 2803
|||||
28 AAAAAAAAAAAAAAAAAA 18

RESULT 1192

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AX394617
LOCUS AX394617 28 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 15 from Patent EP1186673.
ACCESSION AX394617
VERSION AX394617.1 GI:21065730
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 15 13-MAR-2002;
Agilent Technologies Inc (US)
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Query Match
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QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1193
AX394619 29 bp DNA linear PAT 18-MAY-2002
LOCUS AX394619
DEFINITION Sequence 17 from Patent EP1186673.
ACCESSION AX394619
VERSION AX394619.1 GI:21065732
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 17 13-MAR-2002;
Agilent Technologies Inc (US)
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QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1194
AX394621 30 bp DNA linear PAT 18-MAY-2002
LOCUS AX394621
DEFINITION Sequence 19 from Patent EP1186673.
ACCESSION AX394621
VERSION AX394621.1 GI:21065734
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
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TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 19 13-MAR-2002;
Agilent Technologies Inc (US)
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Query Match
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1195
AR242448/c 30 bp mRNA linear PAT 20-DEC-2002
LOCUS AR242448/c
DEFINITION Sequence 23 from patent US 6472509.
ACCESSION AR242448
VERSION AR242448.1 GI:27288865
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1
AUTHORS (bases 1 to 30)
TITLE Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
JOURNAL Patent: US 6472509-A 23 29-OCT-2002;
Agilent Technologies Inc (US)
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Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 30 AAAAAAAAAAAAAAAAAA 13

RESULT 1196
AR280216/c 30 bp mRNA linear PAT 10-APR-2003
LOCUS AR280216/c
DEFINITION Sequence 23 from patent US 6518045.
ACCESSION AR280216
VERSION AR280216.1 GI:29715606
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1
AUTHORS (bases 1 to 30)
TITLE Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
JOURNAL Patent: US 6518045-A 23 11-FEB-2003;
Agilent Technologies Inc (US)
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/organism="unknown"
/mol_type="mRNA"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 30 AAAAAAAAAAAAAAAAAA 13
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RESULT 1197
AR322431/c
LOCUS
DEFINITION Sequence 23 from patent US 6566097.
ACCESSION AR322431
VERSION AR322431.1 GI:33708184
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 30)
TITLE Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
JOURNAL Feline cytokine protein
Patent: US 6566097-A 23 20-MAY-2003;
FEATURES
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/organism="unknown"
/mol_type="mRNA"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 30 AAAAAAAAAAAAAAAAAA 13

RESULT 1198
AX394623
LOCUS
DEFINITION Sequence 21 from Patent Epl186673.
ACCESSION AX394623
VERSION AX394623.1 GI:21065736
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 21 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES
Location/Qualifiers
1..31
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/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 31;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1199
AR051291/c
LOCUS
DEFINITION Sequence 8 from patent US 5830662.
ACCESSION AR051291
VERSION AR051291.1 GI:5974655
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: US 5830662-A 8 03-NOV-1998;
FEATURES
Location/Qualifiers
1..32
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/mol_type="unassigned DNA"

Query Match
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1200
116939/c
LOCUS
DEFINITION Sequence 8 from patent US 5482845.
ACCESSION 116939
VERSION 116939.1 GI:1251847
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 32)
AUTHORS Soares,M.B. and Efstratiadis,A.
TITLE Method for construction of normalized cDNA libraries
JOURNAL Patent: US 5482845-A 8 09-JAN-1996;
FEATURES
Location/Qualifiers
1..32
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/mol_type="unassigned DNA"

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QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1201
145733/c
LOCUS
DEFINITION Sequence 8 from patent US 5637685.
ACCESSION 145733
VERSION 145733.1 GI:2469835
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 32)
AUTHORS Soares,M.B. and Efstratiadis,A.
TITLE Normalized cDNA libraries
JOURNAL Patent: US 5637685-A 8 10-JUN-1997;
FEATURES
Location/Qualifiers
1..32
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1202
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TITLE Method for construction of normalized cDNA libraries
JOURNAL Patent: US 5830662-A 8 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1200
116939/c
LOCUS 116939 32 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 8 from patent US 5482845.
ACCESSION 116939
VERSION 116939.1 GI:1251847
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 32)
AUTHORS Soares,M.B. and Efstratiadis,A.
TITLE Method for construction of normalized cDNA libraries
JOURNAL Patent: US 5482845-A 8 09-JAN-1996;
FEATURES Location/Qualifiers
source 1..32
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/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 32;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1201
145733/c
LOCUS 145733 32 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5637685.
ACCESSION 145733
VERSION 145733.1 GI:2469835
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 32)
AUTHORS Soares,M.B. and Efstratiadis,A.
TITLE Normalized cDNA libraries
JOURNAL Patent: US 5637685-A 8 10-JUN-1997;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1202

AX394625
LOCUS AX394625 32 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 23 from Patent EP1186673.
ACCESSION AX394625
VERSION AX394625.1 GI:21065738
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mobler, P.K. and Delenstarr, G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 23 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match 0.6%; Score 18; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1203
AR014684/c
LOCUS AR014684 32 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 7 from patent US 5773696.
ACCESSION AR014684
VERSION AR014684.1 GI:3972138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS (bases 1 to 32)
TITLE Liang, J., Shah, D., Maganlal, W., Y. Shun. and Rosenberger, C. Annette.
JOURNAL Antifungal polypeptide and methods for controlling plant pathogenic
FEATURES
source Patent: US 5773696-A 7 30-JUN-1998;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 18; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1204
AR341692/c
LOCUS AR341692 32 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 16 from patent US 6573361.
ACCESSION AR341692
VERSION AR341692.1 GI:33734520
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS (bases 1 to 32)
TITLE Bunkers, G.J., Liang, J., Mittanck, C.A., Seale, J.W. and Wu, Y.S.
JOURNAL Antifungal proteins and methods for their use
Patent: US 6573361-A 16 03-JUN-2003;

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1205
AR366811/c
LOCUS AR366811 32 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 8 from patent US 6329504.
ACCESSION AR366811
VERSION AR366811.1 GI:34599783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS (bases 1 to 32)
TITLE Liang, J., Shah, D.M., Wu, Y.S., Rosenberger, C.A. and Hakimi, S.
JOURNAL Antifungal polypeptide and methods for controlling plant pathogenic
FEATURES
source Patent: US 6329504-A 8 11-DEC-2001;
Location/Qualifiers
1..32
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1206
AR432384/c
LOCUS AR432384 32 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6653280.
ACCESSION AR432384
VERSION AR432384.1 GI:40194661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS (bases 1 to 32)
TITLE Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.
JOURNAL Antifungal polypeptide AlyAFP from Alyssum and methods for
controlling plant pathogenic fungi
FEATURES
source Patent: US 6653280-A 7 25-NOV-2003;
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 18; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 32 AAAAAAAAAAAAAAAAAA 15

RESULT 1207

Accession	LOCUS	REFERENCE	AUTHORS	TITLE	VERSION	KEYWORDS	SOURCE	ORGANISM	LOCUS	SEQUENCE	FROM	PATENT	DATE	LENGTH	DB	SCORE	PRED	NO.	CONSERVATIVE	MISMATCHES	INDELS	GAPS
AR409897/c	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
AR409897	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
AR409897.1	GI:40161032																					
AR409897/c	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
AR409897	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
AR409897.1	GI:40161032																					
AR409897/c	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
AR409897	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
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AR409897/c	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
AR409897	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
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AR409897/c	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
AR409897	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;	Pred No. 2.2e+03;	0;	Mismatches 5;	Indels 0;	Gaps 0;	
AR409897.1	GI:40161032																					
AR409897/c	AR409897	Sequence 10 from patent US 6635422.	Keene, J.D., Tenenbaum, S.A. and Carson, C.C.	Methods for isolating and characterizing endogenous mRNA-protein (MRNP) complexes	Patent: US 6635422-A 10 21-OCT-2003;	Location/Qualifiers	1. .32	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 32)	0.6%;	Score 18;	DB 1;	Length 32;	80.8%;						

FEATURES		Location/Qualifiers	
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Matches	17; Conservative	2; Mismatches	0; Indels 0; Gaps 0;
QY	2784	TGAAAAAAAAAAAAAAAAAAAA 2802	
Db	19	DKAAAAAAAAAAAAAAAAAAAA 1	
RESULT 1210			
LOCUS	ARI47331	19 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 6 from patent US 6221584.		
ACCESSION	ARI47331		
VERSION	ARI47331.1 GI:15111134		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 19)		
AUTHORS	Emrich,T., Leying,H., Hinzpeter,M. and Karl,G.		
TITLE	Method of detecting telomerase activity		
JOURNAL	Patent: US 6221584-A 6 24-APR-2001;		
FEATURES	Location/Qualifiers		
source	1..19 /organism="unknown" /mol_type="unassigned DNA"		
Query Match			
Best Local Similarity	0.6%;	Score 17.8;	DB 1; Length 19;
Matches	17; Conservative	2; Mismatches	0; Indels 0; Gaps 0;
QY	2170	TTTTTTTTTTTTTTTTTTAA 2188	
Db	1	TTTTTTTTTTTTTTTTTMM 19	
RESULT 1211			
LOCUS	ARI47331/c	19 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 6 from patent US 6221584.		
ACCESSION	ARI47331		
VERSION	ARI47331.1 GI:15111134		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 19)		
AUTHORS	Emrich,T., Leying,H., Hinzpeter,M. and Karl,G.		
TITLE	Method of detecting telomerase activity		
JOURNAL	Patent: US 6221584-A 6 24-APR-2001;		
FEATURES	Location/Qualifiers		
source	1..19 /organism="unknown" /mol_type="unassigned DNA"		
Query Match			
Best Local Similarity	0.6%;	Score 17.8;	DB 1; Length 19;
Matches	17; Conservative	2; Mismatches	0; Indels 0; Gaps 0;
QY	2784	TGAAAAAAAAAAAAAAAAAAAA 2802	
Db	19	DKAAAAAAAAAAAAAAAAAAAA 1	
RESULT 1212			
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LOCUS	AX103869	22 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence 61 from Patent WO0122972.				
ACCESSION	AX103869				
VERSION	AX103869.1	GI:13920066			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	artificial sequences.				
AUTHORS	1 Krieg,A.M., Schetter,C. and Vollmer,J.C.				
TITLE	Immunostimulatory nucleic acids				
JOURNAL	Patent: WO 0122972-A 61 05-APR-2001;				
	UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical				
	GmbH (DE)				
FEATURES	Location/Qualifiers				
source	1..22				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
Query Match	0.6%; Score 17.8; DB 1; Length 22;				
Best Local Similarity	90.5%; Pred. No. 1e+03;				
Matches	19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	2166	TTTTTTTTTTTTTTTTTTT	2186		
Db	1	TTTTTTTGTTTGTGTTT	21		
RESULT 1213					
LOCUS	AX457060	22 bp	DNA	linear	PAT 06-JUL-2002
DEFINITION	Sequence 21 from Patent WO0231186.				
ACCESSION	AX457060				
VERSION	AX457060.1	GI:21715842			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	artificial sequences.				
AUTHORS	1 Berlin,K.				
TITLE	Method for the detection of cytosine methylations				
JOURNAL	Patent: WO 0231186-A 21 18-APR-2002;				
	Epigenomics AG (DE)				
FEATURES	Location/Qualifiers				
source	1..22				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Primer"				
Query Match	0.6%; Score 17.8; DB 1; Length 22;				
Best Local Similarity	90.5%; Pred. No. 1e+03;				
Matches	19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	2167	TTTTTTTTTTTTTTTTTTTA	2187		
Db	1	TTTTTTTATTTTTATTTA	21		
RESULT 1214					
LOCUS	AX546922	22 bp	DNA	linear	PAT 01-MAR-2003
DEFINITION	Sequence 61 from Patent WO02053141.				
ACCESSION	AX546922				
VERSION	AX546922.1	GI:25812066			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	artificial sequences.				
AUTHORS	1 Bratzler,R.L.				
TITLE	Inhibition of angiogenesis by nucleic acids				

JOURNAL	Patent: WO 02053141-A 61 11-JUL-2002;
FEATURES	Coley Pharmaceutical Group, Inc. (US)
source	Location/Qualifiers
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	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
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Query Match	0.6%;	Score 17.8;	DB 1;	Length 22;
Best Local Similarity	90.5%;	Pred. No. 1e+03;		
Matches	19;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;

QY	2166	TTTTTTTTTTTTTTTTTTTT	2186
Db	1	TTTTTTTGTTTTGTTT	21

RESULT 1215	
AX457061	
LOCUS	AX457061 23 bp DNA linear PAT 06-JUL-2002
DEFINITION	Sequence 22 from Patent WO0231186.
ACCESSION	AX457061
VERSION	AX457061.1 GI:21715843
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1
TITLE	Berlin, K.
JOURNAL	Method for the detection of cytosine methylations
FEATURES	Patent: WO 0231186-A 22 18-APR-2002;
source	EpiGenomics AG (DE)
	Location/Qualifiers
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	/mol_type="unassigned DNA"
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	/note="Primer"

Query Match	0.6%;	Score 17.8;	DB 1;	Length 23;
Best Local Similarity	90.5%;	Pred. No. 1.1e+03;		
Matches	19;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;

QY	2168	TTTTTTTTTTTTTTTTTTAA	2188
Db	2	TTTTTTTAAATTTTAA	22

RESULT 1216	
AR431313	
LOCUS	AR431313 24 bp DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 7 from patent US 6651008.
ACCESSION	AR431313
VERSION	AR431313.1 GI:40193281
KEYWORDS	
SOURCE	unknown.
ORGANISM	unknown.
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 24)
TITLE	Vaisberg, E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
JOURNAL	Database system including computer code for predictive cellular
FEATURES	bioinformatics
source	Patent: US 6651008-A 7 18-NOV-2003;
	Location/Qualifiers
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	/organism="unknown"
	/mol_type="genomic DNA"

Query Match	0.6%;	Score 17.8;	DB 1;	Length 24;
Best Local Similarity	90.5%;	Pred. No. 1.3e+03;		
Matches	19;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;

Db 1 ||||| 1 GAGCCAGGGGGAGCAGGGCT 21

RESULT 1221
AR243409/c
LOCUS AR243409 25 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 202 from patent US 6475789.
ACCESSION AR243409
VERSION AR243409.1 GI:27290620
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit: diagnostic and therapeutic
methods
JOURNAL Patent: US 6475789-A 202 05-NOV-2002;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

QY 789 CCTGTCAAGAGAGCTGTGG 809
Db 21 CCTGCCTGAAGAGAGCTGTGG 1

RESULT 1222
AR265036
LOCUS AR265036 25 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 50 from patent US 6492122.
ACCESSION AR265036
VERSION AR265036.1 GI:29693423
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Weidenhammer,E.M., Wang,L., Xu,X., Heller,M.J. and Kahl,B.F.
TITLE Quantitative analysis methods on active electronic microarrays
JOURNAL Patent: US 6492122-A 50 10-DEC-2002;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 487 GAGCCAGAGGAGCGGGCT 507
Db 1 GAGCCAGGGGGAGCAGGGCT 21

RESULT 1223
AR390565/c
LOCUS AR390565 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 435 from patent US 6610839.
ACCESSION AR390565
VERSION AR390565.1 GI:40112491
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)

AUTHORS Morin,G.B. and Andrews,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 435 26-AUG-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 789 CCTGTCAAGAGAGCTGTGG 809
Db 21 CCTGCCTGAAGAGAGCTGTGG 1

RESULT 1224
AR393179/c
LOCUS AR393179 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 435 from patent US 6617110.
ACCESSION AR393179
VERSION AR393179.1 GI:40118470
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
drug screening
JOURNAL Patent: US 6617110-A 435 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 789 CCTGTCAAGAGAGCTGTGG 809
Db 21 CCTGCCTGAAGAGAGCTGTGG 1

RESULT 1225
AR435375
LOCUS AR435375 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1798 from patent US 6656700.
ACCESSION AR435375
VERSION AR435375.1 GI:40198218
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-B
JOURNAL Patent: US 6656700-A 1798 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 AAGCAATTGTGCTGCTGT 2330
Db 5 AAGCCAGTTGTGCTGCTGT 25

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RESULT 1226
LOCUS AR435376 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1799 from patent US 6656700.
ACCESSION AR435376
VERSION AR435376.1 GI:40198219
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1799 02-DEC-2003;
FEATURES
source
1. .25
/mol_type="genomic DNA"

Query Match. 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 AAGCAATTGTTGCTGCTTGT 2330
Db 4 AAGCCAGTTGTTGCTGCTTGT 24

RESULT 1227
LOCUS AR435377 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1800 from patent US 6656700.
ACCESSION AR435377
VERSION AR435377.1 GI:40198220
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1800 02-DEC-2003;
FEATURES
source
1. .25
/mol_type="genomic DNA"

Query Match. 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 AAGCAATTGTTGCTGCTTGT 2330
Db 3 AAGCCAGTTGTTGCTGCTTGT 23

RESULT 1228
LOCUS AR435378 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1801 from patent US 6656700.
ACCESSION AR435378
VERSION AR435378.1 GI:40198221
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1801 02-DEC-2003;
FEATURES
Location/Qualifiers
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source 1. .25
/mol_type="genomic DNA"

Query Match. 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 AAGCAATTGTTGCTGCTTGT 2330
Db 2 AAGCCAGTTGTTGCTGCTTGT 22

RESULT 1229
LOCUS AR435379 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1802 from patent US 6656700.
ACCESSION AR435379
VERSION AR435379.1 GI:40198222
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1802 02-DEC-2003;
FEATURES
source
1. .25
/mol_type="genomic DNA"

Query Match. 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 AAGCAATTGTTGCTGCTTGT 2330
Db 1 AAGCCAGTTGTTGCTGCTTGT 21
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RESULT 1230
LOCUS AX042571/c 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 137 from Patent WO0065088.
ACCESSION AX042571
VERSION AX042571.1 GI:11341179
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 137 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1. .25
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQAI Homozygote primer sequence"

Query Match. 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAA 2799
Db 21 AGACTTGAAAAAAAAAAAAA 1

RESULT 1231
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QY 2105 GGGGGCCTTCTGTTTAGGA 2125
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match
Best Local Similarity
Matches
QY 2105 GGGGGCCTTCTGTTTAGGA 2125
Db 3 GGGGACCTTCTGTCTTAGGA 23
RESULT 1246
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match
Best Local Similarity
Matches
QY 2105 GGGGGCCTTCTGTTTAGGA 2125
Db 2 GGGGACCTTCTGTCTTAGGA 22
RESULT 1247
LOCUS
DEFINITION
ACCESSION
VERSION
QY 2105 GGGGGCCTTCTGTTTAGGA 2125
Db 2 GGGGACCTTCTGTCTTAGGA 22
RESULT 1247
LOCUS
DEFINITION
ACCESSION
VERSION

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match
Best Local Similarity
Matches
QY 2105 GGGGGCCTTCTGTTTAGGA 2125
Db 1 GGGGACCTTCTGTCTTAGGA 21
RESULT 1248
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match
Best Local Similarity
Matches
QY 2105 GGGGGCCTTCTGTTTAGGA 2125
Db 21 CCTGCTGAAGAGCTGTGG 1
RESULT 1249
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
QY 789 CCTGTCAAGAGAGCTGTGG 809
Db 21 CCTGCTGAAGAGCTGTGG 1
RESULT 1249
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

PN JP 2001081042-A/96
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HARLEY,WILLIAM H ANDREWS
PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
PC C07K5/10,
PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
C12N15/09,
PC C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
G01N33/53,
PC G01N33/566,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
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CC Topology: linear;
FH Key Location/Qualifiers
FT source 1..25
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FT Location/Qualifiers
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 789 CCTGTCAAGAGAGCTGTGG 809
Db 21 CCTGCCTGAAGAGAGCTGTGG 1

RESULT 1250
E33560/c
LOCUS E33560 26 bp DNA linear PAT 31-JAN-2002
DEFINITION Stress-responsive gene promoter.
E33560
VERSION E33560.1 GI:18624133
KEYWORDS JP 2000078977-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 26)
REFERENCE 1
AUTHORS Tsujimoto,Y., Izawa,S., Inoue,Y., Kimura,H. and Sato,N.
TITLE Stress-responsive gene promoter
JOURNAL Patent: JP 2000078977-A 5 21-MAR-2000;
MARUHA CORP

COMMENT OS Artificial Sequence
PN JP 2000078977-A/5
PD 21-MAR-2000
PF 04-SEP-1998 JP 1998251390
PR
PI YOSHIIYUKI TSUJIMOTO,SHINGO IZAWA,YOSHIIHARU INOUE,HIKARU
KIMURA,
PI NOBUYUKI SATO
PC C12N15/09,C12N1/19,C12P21/02//((C12N15/09,C12R1:865),(C12N1/19,
PC C12R1:865)
PC (C12P21/02,C12R1:865),C12N15/00,(C12N15/00,C12R1:865) CC
FH Key Location/Qualifiers
FT source 1..36
FT Location/Qualifiers
1..26
/organism='Artificial Sequence'.
FEATURES
source location/Qualifiers

Query Match 0.6%; Score 17.8; DB 1; Length 26;

Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2784 TCAAAAAAAAAAAAAAAAAA 2804
Db 24 TCAAAAAAAAAAAAAAAAAA 4

RESULT 1251
AR159556/c
LOCUS AR159556 24 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 16 from patent US 6251589.
ACCESSION AR159556
VERSION AR159556.1 GI:16222248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Tsuji,S. and Sanpei,K.
TITLE Method for diagnosing spinocerebellar ataxia type 2 and primers
JOURNAL Patent: US 6251589-A 16 26-JUN-2001;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 46 CGCGCGCGCGCGCGCGCGCAG 69
Db 24 CGCGCGCGCGCGCTGCGCGCGCTG 1

RESULT 1252
AX443659
LOCUS AX443659 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 114 from Patent WO0216649.
ACCESSION AX443659
VERSION AX443659.1 GI:21690937
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE 1
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 114 28-FEB-2002;
Illumina, Inc. (US)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

Query Match 0.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1086 AAGGTGAAGCTGTTCAATTGGCTA 1109
Db 1 AAGGTGTCGCATTCATTGGCTA 24

RESULT 1253
A71580
LOCUS A71580 25 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 13 from Patent WO9813478.
ACCESSION A71580

VERSION A71580.1 GI:4775190
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1004 GAGAGTTGACACAGATCGGTTG 1027
DB 2 GGGAAGTTGCAGAGATGGGTTG 25
RESULT 1254
BD245989
LOCUS BD245989 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Development of novel antibiotics based on bacteriophage genomics.
ACCESSION BD245989
VERSION BD245989.1 GI:33055759
KEYWORDS JP 2002531107-A/724.
SOURCE JP 2002531107-A/724.
ORGANISM unidentified
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Pelletier,J., Gros,P. and Dubow,M.
TITLE Development of novel antibiotics based on bacteriophage genomics
JOURNAL Patent: JP 2002531107-A 724 24-SEP-2002;
COMMENT PHAGETECH INC
OS Staphylococcus aureus bacteriophage 96
PN JP 2002531107-A/724
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
PELLETIER, PHILIPPE GROS, MICHAEL DUBOW
PC C12N15/09, A01N63/00, A61K38/00, A61K45/00, A61P31/04, C07K14/005,
PC C12M1/00,
PC C12N1/21, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC
C12N15/00,
PC A61K37/02
CC Ribosome binding sequence
FH Key Location/Qualifiers
FT source 1.25
FT aureus bacteriophage /organism='Staphylococcus
96'.
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SOURCE location/Qualifiers
1.25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

DB 2 TCATAAAGTATCTTGTAGTAT 25
RESULT 1255
AR237790
LOCUS AR237790 25 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 10 from patent US 6465636.
ACCESSION AR237790
VERSION AR237790.1 GI:27282610
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Stuiiver,M.H., Custers,J.H.H.V. and Simons,L.H.
TITLE Pathogen-inducible promoter
JOURNAL Patent: US 6465636-A 10 15-OCT-2002;
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source location/Qualifiers
1.25
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1004 GAGAGTTGACACAGATCGGTTG 1027
DB 2 GGGAAGTTGCAGAGATGGGTTG 25
RESULT 1256
AX015674
LOCUS AX015674 25 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9950428.
ACCESSION AX015674
VERSION AX015674.1 GI:10041503
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Simons,L.H., Stuiiver,M.H. and Custers,J.H.
TITLE Pathogen-inducible promoter
JOURNAL Patent: WO 9950428-A 10 07-OCT-1999;
SIMONS LAMBERTUS HENRICUS (NL); STUIVER MAARTEN HENDRIK (NL); MOGEN
INT (NL); CUSTERS JEROME HUBERTINA HENRI (NL)
FEATURES
source location/Qualifiers
1.25
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/note="primer"

Query Match
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1004 GAGAGTTGACACAGATCGGTTG 1027
DB 2 GGGAAGTTGCAGAGATGGGTTG 25
RESULT 1257
AX042589
LOCUS AX042589 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 155 from Patent WO0065088.
ACCESSION AX042589
VERSION AX042589.1 GI:11341197
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 155 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
1.25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQAI Homozygote primer sequence"

Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAA 2802
Db 24 AGAAGGAGAGAAAAAAAAAAAAA 1

RESULT 1258
AX042901/c
LOCUS AX042901 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 467 from Patent WO0065088.
ACCESSION AX042901
VERSION AX042901.1 GI:11341509
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
1
REFERENCE
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 467 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="16S rRNA Homozygote Primer Sequence"

Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAA 2804
Db 24 AATTCGAAATAAAAAAAAAAAAAA 1

RESULT 1259
AX043100/c
LOCUS AX043100 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 666 from Patent WO0065088.
ACCESSION AX043100
VERSION AX043100.1 GI:11341708
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
1
REFERENCE
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 666 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
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Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2776 GTTAGAATTGAAAAAAAAAAAAA 2799
Db 24 GTTCTACTTGCAAAAAAAAAAAAAA 1

RESULT 1260
AX043152/c
LOCUS AX043152 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 718 from Patent WO0065088.
ACCESSION AX043152
VERSION AX043152.1 GI:11341760
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
1
REFERENCE
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 718 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPB1 Heterozygote Primer Sequence"

Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2775 TGTAGAAATTGAAAAAAAAAAAAA 2798
Db 24 TGGTACACTTAAAAAAAAAAAAA 1

RESULT 1261
AX043290/c
LOCUS AX043290 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 856 from Patent WO0065088.
ACCESSION AX043290
VERSION AX043290.1 GI:11341898
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
1
REFERENCE
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 856 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
1.25
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQAI Heterozygote Primer Sequence"

Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAA 2802
Db 24 AGAAGGAGAGAAAAAAAAAAAAA 1

RESULT 1262

AX043309/c 25 bp DNA linear PAT 23-NOV-2000
LOCUS AX043309 Sequence 875 from Patent WO0065088.
DEFINITION AX043309
ACCESSION AX043309
VERSION AX043309.1 GI:11341917
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Ulfendahl, P.J. and Wong, K.C.
AUTHORS Primers for identifying typing or classifying nucleic acids
TITLE Patent: WO 0065088-A 875 02-NOV-2000;
JOURNAL Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQAI Heterozygote Primer Sequence"
Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2778 TAGAATTGAAAAAAAAAAAAA 2801
Db 24 TAGAGTTGTAGCAAAAAAAAAAAAA 1
RESULT 1263
AX043412 25 bp DNA linear PAT 23-NOV-2000
LOCUS AX043412 Sequence 978 from Patent WO0065088.
DEFINITION AX043412
ACCESSION AX043412
VERSION AX043412.1 GI:11342020
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Ulfendahl, P.J. and Wong, K.C.
AUTHORS Primers for identifying typing or classifying nucleic acids
TITLE Patent: WO 0065088-A 978 02-NOV-2000;
JOURNAL Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DRB345 Heterozygote Primer Sequence"
Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2167 TTTTCTTTTCTTTTCTTAACT 2190
Db 1 TTTTCTTTTCTTTTCTTGAAGCT 24
RESULT 1264
AX115700 25 bp DNA linear PAT 11-MAY-2001
LOCUS AX115700 Sequence 823 from Patent WO0129262.
DEFINITION AX115700
ACCESSION AX115700
VERSION AX115700.1 GI:14032642
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Picoult-Newburg, L. and Pohl, M.

TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 823 26-APR-2001;
ORCHID Biosciences, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2165 CTTTCTTTTCTTTTCTTTTAA 2188
Db 25 CTGATCTTTTCTTTTCTTTCTTAA 2
RESULT 1265
BD008572 25 bp DNA linear PAT 31-JAN-2002
LOCUS BD008572 Antifungal proteins, DNA coding therefor, and hosts incorporating
DEFINITION same.
ACCESSION BD008572
VERSION BD008572.1 GI:18636945
KEYWORDS JP 2001502525-A/10.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Stuijver, M.H., Custers, J.H.H.V., Buurlage, M.B.S., Melchers, L.S.,
Deventer, J.P.E.V., Lageweg, W. and Ponstein, A.S.
TITLE Antifungal proteins, DNA coding therefor, and hosts incorporating
JOURNAL Patent: JP 2001502525-A 10 27-FEB-2001;
MOGEN INTERNATIONAL NV
COMMENT
OS Unidentified
PN JP 2001502525-A/10
PD 27-FEB-2001
PF 04-SEP-1997 JP 1998515200
PR
PI MAARTEN HENDRIK STUIJVER,
PI JEROME HUBERTUS HENRICUS VICTOR CUSTERS,
PI MARIANNE BEATRIX SELA BUURLAGE, LEO STOERD MELCHERS, PI
JOHANNA PIETERNELLA ELS VAN DEVENTER TROOST, WESSEL LAGEWEG, PI
ANNE SILENE PONSTEIN
PC C12N15/82, C12N9/02, C12Q1/68, C07K16/40, C12N15/62, A01H5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..25 /organism='Unidentified'.
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source Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1004 GAGAGTTGACAGATCGGTTG 1027
Db 2 GGGAAGTTGCAGAAAGATTGGTTG 25
RESULT 1266
BD222040 25 bp DNA linear PAT 17-JUL-2003
LOCUS BD222040 Pathogen-inducible promoter.
DEFINITION BD222040
ACCESSION BD222040
VERSION BD222040.1 GI:33031810

KEYWORDS JP 2002509728-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 25)
AUTHORS Stuiiver,M.H., Custers,J.H.H.V. and Simons,L.H.
TITLE Pathogen-inducible promoter
JOURNAL Patent: JP 2002509728-A 10 02-APR-2002;
ZENECA MOGEN BV
COMMENT OS Artificial Sequence
PN JP 2002509728-A/10
PD 02-APR-2002
PF 25-MAR-1999 JP 2000541316
PR 01-APR-1998 EP 98201024.1
PI MAARTEN HENDRIK STUIVER,JEROME HUBERTINA HENRICUS VICTOR PI
CUSTERS,
PI LAMBERTUS HENRICUS SIMONS
PC C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/
PC 10,C12N15/00,
PC C12N5/00,C12N5/00
CC Description of Artificial Sequence:primer
FH Key Location/Qualifiers
FT source 1..25
FEATURES
source /organism='Artificial Sequence'.
1..25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred.No.1.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1004 GAGAGTTGACACAGATCGGGTTG 1027
Db 2 GGGAAGTTGCAGAGATTGGGTTG 25
RESULT 1267
AR098647 26 bp DNA linear PAT 14-FEB-2001
LOCUS AR098647
DEFINITION Sequence 5 from patent US 6077668.
ACCESSION AR098647
VERSION AR098647.1 GI:12808413
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Koool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 5 20-JUN-2000;
FEATURES
source Location/Qualifiers
1..26
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17.6; DB 1; Length 26;
Best Local Similarity 83.3%; Pred.No.1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2781 AATTGAAAAAAAAAAAAAAAAA 2804
Db 2 AAAAAAAAAAACAAAAAAAAAAAA 25
RESULT 1268
AR204721 26 bp DNA linear PAT 20-JUN-2002
LOCUS AR204721
DEFINITION Sequence 5 from patent US 6368802.
ACCESSION AR204721
VERSION AR204721.1 GI:21502120

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Koool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 5 09-APR-2002;
FEATURES
source Location/Qualifiers
1..26
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.6%; Score 17.6; DB 1; Length 26;
Best Local Similarity 83.3%; Pred.No.1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2781 AATTGAAAAAAAAAAAAAAAAA 2804
Db 2 AAAAAAAAAAACAAAAAAAAAAAA 25
RESULT 1269
AX589115/c 27 bp DNA linear PAT 24-JAN-2003
LOCUS AX589115
DEFINITION Sequence 33 from Patent WO02083179.
ACCESSION AX589115
VERSION AX589115.1 GI:27900764
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS McKerracher,L.
TITLE Fusion proteins
JOURNAL Patent: WO 02083179-A 33 24-OCT-2002;
Bioaxone Therapeutique Inc. (CA)
FEATURES
source Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide used in the cloning of a reverse
HIV Tat sequence in C3Basic3"
Query Match 0.6%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred.No.1.8e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1492 GGAGAAATGGAGAAACACAGAA 1515
Db 26 GAAGAAAGAGAGAAACAAAGAA 3
RESULT 1270
AR098648/c 29 bp DNA linear PAT 14-FEB-2001
LOCUS AR098648
DEFINITION Sequence 6 from patent US 6077668.
ACCESSION AR098648
VERSION AR098648.1 GI:12808414
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Koool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 6 20-JUN-2000;
FEATURES
source Location/Qualifiers
1..29
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match          0.6%; Score 17.6; DB 1; Length 29;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db      29 AAAAAAAAAAACAAAAAAAAAAAA 6

RESULT 1271
LOCUS   AR204722 29 bp DNA linear PAT 20-JUN-2002
DEFINITION
Sequence 6 from patent US 6368802.
ACCESSION AR204722
VERSION   AR204722.1 GI:21502121
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Kool,E.T.
TITLE   Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 6 09-APR-2002;
FEATURES
source   1. .29
         /organism="unknown"
         /mol_type="unassigned DNA"

Query Match          0.6%; Score 17.6; DB 1; Length 29;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db      29 AAAAAAAAAAACAAAAAAAAAAAA 6

RESULT 1272
LOCUS   AX078001 20 bp DNA linear PAT 22-FEB-2001
DEFINITION
Sequence 15 from Patent WO0105435.
ACCESSION AX078001
VERSION   AX078001.1 GI:13157746
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gleave,M.
TITLE   Antisense therapy for hormone-regulated tumors
JOURNAL Patent: WO 0105435-A 15 25-JAN-2001;
          THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
FEATURES
source   1. .20
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"

Query Match          0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2170 TTTT TTTT TTTT TTTT TTTT AA 2188
Db      1 TTTT TTTT TTTT TTTT TTTT CA 19

RESULT 1273
LOCUS   AR211367 20 bp DNA linear PAT 20-JUN-2002
DEFINITION
Sequence 5 from patent US 6399305.
ACCESSION AR211367
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VERSION AR211367.1 GI:21514670
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 20)
          Makino,Y., Abe,Y., Takagi,M., Takenaka,S., Yamashita,K. and
          Ogawa,M.
TITLE   Protection of partial complementary nucleic acid fragment using a
          electroconductive chip and intercalator
JOURNAL Patent: US 6399305-A 5 04-JUN-2002;
FEATURES
source   1. .20
         /organism="unknown"
         /mol_type="unassigned DNA"

Query Match          0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db      20 AAAAAAAAAATAAAAAAAAA 2

RESULT 1274
LOCUS   AR371268 20 bp DNA linear PAT 12-SEP-2003
DEFINITION
Sequence 4 from patent US 6395474.
ACCESSION AR371268
VERSION   AR371268.1 GI:34608200
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 20)
          Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE   Peptide nucleic acids
JOURNAL Patent: US 6395474-A 4 28-MAY-2002;
FEATURES
source   1. .20
         /organism="unknown"
         /mol_type="genomic DNA"

Query Match          0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db      1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1275
LOCUS   AX136903 20 bp DNA linear PAT 30-MAY-2001
DEFINITION
Sequence 5 from Patent EP1065278.
ACCESSION AX136903
VERSION   AX136903.1 GI:14273252
KEYWORDS
SOURCE   synthetic construct
          synthetic construct
          artificial sequences.
REFERENCE
AUTHORS 1
          Makino,Y., Abe,Y., Ogawa,M., Takagi,M., Takenaka,S. and
          Yamashita,K.
TITLE   Detection of partly complementary nucleic acid fragment
JOURNAL Patent: EP 1065278-A 5 03-JAN-2001;
          FUJI PHOTO FILM CO., LTD. (JP)
FEATURES
source   1. .20
         /organism="synthetic construct"
         /mol_type="unassigned DNA"
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/db xref="taxon:32630"
/note="sample nucleic acid fragment"

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 20 AAAAAAAAAATAAAAAAAA 2

RESULT 1276

LOCUS E59328 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION E59328
VERSION E59328.1 GI:18622505
KEYWORDS JP 2000342265-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose,K. and Yoshida,T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 9 12-DEC-2000;
TOAGOSEI CHEM IND CO LTD

COMMENT

OS Artificial Sequence
PN JP 2000342265-A/9
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999154974
PR
PI KUNITHIKO HIROSE,TADAO YOSHIDA
PC C12N15/09,B01D15/08,C12N15/00
CC

FH Key Location/Qualifiers
FT source 1..20
FT /Organism='Artificial Sequence'.
FT

FEATURES

source 1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2169 TTTTCTTTTCTTTTCTTTT 2187
|||||
Db 19 TTTTCTTTTCTTTTCTTTT 1

RESULT 1277

LOCUS AR241831 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 119 from patent US 6472154.
ACCESSION AR241831
VERSION AR241831.1 GI:27287643
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 21)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 119 29-OCT-2002;
FEATURES Location/Qualifiers
1..21

source /organism="unknown"
/mol_type="genomic DNA"

Query Match 0.6%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 21 AAAAAAAAAATAAAAAAAA 3

RESULT 1278

LOCUS AX838821 21 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 26 from Patent WO03076667.
ACCESSION AX838821
VERSION AX838821.1 GI:39922376
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Jeney,C. and Takacs,T.
TITLE Amplification-hybridisation method for detecting and typing
JOURNAL humanpapillomavirus
Patent: WO 03076667-A 26 18-SEP-2003;
Jeney, Csaba (HU) ; Takacs, Tibor (HU)
FEATURES Location/Qualifiers
1..21

source /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer (HICR52)"

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2533 ATACAGGCTATTAGAATT 2551
|||||
Db 3 ATACAGGCTATTAGAATT 21

RESULT 1279

LOCUS E12392 23 bp DNA linear PAT 27-APR-1998
DEFINITION Oligonucleotide primer.
ACCESSION E12392
VERSION E12392.1 GI:3251225
KEYWORDS JP 1996322598-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 23)
AUTHORS Katou,K.
TITLE INDEXING METHOD OF DNA MOLECULE
JOURNAL Patent: JP 1996322598-A 2 10-DEC-1996;
RES DEV CORP OF JAPAN
COMMENT OS None
OC Artificial sequences.
PN JP 1996322598-A/2
PD 10-DEC-1996
PF 12-SEP-1995 JP 1995234122
PR 28-MAR-1995 JP 95P 69695
PI KATOU KIKUYA
PC C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..23
FT /organism="unidentified"
FT /mol_type="genomic DNA"

FEATURES Location/Qualifiers
1..23
source /organism="unidentified"
/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match 0.6%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2165 CTTTCTTTTCTTTTCTTTTCTTTT 2183

Db 4 CTGTTTCTTTTCTTTTCTTTTCTTTT 22

RESULT 1280

E12392/c 23 bp DNA linear PAT 27-APR-1998

DEFINITION Oligonucleotide primer.

E12392

E12392.1 GI:3251225

KEYWORDS JP 1996322598-A/2.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 23)

AUTHORS Katou,K.

TITLE INDEXING METHOD OF DNA MOLECULE

JOURNAL Patent: JP 1996322598-A 2 10-DEC-1996;

RES DEV CORP OF JAPAN

COMMENT

OS None

OC Artificial sequences.

PN JP 1996322598-A/2

PD 10-DEC-1996

PF 12-SEP-1995 JP 1995234122

PR 28-MAR-1995 JP 95P 69695

PI KATOU KIKUYA

PC C12Q1/68,C07H21/02,C07H21/04,C12N15/09;

CC strandedness: Single;

FH topology: Linear;

FH Key Location/Qualifiers

FT source 1. .23

FEATURES /organism='Artificial sequences'.

source 1. .23

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match 0.6%; Score 17.4; DB 1; Length 23;

Best Local Similarity 94.7%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803

Db 23 GAAAAAAAAAAAAAAAAAAAAACA 5

RESULT 1281

I79498 23 bp DNA linear PAT 10-JUN-1998

DEFINITION Sequence 5 from patent US 5707807.

I79498

VERSION I79498.1 GI:3207788

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 23)

Kato,K.

Molecular indexing for expressed gene analysis

Patent: US 5707807-A 5 13-JAN-1998;

Location/Qualifiers

1. .23

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.4; DB 1; Length 23;

Best Local Similarity 94.7%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2165 CTTTCTTTTCTTTTCTTTTCTTTT 2183

Db 4 CTGTTTCTTTTCTTTTCTTTTCTTTT 22

RESULT 1282

I79498/c 23 bp DNA linear PAT 10-JUN-1998

DEFINITION Sequence 5 from patent US 5707807.

I79498

VERSION I79498.1 GI:3207788

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 23)

Kato,K.

Molecular indexing for expressed gene analysis

Patent: US 5707807-A 5 13-JAN-1998;

Location/Qualifiers

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/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.6%; Score 17.4; DB 1; Length 23;

Best Local Similarity 94.7%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803

Db 23 GAAAAAAAAAAAAAAAAAAAAACA 5

RESULT 1283

AR431312/c 24 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 6 from patent US 6651008.

AR431312

VERSION AR431312.1 GI:40193280

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 24)

Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.

Database system including computer code for predictive cellular

bioinformatics

Patent: US 6651008-A 6 18-NOV-2003;

Location/Qualifiers

1. .24

/organism="unknown"

/mol_type="genomic DNA"

Query Match 0.6%; Score 17.4; DB 1; Length 24;

Best Local Similarity 94.7%; Pred. No. 1.5e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

Db 24 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 1284

AR431308/c 24 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 2 from patent US 6651008.

AR431308

VERSION AR431308.1 GI:40193276

modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184
|||||
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 873
AX825164/c
LOCUS AX825164 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 62 from Patent WO03072818.
ACCESSION AX825164
VERSION AX825164.1 GI:39750893

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 62 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 874
BD087491
LOCUS BD087491 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis.
ACCESSION BD087491
VERSION BD087491.1 GI:22633101

KEYWORDS JP 2001525193-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 2 11-DEC-2001;
NANOGEN INC
COMMENT OS Artificial Sequence
PN JP 2001525193-A/2
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER,CARL F EDMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Synthesized with u at 3'
terminus to
CC provide ribonucleic acid base for reactivity; Poly A sequence
CC for reduced
CC secondary structure
CC Key Location/Qualifiers
FH source 1..21
FT /organism='Artificial Sequence'.
FT Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 875
AX825111
LOCUS AX825111 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 9 from Patent WO03072818.
ACCESSION AX825111
VERSION AX825111.1 GI:39750840
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 9 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 870
AX825154/c

LOCUS AX825154 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 52 from Patent WO03072818.
ACCESSION AX825154
VERSION AX825154.1 GI:39750883

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 52 04-SEP-2003;

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
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Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 871
AX825160

LOCUS AX825160 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 58 from Patent WO03072818.
ACCESSION AX825160
VERSION AX825160.1 GI:39750889

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 58 04-SEP-2003;

FEATURES
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/organism="synthetic construct"

misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 872
AX825161

LOCUS AX825161 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 59 from Patent WO03072818.
ACCESSION AX825161
VERSION AX825161.1 GI:39750890

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 59 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers

source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 64 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES
source
1. .21
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
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modified_base 6
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/mod_base=OTHER

modified_base 9
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/mod_base=OTHER

modified_base 12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 15
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/mod_base=OTHER

modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 864
BD080832/c
LOCUS BD080832
DEFINITION Mammaglobin, a secreted mammary specific breast cancer protein.
ACCESSION BD080832
VERSION BD080832.1 GI:22626435
KEYWORDS JP 2001516569-A/10.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mammaglobin, a secreted mammary specific breast cancer protein
JOURNAL Patent: JP 2001516569-A 10 02-OCT-2001;
WASHINGTON UNIVERSITY

COMMENT OS Unidentified
PN JP 2001516569-A/10
PD 02-OCT-2001
PF 18-SEP-1998 JP 2000511779
PR 18-SEP-1997 US 08/933149
PI MARK A WATSON,TIMOTHY P FLEMING
PC C12N15/09,A61K35/26,A61K39/00,A61K39/395,A61K39/395,
A61P35/00,
PC C07K14/47,C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Mammaglobin, a secreted mammary specific breast cancer protein
FH Key Location/Qualifiers

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FT /organism='Unidentified'.
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1. .21
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 865
BD224108/c
LOCUS BD224108
DEFINITION Mammaglobin, breast cancer secretory protein specific to mamma.
ACCESSION BD224108
VERSION BD224108.1 GI:33033878
KEYWORDS JP 2002525098-A/10.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mammaglobin, breast cancer secretory protein specific to mamma
JOURNAL Patent: JP 2002525098-A 10 13-AUG-2002;
WASHINGTON UNIVERSITY

COMMENT OS Artificial Sequence
PN JP 2002525098-A/10
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572241
PR 29-SEP-1998 US 09/162622
PI MARK A WATSON,TIMOTHY P FLEMING
PC C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/577//G01N33/574, PC
C12N15/00

CC Description of Artificial Sequence:Synthetic
FH Key Location/Qualifiers
FT source 1. .21
FT /organism='Artificial Sequence'.
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1. .21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 866
AR153849
LOCUS AR153849
DEFINITION Sequence 2 from patent US 6238624.
ACCESSION AR153849
VERSION AR153849.1 GI:15121902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
TITLE Methods for transport in molecular biological analysis and

JOURNAL cancer protein
Patent: US 5668267-A 13 16-SEP-1997;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 21 AAAAAAAAAAAAAAAAAA 3
RESULT 859
AR322245/c
LOCUS AR322245 21 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 13 from patent US 6566072.
ACCESSION AR322245
VERSION AR322245.1 GI:33707814
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mammaglobin, a secreted mammary-specific breast cancer protein
JOURNAL Patent: US 6566072-A 13 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 21 AAAAAAAAAAAAAAAAAA 3
RESULT 860
AX104720/c
LOCUS AX104720 21 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 912 from Patent WO0122972.
ACCESSION AX104720
VERSION AX104720.1 GI:13920917
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 912 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 21 AAAAAAAAAAAAAAAAAA 3

RESULT 861
AX355812/c
LOCUS AX355812 21 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 840 from Patent WO0197843.
ACCESSION AX355812
VERSION AX355812.1 GI:18620480
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 840 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"
Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 21 AAAAAAAAAAAAAAAAAA 3
RESULT 862
AX547773/c
LOCUS AX547773 21 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 912 from Patent WO02053141.
ACCESSION AX547773
VERSION AX547773.1 GI:25812917
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 912 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 21 AAAAAAAAAAAAAAAAAA 3
RESULT 863
AX825166/c
LOCUS AX825166 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 64 from Patent WO03072818.
ACCESSION AX825166
VERSION AX825166.1 GI:39750895
KEYWORDS

Unclassified.
1 (bases 1 to 21)
Watson,M.A. and Fleming,T.P.
Mammaglobin, a mammary-specific breast cancer protein
Patent: US 5968754-A 13 19-OCT-1999;
Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 854
AR084521
LOCUS AR084521 linear PAT 01-SEP-2000
DEFINITION Sequence 10 from patent US 5981185.
ACCESSION AR084521
VERSION AR084521.1 GI:10011292
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 21)
Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 10 09-NOV-1999;
Location/Qualifiers
1. .21
/organism="unknown"
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Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 855
AR084524/c
LOCUS AR084524 linear PAT 01-SEP-2000
DEFINITION Sequence 13 from patent US 5981185.
ACCESSION AR084524
VERSION AR084524.1 GI:10011295
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 21)
Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 13 09-NOV-1999;
Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 856
AR093143/c
LOCUS AR093143 linear PAT 08-SEP-2000
DEFINITION Sequence 12 from patent US 5998596.
ACCESSION AR093143
VERSION AR093143.1 GI:10019895
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 21)
Bergan,R. and Neckers,L.
Inhibition of protein kinase activity by aptameric action of
oligonucleotides
Patent: US 5998596-A 12 07-DEC-1999;
Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
| | | | | | | | | | | | | | | | | | | | | |
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 857
AR095412/c
LOCUS AR095412 linear PAT 08-SEP-2000
DEFINITION Sequence 13 from patent US 6004756.
ACCESSION AR095412
VERSION AR095412.1 GI:10023262
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 21)
Watson,M.A. and Fleming,T.P.
Method for detecting the presence of breast cancer by detecting an
increase in mammaglobin mRNA expression
Patent: US 6004756-A 13 21-DEC-1999;
Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 858
I65744/c
LOCUS I65744 linear PAT 07-OCT-1997
DEFINITION Sequence 13 from patent US 5668267.
ACCESSION I65744
VERSION I65744.1 GI:2482314
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 21)
Watson,M.A. and Fleming,T.P.
Polynucleotides encoding mammaglobin, a mammary-specific breast

Qy	2169	TTTTTTTTTTTTTTTTTTA	2187
Db	1	TTTTTTTTTTTTTTTTTTA	19
RESULT 851			
LOCUS	AR140559/c		PAT 16-JUN-2001
DEFINITION	Sequence 34 from patent US 6207802.	20 bp	DNA
ACCESSION	AR140559		
VERSION	AR140559.1	GI:14483055	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Zsebo,K.M.; Bosselman,R.A.; Suggs,S.V. and Martin,F.H.		
TITLE	Stem cell factor and compositions		
JOURNAL	Patent: US 6207802-A 34 27-MAR-2001;		
FEATURES	Location/Qualifiers		
source	1..20		
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Query Match	0.7%; Score 19; DB 1; Length 20;		
Best Local Similarity	100.0%; Pred.No. 4.7e+02;		
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	2785	GAAAAAAAAAAAAAAA 2803	
Db	19	GAAAAAAAAAAAAAAA 1	
RESULT 852			
AX078001/c			PAT 22-FEB-2001
LOCUS	AX078001	20 bp	DNA
DEFINITION	Sequence 15 from Patent WO0105435.		
ACCESSION	AX078001		
VERSION	AX078001.1	GI:13157746	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Gleave,M.		
TITLE	Antisense therapy for hormone-regulated tumors		
JOURNAL	Patent: WO 0105435-A 15 25-JAN-2001;		
	THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)		
FEATURES	Location/Qualifiers		
source	1..20		
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	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	0.7%; Score 19; DB 1; Length 20;		
Best Local Similarity	100.0%; Pred.No. 4.7e+02;		
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	2783	TTGAAAAAAAAAAAAAAA 2801	
Db	19	TTGAAAAAAAAAAAAAAA 1	
RESULT 853			
AR080294/c			PAT 31-AUG-2000
LOCUS	AR080294	21 bp	DNA
DEFINITION	Sequence 13 from patent US 5968754.		
ACCESSION	AR080294		
VERSION	AR080294.1	GI:10007029	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		


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Oligomer Sequence-Synthetic Probe Sequence"

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 841
AX741052
LOCUS AX741052 20 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 26 from Patent WO03027328.
ACCESSION AX741052
VERSION AX741052.1 GI:30523913
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE Methods, kits and compositions pertaining to the suppression of
detectable probe binding to randomly distributed repeat sequences
in genomic nucleic acid
JOURNAL Patent: WO 03027328-A 26 03-APR-2003;
Boston Probes, Inc. (US); DakoCytomation Denmark A/S (DK)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 842
BD008523
LOCUS BD008523 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial
infections.
ACCESSION BD008523
VERSION BD008523.1 GI:18636896
KEYWORDS JP 2001503969-A/26.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Hiyama,J., Visser,E.S., Skinner,M.A., Scott,L.M. and
Prestidge,R.L.
TITLE Compounds and methods for treatment and diagnosis of Mycobacterial
infections
JOURNAL Patent: JP 2001503969-A 26 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT OS Unidentified
PN JP 2001503969-A/26
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR
PI PAUL TAN,JUN HIYAMA,ELIZABETH S VISSER,MARGOT A SKINNER, PI
LINDA M SCOTT,
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PI ROSS L PRESTIDGE
PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.
FEATURES
source
Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 843
BD080522/c
LOCUS BD080522 20 bp RNA linear PAT 27-AUG-2002
DEFINITION Ribonucleoside-derivative and method for preparing the same.
ACCESSION BD080522
VERSION BD080522.1 GI:22626125
KEYWORDS JP 2001515087-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pitsch,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: JP 2001515087-A 1 18-SEP-2001;
STEFAN PITSCH,PATRICK A WEISS,LUZI JENNY
COMMENT OS Artificial Sequence
PN JP 2001515087-A/1
PD 18-SEP-2001
PF 17-AUG-1998 JP 2000509723
PR 18-AUG-1997 CH 1931/97
PI STEFAN PITSCH,PATRICK A WEISS,LUZI JENNY
PC C07H19/06,C07F7/18,C07H19/16,C07H21/02,C07H23/00 CC
Description of Artificial Sequence:synthetic polynucleotide FH
Key Location/Qualifiers
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FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..20
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/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 844
BD107450/c
LOCUS BD107450 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of detecting single base polymorphism.
ACCESSION BD107450
VERSION BD107450.1 GI:23202268
KEYWORDS JP 2002034599-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
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ACCESSION AX556124
VERSION AX556124.1 GI:25899506
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0246472-A 55 13-JUN-2002;
Nanosphere, Inc. (US)
FEATURES
source
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAA 19
RESULT 837
AX556139
LOCUS AX556139 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 70 from Patent WO0246472.
ACCESSION AX556139
VERSION AX556139.1 GI:25899521
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0246472-A 70 13-JUN-2002;
Nanosphere, Inc. (US)
FEATURES
source
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
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Db 1 AAAAAAAAAAAAAAAAAAAAA 19
RESULT 838
AX664307
LOCUS AX664307 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 5 from Patent WO0246398.
ACCESSION AX664307
VERSION AX664307.1 GI:29164237
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1

AUTHORS Willson,R.C. and Murphy,J.C.
TITLE Nucleic acid separation using immobilized metal affinity chromatography
JOURNAL Patent: WO 0246398-A 5 13-JUN-2002;
The University of Houston System (US)
FEATURES
source
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Sequence"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAA 19
RESULT 839
AX664308/c
LOCUS AX664308 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 6 from Patent WO0246398.
ACCESSION AX664308
VERSION AX664308.1 GI:29164238
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Willson,R.C. and Murphy,J.C.
TITLE Nucleic acid separation using immobilized metal affinity chromatography
JOURNAL Patent: WO 0246398-A 6 13-JUN-2002;
The University of Houston System (US)
FEATURES
source
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Sequence"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
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Db 20 AAAAAAAAAAAAAAAAAAAAA 2
RESULT 840
AX741040/c
LOCUS AX741040 20 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 14 from Patent WO03027328.
ACCESSION AX741040
VERSION AX741040.1 GI:30523901
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE Methods, kits and compositions pertaining to the suppression of detectable probe binding to randomly distributed repeat sequences in genomic nucleic acid
JOURNAL Patent: WO 03027328-A 14 03-APR-2003;
Boston Probes, Inc. (US); DakoCytomation Denmark A/S (DK)
FEATURES
source
1.20
/organism="synthetic construct"

FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 832
AX465326
LOCUS AX465326 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 70 from Patent WO0218643.
ACCESSION AX465326
VERSION AX465326.1 GI:21899689
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0218643-A 70 07-MAR-2002;
Nanosphere, Inc. (US)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 833
AX547087/c
LOCUS AX547087 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 226 from Patent WO02053141.
ACCESSION AX547087
VERSION AX547087.1 GI:25812231
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 226 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 834
AX547417/c
LOCUS AX547417 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 556 from Patent WO02053141.
ACCESSION AX547417
VERSION AX547417.1 GI:25812561
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 556 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 835
AX547421
LOCUS AX547421 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 560 from Patent WO02053141.
ACCESSION AX547421
VERSION AX547421.1 GI:25812565
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 560 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 836
AX556124
LOCUS AX556124 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 55 from Patent WO0246472.

LOCUS AX355810 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 838 from Patent WO0197843.
ACCESSION AX355810
VERSION AX355810.1 GI:18620478
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 838 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source 1: .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2
RESULT 828
AX355811/c
LOCUS AX355811 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 839 from Patent WO0197843.
ACCESSION AX355811
VERSION AX355811.1 GI:18620479
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 839 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source 1: .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2
RESULT 829
AX440125
LOCUS AX440125 20 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 55 from Patent WO0173123.
ACCESSION AX440125
VERSION AX440125.1 GI:21664936
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A., Park, S.J. and Li, Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0173123-A 55 04-OCT-2001;
Nanosphere, Inc. (US)
FEATURES
source 1: .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 830
AX440140
LOCUS AX440140 20 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 70 from Patent WO0173123.
ACCESSION AX440140
VERSION AX440140.1 GI:21664951
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A., Park, S.J. and Li, Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0173123-A 70 04-OCT-2001;
Nanosphere, Inc. (US)
FEATURES
source 1: .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 831
AX465311
LOCUS AX465311 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 55 from Patent WO0218643.
ACCESSION AX465311
VERSION AX465311.1 GI:21899674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A., Garimella, V., Li, Z. and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0218643-A 55 07-MAR-2002;
Nanosphere, Inc. (US)

FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAA 2

RESULT 823
AX104368
LOCUS AX104368 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 560 from Patent WO0122972.
ACCESSION AX104368
VERSION AX104368.1 GI:13920565
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C..
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 560 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1. .20
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 824
AX196224
LOCUS AX196224 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 55 from Patent WO0151665.
ACCESSION AX196224
VERSION AX196224.1 GI:15386427
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A. and Li,Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0151665-A 55 19-JUL-2001;
Nanosphere, Inc. (US)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="random synthetic sequence"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 825
AX196239
LOCUS AX196239 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 70 from Patent WO0151665.
ACCESSION AX196239
VERSION AX196239.1 GI:15386442
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A. and Li,Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0151665-A 70 19-JUL-2001;
Nanosphere, Inc. (US)
FEATURES
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Location/Qualifiers
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/note="random synthetic sequence"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 826
AX354974
LOCUS AX354974 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 2 from Patent WO0197843.
ACCESSION AX354974
VERSION AX354974.1 GI:18619641
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 2 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 827
AX355810/c

Thu Jun 10 13:10:06 2004

DEFINITION Sequence 9 from Patent WO0067023.
ACCESSION AX045779
VERSION AX045779.1 GI:11344146
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 9 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
misc_feature 1
/note="modified with digoxigenin"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAA 2
RESULT 819
AX045787/c
LOCUS AX045787 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 17 from Patent WO0067023.
ACCESSION AX045787
VERSION AX045787.1 GI:11344154
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 17 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
misc_feature 1
/note="phosphorothioate backbone"
misc_feature 1
/note="modified with digoxigenin"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAA 2
RESULT 820
AX045790/c
LOCUS AX045790 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 20 from Patent WO0067023.
ACCESSION AX045790
VERSION AX045790.1 GI:11344157

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 20 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAA 2
RESULT 821
AX104034/c
LOCUS AX104034 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 226 from Patent WO0122972.
ACCESSION AX104034
VERSION AX104034.1 GI:13920231
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 226 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAA 2
RESULT 822
AX104364/c
LOCUS AX104364 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 556 from Patent WO0122972.
ACCESSION AX104364
VERSION AX104364.1 GI:13920561
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 556 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
thereof
JOURNAL Patent: US 6582921-A 55 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 814
AR365970
LOCUS AR365970 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 83 from patent US 6328978.
ACCESSION AR365970
VERSION AR365970.1 GI:34598223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watson,J.D., Tan,P.L.J. and Prestidge,R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 83 11-DEC-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 815
AR382312
LOCUS AR382312 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 55 from patent US 6610491.
ACCESSION AR382312
VERSION AR382312.1 GI:40090724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
thereof
JOURNAL Patent: US 6610491-A 55 26-AUG-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 816
AR429653
LOCUS AR429653 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 55 from patent US 6645721.
ACCESSION AR429653
VERSION AR429653.1 GI:40189949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
thereof
JOURNAL Patent: US 6645721-A 55 11-NOV-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 817
AX004876/c
LOCUS AX004876 20 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 5 from Patent WO9910527.
ACCESSION AX004876
VERSION AX004876.1 GI:9928276
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Bayer,E. and Schewitz,J.
TITLE Method for isolating anionic organic substances from aqueous
systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 5 04-MAR-1999;
FEATURES SUEDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="phosphorothioate oligonucleotide"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 818
AX045779/c
LOCUS AX045779 20 bp DNA linear PAT 24-NOV-2000

Thu Jun 10 13:10:06 2004

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6406704-A 83 18-JUN-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 809
AR222466 AR222466 20 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 26 from patent US 6429300.
DEFINITION AR222466
ACCESSION AR222466
VERSION AR222466.1 GI:23329997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurz, M., Lohse, P. and Wagner, R.
TITLE peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 26 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 810
AR236083/c AR236083 20 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 1 from patent US 6462184.
DEFINITION AR236083
ACCESSION AR236083
VERSION AR236083.1 GI:27279782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M. and Maier, M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 1 08-OCT-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2
RESULT 811
AR274394 AR274394 20 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 55 from patent US 6506564.
DEFINITION AR274394
ACCESSION AR274394
VERSION AR274394.1 GI:29706840
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: US 6506564-A 55 14-JAN-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 812
AR343047/c AR343047 20 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 10 from patent US 6576752.
DEFINITION AR343047
ACCESSION AR343047
VERSION AR343047.1 GI:33738375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M., Lomberg, H., Salo, H. and Virta, P.
TITLE Aminoxy functionalized oligomers
JOURNAL Patent: US 6576752-A 10 10-JUN-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2
RESULT 813
AR344936 AR344936 20 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 55 from patent US 6582921.
DEFINITION AR344936
ACCESSION AR344936
VERSION AR344936.1 GI:33741017
KEYWORDS
SOURCE Unknown.

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 804
AR154115/c
LOCUS AR154115 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 14 from patent US 6238865.
ACCESSION AR154115
VERSION AR154115.1 GI:15122168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS Huang,Z. and Szostak,J.W.
TITLE Simple and efficient method to label and modify 3'-termini of RNA using DNA polymerase and a synthetic template with defined overhang nucleotides
JOURNAL Patent: US 6238865-A 14 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 805
AR164658
LOCUS AR164658 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 13 from patent US 6274321.
ACCESSION AR164658
VERSION AR164658.1 GI:16237754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS Blumberg,B.
TITLE High throughput functional screening of cDNAs
JOURNAL Patent: US 6274321-A 13 14-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 806
E12676/c
LOCUS E12676 20 bp DNA linear PAT 27-APR-1998
DEFINITION Anti-HTLV-1 antisense oligonucleotide.
ACCESSION E12676
VERSION E12676.1 GI:3251508
KEYWORDS JP 1997052898-A/10.
SOURCE unidentified
ORGANISM unidentified

unclassified.
1 (bases 1 to 20)
Mizuguchi,M., Kurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.
ANTI-HTLV-I ANTI-SENSE OLIGONUCLEOTIDE
Patent: JP 1997052898-A 10 25-FEB-1997;
SOYAKU GIJUTSU KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1997052898-A/10
PD 25-FEB-1997
PF 09-AUG-1995 JP 1995224606
PI MIZUGUCHI MASATSUGU, KUROSAKI NAKO, MAKINO KEISUKE, PI
KOYANAGI YOSHIO,
PI YAMAMOTO NAOKI
PC C07H21/04//A61K31/70;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH Key Location/Qualifiers
FH source 1..20
FT /organism='Artificial sequences'.
FT Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 807
I36180/c
LOCUS I36180 20 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 16 from patent US 5605662.
ACCESSION I36180
VERSION I36180.1 GI:2086693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS Heller,M.J. and Tu,E.
TITLE Active programmable electronic devices for molecular biological analysis and diagnostics
JOURNAL Patent: US 5605662-A 16 25-FEB-1997;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 808
AR213738
LOCUS AR213738 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 83 from patent US 6406704.
ACCESSION AR213738
VERSION AR213738.1 GI:23311025

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Visser,E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6160093-A 83 12-DEC-2000;
FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 802
AR123335
LOCUS AR123335 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6169176.
ACCESSION AR123335
VERSION AR123335.1 GI:14108301
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bruice,T.C. and Dev,A.P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 1 02-JAN-2001;
FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 803
AR141070/c
LOCUS AR141070 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6207819.
ACCESSION AR141070
VERSION AR141070.1 GI:14483566
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 1 27-MAR-2001;
FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 799
AR093312
LOCUS AR093312 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 83 from patent US 6001361.
ACCESSION AR093312
VERSION AR093312.1 GI:10020062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Hiyama,J., Visser,E., Skinner,M., Scott,L. and Prestidge,R.
TITLE Mycobacterium vaccae antigens
JOURNAL Patent: US 6001361-A 83 14-DEC-1999;
FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 800
AR118970/c
LOCUS AR118970 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 96 from patent US 6150092.
ACCESSION AR118970
VERSION AR118970.1 GI:14100880
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 96 21-NOV-2000;
FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
 |||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 801
AR121692
LOCUS AR121692 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 83 from patent US 6160093.
ACCESSION AR121692
VERSION AR121692.1 GI:14105268
KEYWORDS

DEFINITION Prostatic cancer gene.
ACCESSION BD196900
VERSION BD196900.1 GI:33006670
KEYWORDS JP 2002516657-A/489.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
TITLE Prostatic cancer gene
JOURNAL Patent: JP 2002516657-A 489 11-JUN-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002516657-A/489
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
,C12N15/00,C12N5/00,
PC C12N5/00,C12N15/00
CC potential microsequencing oligo for 4-4-187.mis2 FH Key
FT primer bind 1..19.
Location/Qualifiers
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 795
AR064875/c
LOCUS AR064875 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5849480.
ACCESSION AR064875
VERSION AR064875.1 GI:5995091
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cros,P., Kurfurst,R., Battail,N. and Piga,N.
TITLE Process and device for assaying a hapten
JOURNAL Patent: US 5849480-A 5 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
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Db 20 AAAAAAAAAAAAAAAAAAAAAA 2
RESULT 796
AR080000
LOCUS AR080000 20 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5968524.
ACCESSION AR080000
VERSION AR080000.1 GI:10006735
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watson,J.D. and Tan,P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated psoriasis
JOURNAL Patent: US 5968524-A 83 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 797
AR085926
LOCUS AR085926 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 83 from patent US 5985287.
ACCESSION AR085926
VERSION AR085926.1 GI:10012692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Skinner,M. and Prestidge,R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 83 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 798
AR087520/c
LOCUS AR087520 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5986084.
ACCESSION AR087520
VERSION AR087520.1 GI:10014283
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pitsch,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: US 5986084-A 1 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

designating self address, compartment device, mechanism, method and operation for molecular biological analysis and diagnosis.

ACCESSION BD087505
VERSION BD087505.1 GI:22633115
KEYWORDS JP 2001525193-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of designating self address, compartment device, mechanism, method and operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 16 11-DEC-2001;
NANOGEN INC
COMMENT OS Artificial Sequence
PN JP 2001525193-A/16
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER,CARL F EDMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Amine
conjugate to provide
CC with dyes reactivity
FH Key Location/Qualifiers
FT source 1..19 /organism='Artificial Sequence'.
FT

FEATURES
source
1..19 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
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Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 792
BD087505/c
LOCUS
DEFINITION Self-assembling microelectronic integration system capable of designating self address, compartment device, mechanism, method and operation for molecular biological analysis and diagnosis.
ACCESSION BD087505
VERSION BD087505.1 GI:22633115
KEYWORDS JP 2001525193-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 19)
AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of designating self address, compartment device, mechanism, method and operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 16 11-DEC-2001;
NANOGEN INC
COMMENT OS Artificial Sequence
PN JP 2001525193-A/16
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI

NERENBERG,
PI MICHAEL J HELLER,CARL F EDMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Amine
conjugate to provide reactivity
CC with dyes Location/Qualifiers
FH Key 1..19
FT source /organism='Artificial Sequence'.
FT

FEATURES
source
1..19 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2804
|||||
Db 19 AAAAAA AAAAAA AAAAAA 1

RESULT 793
BD196900
LOCUS
DEFINITION Prostatic cancer gene.
ACCESSION BD196900
VERSION BD196900.1 GI:33006670
KEYWORDS JP 2002516657-A/489.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
TITLE Prostatic cancer gene
JOURNAL Patent: JP 2002516657-A 489 11-JUN-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002516657-A/489
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
C12N15/00,C12N5/00,
PC C12N5/00,C12N15/00
CC potential microsequencing oligo for 4-4-187.mis2 FH Key
Location/Qualifiers
FT primer_bind 1..19.
FT source 1..19 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 794
BD196900/c
LOCUS
BD196900 19 bp DNA linear PAT 17-JUL-2003

ORGANISM	Unknown.	Unclassified.	REFERENCE	1 (bases 1 to 19)	Score 19; DB 1; Length 19;	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AUTHORS	Cook, P.D., Manoharan, M., Maier, M. and An, H.					
TITLE	C3'-methylene hydrogen phosphonate oligomers and related compounds					
JOURNAL	Patent: US 6639061-A 1 28-OCT-2003;					
FEATURES	Location/Qualifiers					
source	1. .19					
	/organism="unknown"					
	/mol_type="genomic DNA"					
Query Match	0.7%; Score 19; DB 1; Length 19;					
Best Local Similarity	100.0%; Pred. No. 4e+02;					
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2786 AAAAAAAAAAAAAAAAAAAAAA 2804					
Db	19 AAAAAAAAAAAAAAAAAAAAAA 1					
RESULT 787						
AR432616						
LOCUS	AR432616	19 bp	DNA	linear	PAT 18-DEC-2003	
DEFINITION	Sequence 6 from patent US 6653458.					
ACCESSION	AR432616					
VERSION	AR432616.1	GI:40195149				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
Unclassified.						
REFERENCE	1 (bases 1 to 19)					
AUTHORS	Manoharan, M., Cook, P.D. and Guinosso, C.J.					
TITLE	Modified oligonucleotides					
JOURNAL	Patent: US 6653458-A 6 25-NOV-2003;					
FEATURES	Location/Qualifiers					
source	1. .19					
	/organism="unknown"					
	/mol_type="genomic DNA"					
Query Match	0.7%; Score 19; DB 1; Length 19;					
Best Local Similarity	100.0%; Pred. No. 4e+02;					
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184					
Db	1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19					
RESULT 788						
AR432616/c						
LOCUS	AR432616	19 bp	DNA	linear	PAT 18-DEC-2003	
DEFINITION	Sequence 6 from patent US 6653458.					
ACCESSION	AR432616					
VERSION	AR432616.1	GI:40195149				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
Unclassified.						
REFERENCE	1 (bases 1 to 19)					
AUTHORS	Manoharan, M., Cook, P.D. and Guinosso, C.J.					
TITLE	Modified oligonucleotides					
JOURNAL	Patent: US 6653458-A 6 25-NOV-2003;					
FEATURES	Location/Qualifiers					
source	1. .19					
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Best Local Similarity	100.0%; Pred. No. 4e+02;					
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2786 AAAAAAAAAAAAAAAAAAAAAA 2804					

Thu Jun 10 13:10:06 2004

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 15 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
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QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
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RESULT 782
AR403614/c 19 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 15 from patent US 6624294.
ACCESSION AR403614
VERSION AR403614.1 GI:40151200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 15 23-SEP-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
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RESULT 782
AR403614/c 19 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 15 from patent US 6624294.
ACCESSION AR403614
VERSION AR403614.1 GI:40151200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 15 23-SEP-2003;
FEATURES Location/Qualifiers
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 783
AR403623 19 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 25 from patent US 6624294.
ACCESSION AR403623
VERSION AR403623.1 GI:40151209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 25 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
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RESULT 785
AR412338 19 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 1 from patent US 6639061.
ACCESSION AR412338
VERSION AR412338.1 GI:40167448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
Cook,P.D., Manoharan,M., Maier,M. and An,H.
TITLE C3'-methylene hydrogen phosphonate oligomers and related compounds
JOURNAL Patent: US 6639061-A 1 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
|||||
RESULT 786
AR412338/c 19 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 1 from patent US 6639061.
ACCESSION AR412338
VERSION AR412338.1 GI:40167448
KEYWORDS
SOURCE Unknown.

Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
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RESULT 784
AR403623/c 19 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 25 from patent US 6624294.
ACCESSION AR403623
VERSION AR403623.1 GI:40151209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 25 23-SEP-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 4e+02;
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QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 2804
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Db 19 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 1
|||||
RESULT 785
AR412338 19 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 1 from patent US 6639061.
ACCESSION AR412338
VERSION AR412338.1 GI:40167448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
Cook,P.D., Manoharan,M., Maier,M. and An,H.
TITLE C3'-methylene hydrogen phosphonate oligomers and related compounds
JOURNAL Patent: US 6639061-A 1 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
|||||
RESULT 786
AR412338/c 19 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 1 from patent US 6639061.
ACCESSION AR412338
VERSION AR412338.1 GI:40167448
KEYWORDS
SOURCE Unknown.

VERSION AR403608.1 GI:40151194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 8 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 777
AR403612
LOCUS AR403612 19 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6624294.
ACCESSION AR403612
VERSION AR403612.1 GI:40151198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 12 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
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/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
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Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 778
AR403612/c
LOCUS AR403612 19 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6624294.
ACCESSION AR403612
VERSION AR403612.1 GI:40151198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 12 23-SEP-2003;
FEATURES Location/Qualifiers
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 779
AR403613
LOCUS AR403613 19 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6624294.
ACCESSION AR403613
VERSION AR403613.1 GI:40151199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 14 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
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Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 780
AR403613/c
LOCUS AR403613 19 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6624294.
ACCESSION AR403613
VERSION AR403613.1 GI:40151199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 14 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 781
AR403614
LOCUS AR403614 19 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 15 from patent US 6624294.
ACCESSION AR403614
VERSION AR403614.1 GI:40151200

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   Unclassified.
AUTHORS     1 (bases 1 to 19)
              Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
              Prakash,T.P.
TITLE       Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL     Patent: US 6624294-A 7 23-SEP-2003;
FEATURES    Location/Qualifiers
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RESULT	776
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LOCUS	
DEFINITION	
ACCESSION	

AR403608/c	AR403608	19 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	Sequence	8	from patent	US 6624294.	
DEFINITION	AR403608				
ACCESSION					

DEFINITION Sequence 3 from patent US 6624294;
ACCESSION AR403603
VERSION AR403603.1 GI:40151189
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 3 23-SEP-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 767
AR403604
LOCUS AR403604 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6624294.
ACCESSION AR403604
VERSION AR403604.1 GI:40151190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 4 23-SEP-2003;
FEATURES Location/Qualifiers
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1..19
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/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 767
AR403604
LOCUS AR403604 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6624294.
ACCESSION AR403604
VERSION AR403604.1 GI:40151190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 4 23-SEP-2003;
FEATURES Location/Qualifiers
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 768
AR403604/c
LOCUS AR403604 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6624294.
ACCESSION AR403604
VERSION AR403604.1 GI:40151190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 4 23-SEP-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 769
AR403605
LOCUS AR403605 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6624294.
ACCESSION AR403605
VERSION AR403605.1 GI:40151191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 5 23-SEP-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
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Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 770
AR403605/c
LOCUS AR403605 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6624294.
ACCESSION AR403605
VERSION AR403605.1 GI:40151191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 5 23-SEP-2003;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 771
AR403606
LOCUS AR403606 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6624294.

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches 19; Conservative	100.0%; Pred. No. 4e+02;	0.7%;	DB 1;	Length 19;	0;	0;
Qy	2166	TTTTTTTTTTTTTTTTTTT	2184			
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DEFINITION	Sequence 2 from patent US 6624294.					
ACCESSION	AR403602					
VERSION	AR403602.1	GI:40151188				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 19)					
AUTHORS	Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.					
TITLE	Regioselective synthesis of 2'-O-modified nucleosides					
JOURNAL	Patent: US 6624294-A 2 23-SEP-2003;					
FEATURES	Location/Qualifiers					
source	1..19					
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	/mol_type="genomic DNA"					
Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches 19; Conservative	100.0%; Pred. No. 4e+02;	0.7%;	DB 1;	Length 19;	0;	0;
Qy	2786	AAAAAAAAAAAAAAAAAAAAA	2804			
Db	19	AAAAAAAAAAAAAAAAAAAAA	1			
RESULT 765	AR403603					
LOCUS	AR403603	19 bp	DNA	linear		PAT 18-DEC-2003
DEFINITION	Sequence 3 from patent US 6624294.					
ACCESSION	AR403603					
VERSION	AR403603.1	GI:40151189				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 19)					
AUTHORS	Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.					
TITLE	Regioselective synthesis of 2'-O-modified nucleosides					
JOURNAL	Patent: US 6624294-A 3 23-SEP-2003;					
FEATURES	Location/Qualifiers					
source	1..19					
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Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
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Qy	2166	TTTTTTTTTTTTTTTTTTT	2184			
Db	1	TTTTTTTTTTTTTTTTTTT	19			
RESULT 766	AR403603/c					
LOCUS	AR403603	19 bp	DNA	linear		PAT 18-DEC-2003

Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 756
AR367447/c
LOCUS AR367447 19 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6329519.
ACCESSION AR367447
VERSION AR367447.1 GI:34600659
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood,S.P., Moser,H.E., Altmann,K.-H. and Douglas,M.E.
TITLE Intermediates for oligonucleotide synthesis
JOURNAL Patent: US 6329519-A 4 11-DEC-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 757
AR399177
LOCUS AR399177 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6617442.
ACCESSION AR399177
VERSION AR399177.1 GI:40137667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase H1 and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 17 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 758
AR399177/c
LOCUS AR399177 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6617442.
ACCESSION AR399177
VERSION AR399177.1 GI:40137667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase H1 and oligonucleotide compositions thereof

JOURNAL Patent: US 6617442-A 17 09-SEP-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 759
AR399178
LOCUS AR399178 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6617442.
ACCESSION AR399178
VERSION AR399178.1 GI:40137669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase H1 and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 18 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 760
AR399178/c
LOCUS AR399178 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6617442.
ACCESSION AR399178
VERSION AR399178.1 GI:40137669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase H1 and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 18 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 761
AR403601

JOURNAL Patent: US 6465628-A 1 15-OCT-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 746
AR237463/c
LOCUS AR237463 19 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6465628.
ACCESSION AR237463
VERSION AR237463.1 GI:27282213
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and Guzaev,A.
TITLE Process for the synthesis of oligomeric compounds
JOURNAL Patent: US 6465628-A 1 15-OCT-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 747
AR221589
LOCUS AR221589 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 10 from patent US 6562960.
ACCESSION AR321589
VERSION AR321589.1 GI:33706818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Baxter,A.D., Collingwood,S.P., Douglas,M.E. and Taylor,R.J.
TITLE Oligonucleotide analogues
JOURNAL Patent: US 6562960-A 10 13-MAY-2003;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 748

AR321589/c
LOCUS AR321589 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 10 from patent US 6562960.
ACCESSION AR321589
VERSION AR321589.1 GI:33706818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Baxter,A.D., Collingwood,S.P., Douglas,M.E. and Taylor,R.J.
TITLE Oligonucleotide analogues
JOURNAL Patent: US 6562960-A 10 13-MAY-2003;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 749
AR359804
LOCUS AR359804 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 3 from patent US 6593466.
ACCESSION AR359804
VERSION AR359804.1 GI:33766602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Guanidinium functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 3 15-JUL-2003;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 750
AR359804/c
LOCUS AR359804 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 3 from patent US 6593466.
ACCESSION AR359804
VERSION AR359804.1 GI:33766602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Guanidinium functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 3 15-JUL-2003;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 15 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 741
AR213512 AR213512 19 bp DNA linear PAT 25-SEP-2002
LOCUS
DEFINITION Sequence 25 from patent US 6403779.
ACCESSION AR213512
VERSION AR213512.1 GI:23310743
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 25 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184
|||||
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 742
AR213512/c AR213512 19 bp DNA linear PAT 25-SEP-2002
LOCUS
DEFINITION Sequence 25 from patent US 6403779.
ACCESSION AR213512
VERSION AR213512.1 GI:23310743
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 25 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 743
AR222465 AR222465 19 bp DNA linear PAT 26-SEP-2002
LOCUS
DEFINITION Sequence 25 from patent US 6429300.
ACCESSION AR222465
VERSION AR222465.1 GI:23329996
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 25 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 744
AR222465/c AR222465 19 bp DNA linear PAT 26-SEP-2002
LOCUS
DEFINITION Sequence 25 from patent US 6429300.
ACCESSION AR222465
VERSION AR222465.1 GI:23329996
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 25 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184
|||||
Db 19 TTTTTTTTTTTTTTTTTT 1

RESULT 745
AR237463 AR237463 19 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 1 from patent US 6465628.
ACCESSION AR237463
VERSION AR237463.1 GI:27282213
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE Process for the synthesis of oligomeric compounds

Unclassified.
1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
Regioselective synthesis of 2'-O-modified nucleosides
Patent: US 6403779-A 6 11-JUN-2002;
Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 731
AR213496
LOCUS AR213496 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 7 from patent US 6403779.
ACCESSION AR213496
VERSION AR213496.1 GI:23310727
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 7 11-JUN-2002;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2184
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 732
AR213496/C
LOCUS AR213496 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 7 from patent US 6403779.
ACCESSION AR213496
VERSION AR213496.1 GI:23310727
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 7 11-JUN-2002;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 733
AR213497
LOCUS AR213497 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6403779.
ACCESSION AR213497
VERSION AR213497.1 GI:23310728
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 8 11-JUN-2002;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2184
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 734
AR213497/c
LOCUS AR213497 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6403779.
ACCESSION AR213497
VERSION AR213497.1 GI:23310728
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 8 11-JUN-2002;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 735
AR213501
LOCUS AR213501 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 12 from patent US 6403779.
ACCESSION AR213501
VERSION AR213501.1 GI:23310732
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 4 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 726
AR213493/c
LOCUS AR213493 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 4 from patent US 6403779.
ACCESSION AR213493
VERSION AR213493.1 GI:23310724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 4 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 727
AR213494
LOCUS AR213494 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 5 from patent US 6403779.
ACCESSION AR213494
VERSION AR213494.1 GI:23310725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 5 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 730
AR213495/c
LOCUS AR213495 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 6 from patent US 6403779.
ACCESSION AR213495
VERSION AR213495.1 GI:23310726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 728
AR213494/c
LOCUS AR213494 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 5 from patent US 6403779.
ACCESSION AR213494
VERSION AR213494.1 GI:23310725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 5 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 1
RESULT 729
AR213495
LOCUS AR213495 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 6 from patent US 6403779.
ACCESSION AR213495
VERSION AR213495.1 GI:23310726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 6 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 730
AR213495/c
LOCUS AR213495 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 6 from patent US 6403779.
ACCESSION AR213495
VERSION AR213495.1 GI:23310726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Matches	19;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
 |||||
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 723
 AR213492
 LOCUS AR213492 19 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 3 from patent US 6403779.
 ACCESSION AR213492
 VERSION AR213492.1 GI:23310723
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
 Prakash,T.P.
 TITLE Regioselective synthesis of 2'-O-modified nucleosides
 JOURNAL Patent: US 6403779-A 3 11-JUN-2002;
 FEATURES
 source Location/Qualifiers
 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match	0.7%;	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
Matches	19;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 724
 AR213492/c
 LOCUS AR213492 19 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 3 from patent US 6403779.
 ACCESSION AR213492
 VERSION AR213492.1 GI:23310723
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
 Prakash,T.P.
 TITLE Regioselective synthesis of 2'-O-modified nucleosides
 JOURNAL Patent: US 6403779-A 3 11-JUN-2002;
 FEATURES
 source Location/Qualifiers
 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match	0.7%;	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
Matches	19;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
 |||||
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 725
 AR213493
 LOCUS AR213493 19 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 4 from patent US 6403779.
 ACCESSION AR213493
 VERSION AR213493.1 GI:23310724
 KEYWORDS
 SOURCE Unknown.

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 18 09-APR-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 716
AR205801/c
LOCUS AR205801 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 18 from patent US 6369209.
ACCESSION AR205801
VERSION AR205801.1 GI:21503476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 18 09-APR-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 717
AR205809
LOCUS AR205809 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 26 from patent US 6369209.
ACCESSION AR205809
VERSION AR205809.1 GI:21503486
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 26 09-APR-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 720
AR213490/c
LOCUS AR213490 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 1 from patent US 6403779.
ACCESSION AR213490
VERSION AR213490.1 GI:23310721
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 1 11-JUN-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 718
AR205809/c
LOCUS AR205809 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 26 from patent US 6369209.
ACCESSION AR205809
VERSION AR205809.1 GI:21503486
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 26 09-APR-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 719
AR213490
LOCUS AR213490 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 1 from patent US 6403779.
ACCESSION AR213490
VERSION AR213490.1 GI:23310721
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 1 11-JUN-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 720
AR213490/c
LOCUS AR213490 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 1 from patent US 6403779.
ACCESSION AR213490
VERSION AR213490.1 GI:23310721
KEYWORDS

VERSION AR205798.1 GI:21503472
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 15 09-APR-2002;
FEATURES Location/Qualifiers
source 1..19
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/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
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Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 711
AR205799
LOCUS AR205799 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 16 from patent US 6369209.
ACCESSION AR205799
VERSION AR205799.1 GI:21503473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 16 09-APR-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 712
AR205799/c
LOCUS AR205799 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 16 from patent US 6369209.
ACCESSION AR205799
VERSION AR205799.1 GI:21503473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 16 09-APR-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 713
AR205800
LOCUS AR205800 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 17 from patent US 6369209.
ACCESSION AR205800
VERSION AR205800.1 GI:21503474
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 17 09-APR-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 714
AR205800/c
LOCUS AR205800 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 17 from patent US 6369209.
ACCESSION AR205800
VERSION AR205800.1 GI:21503474
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 17 09-APR-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 715
AR205801
LOCUS AR205801 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 18 from patent US 6369209.
ACCESSION AR205801
VERSION AR205801.1 GI:21503476


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RESULT 701
BD274439
LOCUS
DEFINITION
  BD274439
  Oligonucleotides having A-DNA form and B-DNA form conformational
  geometry.
ACCESSION
  BD274439
VERSION
  BD274439.1 GI:33084207
KEYWORDS
  JP 2002543215-A/16.
SOURCE
  synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Manoharan,M. and Mohan,V.
TITLE
  Oligonucleotides having A-DNA form and B-DNA form conformational
  geometry
JOURNAL
  Patent: JP 2002543215-A 16 17-DEC-2002;
COMMENT
  ISIS PHARMACEUTICALS INC
  OS Artificial Sequence
  PN JP 2002543215-A/16
  PD 17-DEC-2002
  PF 03-MAY-2000 JP 2000615638
  PR 03-MAY-1999 US 09/303586
  PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
  PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
  C12N15/00
  CC Oligonucleotide
  CC 2' - O-MOE linkage
  CC 2' - O-MOE linkage
  CC 2' - O-MOE linkage
  FH Key Location/Qualifiers
  FT misc_feature (16)..(17)
  FT misc_feature (17)..(18)
  FT misc_feature (18)..(19).
  FT Location/Qualifiers
  1..19
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  /db_xref="taxon:32630"
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    Query Match 0.7%; Score 19; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 702
BD274439/c
LOCUS
DEFINITION
  BD274439
  Oligonucleotides having A-DNA form and B-DNA form conformational
  geometry.
ACCESSION
  BD274439
VERSION
  BD274439.1 GI:33084207
KEYWORDS
  JP 2002543215-A/16.
SOURCE
  synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Manoharan,M. and Mohan,V.
TITLE
  Oligonucleotides having A-DNA form and B-DNA form conformational
  geometry
JOURNAL
  Patent: JP 2002543215-A 16 17-DEC-2002;
COMMENT
  ISIS PHARMACEUTICALS INC
  OS Artificial Sequence
  PN JP 2002543215-A/16
  PD 17-DEC-2002
  PF 03-MAY-2000 JP 2000615638
  PR 03-MAY-1999 US 09/303586
  PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
  PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
  C12N15/00
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CC Oligonucleotide
CC 2' - O-MOE linkage
CC 2' - O-MOE linkage
CC 2' - O-MOE linkage
FH Key Location/Qualifiers
FT misc_feature (16)..(17)
FT misc_feature (17)..(18)
FT misc_feature (18)..(19).
FT Location/Qualifiers
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  /mol_type="genomic DNA"
  /db_xref="taxon:32630"
FEATURES
  source
    Query Match 0.7%; Score 19; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 703
BD274440
LOCUS
DEFINITION
  BD274440
  Oligonucleotides having A-DNA form and B-DNA form conformational
  geometry.
ACCESSION
  BD274440
VERSION
  BD274440.1 GI:33084208
KEYWORDS
  JP 2002543215-A/17.
SOURCE
  synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Manoharan,M. and Mohan,V.
TITLE
  Oligonucleotides having A-DNA form and B-DNA form conformational
  geometry
JOURNAL
  Patent: JP 2002543215-A 17 17-DEC-2002;
COMMENT
  ISIS PHARMACEUTICALS INC
  OS Artificial Sequence
  PN JP 2002543215-A/17
  PD 17-DEC-2002
  PF 03-MAY-2000 JP 2000615638
  PR 03-MAY-1999 US 09/303586
  PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
  PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
  C12N15/00
  CC Oligonucleotide
  CC sub O linkage
  CC 3' - O-MOE linkage; sub O linkage
  CC 3' - O-MOE linkage; sub O linkage
  CC 3' - O-MOE linkage; sub O linkage
  CC 3' - O-MOE linkage
  FH Key Location/Qualifiers
  FT misc_feature (15)..(16)
  FT misc_feature (16)..(17)
  FT misc_feature (17)..(18)
  FT misc_feature (18)..(19).
  FT misc_feature (19)..(19).
  FT Location/Qualifiers
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  /mol_type="genomic DNA"
  /db_xref="taxon:32630"
FEATURES
  source
    Query Match 0.7%; Score 19; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 4e+02;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19
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PC	C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
PC	C12N15/00
CC	Oligonucleotide
CC	3' - O-MOE linkage
CC	3' - O-MOE linkage
CC	3' - O-MOE linkage
FH	Key Location/Qualifiers
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FT	misc feature (17) . . (18)
FT	misc feature (18) . . (19) .
FEATURES	Location/Qualifiers
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	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
Query Match	0.7%; Score 19; DB 1; Length 19;
Best Local Similarity	100.0%; Pred. No. 4e+02;
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db	1 TTTT TTTT TTTT TTTT TTTT TTTT 19
RESULT 700	
BD274438/c	
LOCUS	BD274438 19 bp DNA linear PAT 17-JUL-2003
DEFINITION	Oligonucleotides having A-DNA form and B-DNA form conformational geometry.
ACCESSION	BD274438
VERSION	BD274438.1 GI:33084206
KEYWORDS	JP 2002543215-A/15.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	1 (bases 1 to 19)
AUTHORS	Manoharan,M. and Mohan,V.
TITLE	Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL	Patent: JP 2002543215-A 15 17-DEC-2002;
COMMENT	ISIS PHARMACEUTICALS INC
	OS Artificial Sequence
	PN JP 2002543215-A/15
	PD 17-DEC-2002
	PF 03-MAY-2000 JP 2000615638
	PR 03-MAY-1999 US 09/303586
	PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
	PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
	PC C12N15/00
CC	Oligonucleotide
CC	3' - O-MOE linkage
CC	3' - O-MOE linkage
CC	3' - O-MOE linkage
FH	Key Location/Qualifiers
FT	misc feature (16) . . (17)
FT	misc feature (17) . . (18)
FT	misc feature (18) . . (19) .
FEATURES	Location/Qualifiers
source	1. .19
	/organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
Query Match	0.7%; Score 19; DB 1; Length 19;
Best Local Similarity	100.0%; Pred. No. 4e+02;
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db	19 AAAAAAAAAAAAAAAAAAAAAA 1


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/mol_type="unassigned DNA"

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    2166 TTTT-----TTTTTTTTTT 2184
Db     1 TTTT-----TTTTTTTTTT 19

RESULT 690
AR135305/c
LOCUS          AR135305          19 bp      DNA           linear       PAT 16-MAY-2001
DEFINITION     Sequence 34 from patent US 6194598.
ACCESSION      AR135305
VERSION        AR135305.1 GI:14124210
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
               Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE          Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL        Patent: US 6194598-A 34 27-FEB-2001;
FEATURES       Location/Qualifiers
                source
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                    /organism="unknown"
                    /mol_type="unassigned DNA"

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    2786 AAAAAAAAAAAAAA----- 2804
Db     19 AAAAAAAAAAAAAA----- 1

RESULT 691
AR135315
LOCUS          AR135315          19 bp      DNA           linear       PAT 16-MAY-2001
DEFINITION     Sequence 44 from patent US 6194598.
ACCESSION      AR135315
VERSION        AR135315.1 GI:14124220
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
               Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE          Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL        Patent: US 6194598-A 44 27-FEB-2001;
FEATURES       Location/Qualifiers
                source
                  1..19
                    /organism="unknown"
                    /mol_type="unassigned DNA"

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    2166 TTTT-----TTTTTTTTTT 2184
Db     1 TTTT-----TTTTTTTTTT 19

RESULT 692
AR135315/c
LOCUS          AR135315          19 bp      DNA           linear       PAT 16-MAY-2001
DEFINITION     Sequence 44 from patent US 6194598.
ACCESSION      AR135315
VERSION        AR135315.1 GI:14124220
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/mol_type="unassigned DNA"

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
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Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 677
AR135295
LOCUS AR135295 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6194598.
ACCESSION AR135295
VERSION AR135295.1 GI:14124200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 24 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 678
AR135296/c
LOCUS AR135296 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6194598.
ACCESSION AR135296
VERSION AR135296.1 GI:14124201
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 24 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 678
AR135296/c
LOCUS AR135296 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6194598.
ACCESSION AR135296
VERSION AR135296.1 GI:14124201
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 25 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
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Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 681
AR135297
LOCUS AR135297 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 26 from patent US 6194598.
ACCESSION AR135297
VERSION AR135297.1 GI:14124202
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 26 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 679
AR135296
LOCUS AR135296 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6194598.
ACCESSION AR135296
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REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 21 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 672
AR135292/c
LOCUS AR135292 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6194598.
ACCESSION AR135292
VERSION AR135292.1 GI:14124197
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 21 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2804
|||||
Db 19 AAAAAA AAAAAA AAAAAA 1

RESULT 673
AR135293
LOCUS AR135293 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6194598.
ACCESSION AR135293
VERSION AR135293.1 GI:14124198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 22 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 674
AR135293/c
LOCUS AR135293 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6194598.
ACCESSION AR135293
VERSION AR135293.1 GI:14124198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 22 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2804
|||||
Db 19 AAAAAA AAAAAA AAAAAA 1

RESULT 675
AR135294
LOCUS AR135294 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6194598.
ACCESSION AR135294
VERSION AR135294.1 GI:14124199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 23 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 676
AR135294/c
LOCUS AR135294 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6194598.
ACCESSION AR135294
VERSION AR135294.1 GI:14124199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 23 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19


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RESULT 661
AR124854
LOCUS AR124854 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6172209.
ACCESSION AR124854
VERSION AR124854.1 GI:14110215
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 31 09-JAN-2001;
FEATURES
    source
        Query Match 0.7%; Score 19; DB 1; Length 19;
        Best Local Similarity 100.0%; Pred. No. 4e+02;
        Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 662
AR124854/c
LOCUS AR124854 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6172209.
ACCESSION AR124854
VERSION AR124854.1 GI:14110215
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 31 09-JAN-2001;
FEATURES
    source
        Query Match 0.7%; Score 19; DB 1; Length 19;
        Best Local Similarity 100.0%; Pred. No. 4e+02;
        Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 663
AR124856
LOCUS AR124856 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 33 from patent US 6172209.
ACCESSION AR124856
VERSION AR124856.1 GI:14110217
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 33 09-JAN-2001;
FEATURES
    source
        Query Match 0.7%; Score 19; DB 1; Length 19;
        Best Local Similarity 100.0%; Pred. No. 4e+02;
        Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 664
AR124856/c
LOCUS AR124856 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 33 from patent US 6172209.
ACCESSION AR124856
VERSION AR124856.1 GI:14110217
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 33 09-JAN-2001;
FEATURES
    source
        Query Match 0.7%; Score 19; DB 1; Length 19;
        Best Local Similarity 100.0%; Pred. No. 4e+02;
        Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1
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source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 664
AR124856/c
LOCUS AR124856 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 33 from patent US 6172209.
ACCESSION AR124856
VERSION AR124856.1 GI:14110217
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 33 09-JAN-2001;
FEATURES
    source
        Query Match 0.7%; Score 19; DB 1; Length 19;
        Best Local Similarity 100.0%; Pred. No. 4e+02;
        Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 665
AR124857
LOCUS AR124857 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 34 from patent US 6172209.
ACCESSION AR124857
VERSION AR124857.1 GI:14110218
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 34 09-JAN-2001;
FEATURES
    source
        Query Match 0.7%; Score 19; DB 1; Length 19;
        Best Local Similarity 100.0%; Pred. No. 4e+02;
        Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 666
AR124857/c
LOCUS AR124857 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 34 from patent US 6172209.
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FEATURES
source Location/Qualifiers
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 651
AR124846
LOCUS AR124846 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6172209.
ACCESSION AR124846
VERSION AR124846.1 GI:14110207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 23 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 652
AR124846/c
LOCUS AR124846 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6172209.
ACCESSION AR124846
VERSION AR124846.1 GI:14110207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 23 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 653
AR124847
LOCUS AR124847 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6172209.
ACCESSION AR124848
VERSION AR124848.1 GI:14110209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 25 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 652
AR124846/c
LOCUS AR124846 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6172209.
ACCESSION AR124846
VERSION AR124846.1 GI:14110207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 23 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .19
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 653
AR124847
LOCUS AR124847 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6172209.
ACCESSION AR124848
VERSION AR124848.1 GI:14110209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 25 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

DEFINITION Sequence 24 from patent US 6172209.
ACCESSION AR124847
VERSION AR124847.1 GI:14110208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 24 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 654
AR124847/c
LOCUS AR124847 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6172209.
ACCESSION AR124847
VERSION AR124847.1 GI:14110208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 24 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 655
AR124848
LOCUS AR124848 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6172209.
ACCESSION AR124848
VERSION AR124848.1 GI:14110209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 25 09-JAN-2001;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 20 09-JAN-2001;
FEATURES Location/Qualifiers
source
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/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 646
AR124843/c
LOCUS AR124843 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6172209.
ACCESSION AR124843
VERSION AR124843.1 GI:14110204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 20 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
|||||
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1
RESULT 647
AR124844
LOCUS AR124844 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6172209.
ACCESSION AR124844
VERSION AR124844.1 GI:14110205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 21 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

Db 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 648
AR124844/c
LOCUS AR124844 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6172209.
ACCESSION AR124844
VERSION AR124844.1 GI:14110205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 21 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
|||||
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1
RESULT 649
AR124845
LOCUS AR124845 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6172209.
ACCESSION AR124845
VERSION AR124845.1 GI:14110206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 22 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19
RESULT 650
AR124845/c
LOCUS AR124845 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6172209.
ACCESSION AR124845
VERSION AR124845.1 GI:14110206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 22 09-JAN-2001;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 630
AR111950/c
LOCUS AR111950 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 24 from patent US 6127533.
ACCESSION AR111950
VERSION AR111950.1 GI:12828798
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 24 03-OCT-2000;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2804
|||||
Db 19 AAAAAA AAAAAA AAAAAA 1

RESULT 631
AR111951
LOCUS AR111951 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 25 from patent US 6127533.
ACCESSION AR111951
VERSION AR111951.1 GI:12828799
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 25 03-OCT-2000;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 632
AR111951/c
LOCUS AR111951 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 25 from patent US 6127533.
ACCESSION AR111951
VERSION AR111951.1 GI:12828799
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 25 03-OCT-2000;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2804
|||||
Db 19 AAAAAA AAAAAA AAAAAA 1

RESULT 633
AR111952
LOCUS AR111952 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 26 from patent US 6127533.
ACCESSION AR111952
VERSION AR111952.1 GI:12828800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 26 03-OCT-2000;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 634
AR111952/c
LOCUS AR111952 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 26 from patent US 6127533.
ACCESSION AR111952
VERSION AR111952.1 GI:12828800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 26 03-OCT-2000;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2804

TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 21 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 625

AR111948
LOCUS AR111948 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 22 from patent US 6127533.
ACCESSION AR111948
VERSION AR111948.1 GI:12828796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 22 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 626

AR111948/c
LOCUS AR111948 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 22 from patent US 6127533.
ACCESSION AR111948
VERSION AR111948.1 GI:12828796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 22 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 627

AR111949
LOCUS AR111949 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 23 from patent US 6127533.
ACCESSION AR111949
VERSION AR111949.1 GI:12828797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 23 03-OCT-2000;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 628

AR111949/c
LOCUS AR111949 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 23 from patent US 6127533.
ACCESSION AR111949
VERSION AR111949.1 GI:12828797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 23 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 629

AR111950
LOCUS AR111950 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 24 from patent US 6127533.
ACCESSION AR111950
VERSION AR111950.1 GI:12828798
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 24 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"


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PF 23-JAN-2002 WO 2002JP000467
PR 23-JAN-2001 JP 01P 014510
PI TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
PC C12P21/02,C12N15/53,C12N15/63,C12N1/21//((C12P21/02,C12R1:91),
CC (C12N15/53,C12R1:01),(C12N1/21,C12R1:01)
CC Process for producing cytochrome c
FH Key
FT source
FT 1..33
    Location/Qualifiers
    1..33
        /organism="Artificial Sequence"
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
Best Local Similarity 0.7%; Score 19.2; DB 1; Length 33;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804
Db 33 AAAAAA 10

RESULT 615
A68209
LOCUS A68209 19 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 4 from Patent WO9747636.
ACCESSION A68209
VERSION A68209.1 GI:4759376
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood,S.P.; Moser,H.E., Altmann,K. and Douglas,M.E.
TITLE INTERMEDIATES FOR OLIGONUCLEOTIDE SYNTHESIS
JOURNAL Patent: WO 9747636-A 4 18-DEC-1997;
CIBA GEIGY AG (CH)
FEATURES
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Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT 2184
Db 1 TTTT 19

RESULT 616
A68209/c
LOCUS A68209 19 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 4 from Patent WO9747636.
ACCESSION A68209
VERSION A68209.1 GI:4759376
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood,S.P.; Moser,H.E., Altmann,K. and Douglas,M.E.
TITLE INTERMEDIATES FOR OLIGONUCLEOTIDE SYNTHESIS
JOURNAL Patent: WO 9747636-A 4 18-DEC-1997;
CIBA GEIGY AG (CH)
FEATURES
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        /organism="unidentified"
        /mol_type="unassigned DNA"
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/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA 2804
Db 19 AAAAAA 1

RESULT 617
AR048767
LOCUS AR048767 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5821354.
ACCESSION AR048767
VERSION AR048767.1 GI:5971110
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Leclerc,G. and Martel,R.
TITLE Radiolabeled DNA oligonucleotide and method of preparation
JOURNAL Patent: US 5821354-A 1 13-OCT-1998;
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        /organism="unknown"
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Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT 2184
Db 1 TTTT 19

RESULT 618
AR048767/c
LOCUS AR048767 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5821354.
ACCESSION AR048767
VERSION AR048767.1 GI:5971110
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Leclerc,G. and Martel,R.
TITLE Radiolabeled DNA oligonucleotide and method of preparation
JOURNAL Patent: US 5821354-A 1 13-OCT-1998;
FEATURES
    source
    1..19
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.7%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA 2804
Db 19 AAAAAA 1

RESULT 619
AR111371
LOCUS AR111371 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6127124.
ACCESSION AR111371
VERSION AR111371.1 GI:12828219
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JOURNAL Patent: EP 1207210-A 7 22-MAY-2002;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
Query Match 0.7%; Score 19.2; DB 1; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 2 AAAAAA 25
RESULT 608
BD165919
LOCUS BD165919 29 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for melting curve analysis of repetitive PCR products.
ACCESSION BD165919
VERSION BD165919.1 GI:27871731
KEYWORDS JP 2002191384-A/7.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 29)
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: JP 2002191384-A 7 09-JUL-2002;
F HOFFMANN LA ROCHE AG
COMMENT OS Homo sapiens (human)
PN JP 2002191384-A/7
PD 09-JUL-2002
PF 13-NOV-2001 JP 2001348017
PR 15-NOV-2000 EP 00124897.0
PI WOLFGANG DIETMAIER
PC C12N15/09,C12Q1/68,C12N15/00
CC Method for melting curve analysis of repetitive PCR products
FH Key Location/Qualifiers
FT source 1. .29
FT /organism='Homo sapiens (human)'.
FEATURES
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1. .29
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.7%; Score 19.2; DB 1; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 2 AAAAAA 25
RESULT 609
BD274324
LOCUS BD274324 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.
ACCESSION BD274324
VERSION BD274324.1 GI:33084092
KEYWORDS JP 2002526030-A/291.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug discovery

JOURNAL Patent: JP 2002526030-A 291 20-AUG-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002526030-A/291
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide.
FH Key Location/Qualifiers
FT misc feature (28)..(29).
FEATURES
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1. .29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 19.2; DB 1; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2778 TAGAATTGAAAAA 2801
Db 4 TAGACCTAAAAA 27
RESULT 610
BD274342
LOCUS BD274342 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.
ACCESSION BD274342
VERSION BD274342.1 GI:33084110
KEYWORDS JP 2002526030-A/309.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug discovery
JOURNAL Patent: JP 2002526030-A 309 20-AUG-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002526030-A/309
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc feature (28)..(29).
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Query Match 0.7%; Score 19.2; DB 1; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2778 TAGAATTGAAAAA 2801
Db 4 TAGACCTAAAAA 27
RESULT 611
E04206
LOCUS E04206 29 bp DNA linear PAT 29-SEP-1997
DEFINITION single strand DNA sequence of Type C hepatitis virus.

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 604
BD175131/c

LOCUS
DEFINITION Androgen receptor complex-associated protein.
ACCESSION BD175131
VERSION BD175131.1 GI:29120825
KEYWORDS JP 2002262871-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Chan,T.Z.
TITLE Androgen receptor complex-associated protein
JOURNAL Patent: JP 2002262871-A 12 17-SEP-2002;
VETERANS GENERAL HOSPITAL
COMMENT OS Artificial Sequence
PN JP 2002262871-A/12
PD 17-SEP-2002
PF 28-FEB-2001 JP 2001055192
PI TAI ZHAI CHAN
PC C12N15/09,C07K14/47,C12N1/19,C12N1/21,C12N5/10 PC
,C12P21/02,C12Q1/68,
PC G01N33/15,G01N33/50,G01N33/566,C12N15/00,C12N5/00 CC n =
A,T,C or G
CC synthetically generated primer
FH key Location/Qualifiers
FT misc feature (1)..(27).
Location/Qualifiers

FEATURES
source
1..27
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19.2; DB 1; Length 27;
Best Local Similarity 87.5%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 605
BD234339/c

LOCUS
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION BD234339
VERSION BD234339.1 GI:33044109
KEYWORDS JP 2002532085-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Romantchikov,Y.
TITLE Improved method for inserting nucleic acid into cyclic vector
JOURNAL Patent: JP 2002532085-A 12 02-OCT-2002;
YURI ROMANTCHIKOV
COMMENT OS Artificial Sequence
PN JP 2002532085-A/12
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588337
PR 17-DEC-1998 US 09/213834
PI YURI ROMANTCHIKOV
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/00,C12N5/00
CC Cloning Vector
FH key Location/Qualifiers

FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Query Match 0.7%; Score 19.2; DB 1; Length 28;
Best Local Similarity 87.5%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

FT source 1..28
/organism='Artificial Sequence'.
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Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"

Query Match 0.7%; Score 19.2; DB 1; Length 28;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 606
BD234335/c

LOCUS
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION BD234335
VERSION BD234335.1 GI:33044105
KEYWORDS JP 2002532085-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Romantchikov,Y.
TITLE Improved method for inserting nucleic acid into cyclic vector
JOURNAL Patent: JP 2002532085-A 8 02-OCT-2002;
YURI ROMANTCHIKOV
COMMENT OS Artificial Sequence
PN JP 2002532085-A/8
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588337
PR 17-DEC-1998 US 09/213834
PI YURI ROMANTCHIKOV
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/00,C12N5/00
CC Cloning Vector
FH key Location/Qualifiers
FT source 1..28
/organism='Artificial Sequence'.
FEATURES
source
1..28
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19.2; DB 1; Length 28;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 607
AX430216

LOCUS
DEFINITION Sequence 7 from Patent EP1207210.
ACCESSION AX430216
VERSION AX430216.1 GI:21655581
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive pcr products

LOCUS BD187513 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Probe carrier, Method and Apparatus for producing Probe carrier.
ACCESSION BD187513
VERSION BD187513.1 GI:32997252
KEYWORDS JP 2003014773-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Okamura,N., Okamoto,T. and Kameyama,M.
TITLE Probe carrier, Method and Apparatus for producing Probe carrier
JOURNAL Patent: JP 2003014773-A 3 15-JAN-2003;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2003014773-A/3
PD 15-JAN-2003
PF 28-MAR-2002 JP 2002093024
PI nobuyuki okamura,tadashi okamoto,makoto kameyama CC Designed
oligonucleotide to be hybridized with the designed CC
oligonucleotide
CC 'tttttttttttttttttttttttttttt'
FH Key Location/Qualifiers.
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 1 AAAAAA 24
RESULT 593
BD187514/c
LOCUS BD187514 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Probe carrier, Method and Apparatus for producing Probe carrier.
ACCESSION BD187514
VERSION BD187514.1 GI:32997253
KEYWORDS JP 2003014773-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Okamura,N., Okamoto,T. and Kameyama,M.
TITLE Probe carrier, Method and Apparatus for producing Probe carrier
JOURNAL Patent: JP 2003014773-A 4 15-JAN-2003;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2003014773-A/4
PD 15-JAN-2003
PF 28-MAR-2002 JP 2002093024
PI nobuyuki okamura,tadashi okamoto,makoto kameyama CC Designed
oligonucleotide used as a probe to be stabilized CC on a surface
of a
CC carrier
FH Key Location/Qualifiers.
FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 1 AAAAAA 24

Db 25 AAAAAA 2
RESULT 594
BD204988/c
LOCUS BD204988 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Protein array enabling site specification.
ACCESSION BD204988
VERSION BD204988.1 GI:33014758
KEYWORDS JP 2002510505-A/23.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kuimelis,R.G. and Wagner,R.
TITLE Protein array enabling site specification
JOURNAL Patent: JP 2002510505-A 23 09-APR-2002;
PHYLOS INC
COMMENT OS Artificial Sequence
PN JP 2002510505-A/23
PD 09-APR-2002
PF 31-MAR-1999 JP 2000542484
PR 03-APR-1998 US 60/080686
PI ROBERT G KUIMELIS,RICHARD WAGNER
PC C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
G01N33/68,
PC C12N15/00
CC Capture probe sequence
FH Key Location/Qualifiers
FT source 1. .25
/organism='Artificial Sequence'.
FEATURES
source
1. .25
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 25 AAAAAA 2
RESULT 595
I29929
LOCUS I29929 25 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 42 from patent US 5578468.
ACCESSION I29929
VERSION I29929.1 GI:1820720
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Pickup,D.J., Patel,D. and Antczak,J.B.
TITLE Site-specific RNA cleavage
JOURNAL Patent: US 5578468-A 42 26-NOV-1996;
FEATURES
source
1. .25
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 2 AAAAAA 25

REFERENCE 1 (bases 1 to 25)
AUTHORS Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
TITLE Hybridization assay signal enhancement
JOURNAL Patent: US 6103474-A 5 15-AUG-2000;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 25 AAAAAAAAAA 2
RESULT 588
BD234336/c
LOCUS BD234336 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION BD234336
VERSION BD234336.1 GI:33044106
KEYWORDS JP 2002532085-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Romantchikov,Y.
TITLE Improved method for inserting nucleic acid into cyclic vector
JOURNAL Patent: JP 2002532085-A 9 02-OCT-2002;
YURI ROMANTCHIKOV
OS Artificial Sequence
PN JP 2002532085-A/9
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588337
PR 17-DEC-1998 US 09/213834
PI YURI ROMANTCHIKOV
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
CC 00
CC Cloning Vector
FH Key Location/Qualifiers
FT source 1..25
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 25 AAAAAAAAAA 2
RESULT 589
I58009/c
LOCUS I58009 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 2 from patent US 5610287.
ACCESSION I58009
VERSION I58009.1 GI:2483073
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Nikiforov,T. and Knapp,M.R.
TITLE Method for immobilizing nucleic acid molecules

JOURNAL Patent: US 5610287-A 2 11-MAR-1997;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 25 AAAAAAAAAA 2
RESULT 590
I96072/c
LOCUS I96072 25 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 2 from patent US 5734020.
ACCESSION I96072
VERSION I96072.1 GI:3940542
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Wong,Y.N.
TITLE Production and use of magnetic porous inorganic materials
JOURNAL Patent: US 5734020-A 2 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 25 AAAAAAAAAA 2
RESULT 591
AR288252/c
LOCUS AR288252 25 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 23 from patent US 6537749.
ACCESSION AR288252
VERSION AR288252.1 GI:31675536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kuimelis,R.G. and Wagner,R.
TITLE Addressable protein arrays
JOURNAL Patent: US 6537749-A 23 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 25 AAAAAAAAAA 2
RESULT 592
BD187513

RESULT 583
AX750585/C
LOCUS AX750585 24 bp DNA linear PAT 20-JUN-2003
DEFINITION Sequence 11 from Patent WO0221134.
ACCESSION AX750585
VERSION AX750585.1 GI:32133003
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mack,D. and Gish,K.C.
TITLE Methods of diagnosing breast cancer and screening for modulators
JOURNAL Patent: WO 0221134-A 11 14-MAR-2002;
EOS Biotechnology, Inc. (US)
FEATURES
source 1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7-(dT)-24 primer"
Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 24 AAAAAA 1
RESULT 584
AX829247/C
LOCUS AX829247 24 bp DNA linear PAT 12-DEC-2003
DEFINITION Sequence 140 from Patent WO02059377.
ACCESSION AX829247
VERSION AX829247.1 GI:39838972
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mack,D.H., Gish,K.C. and Afar,D.
TITLE Methods of diagnosis of breast cancer, compositions and methods of
screening for modulators of breast cancer
JOURNAL Patent: WO 02059377-A 140 01-AUG-2002;
EOS Biotechnology, Inc. (US)
FEATURES
source 1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence:T7-T24 oligo"
modified_base 8. .24
/note="t at positions 8-24 may be present or absent"
/mod_base=OTHER
Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 24 AAAAAA 1
RESULT 585
BD136714
LOCUS BD136714 24 bp DNA linear PAT 18-SEP-2002
DEFINITION Quantitative assay of nucleic acid amplification product.
ACCESSION BD136714

VERSION BD136714.1 GI:23231659
KEYWORDS JP 2002504350-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Patel,R. and Kurn,N.
TITLE Quantitative assay of nucleic acid amplification product
JOURNAL Patent: JP 2002504350-A 4 12-FEB-2002;
DADE BEHRING INC
COMMENT OS Artificial Sequence
PN JP 2002504350-A/4
PD 12-FEB-2002
PF 17-FEB-1999 JP 2000532556
PR 18-FEB-1998 US 09/025639
PI RAJESH PATEL,NURITH KURN
PC C12Q1/68,C12N15/09,C12N15/00
CC Synthetic DNA Probe
FH Key
FT misc_binding (1). .(24).
Location/Qualifiers
source 1. .24
/organism="synthetic construct"
/mol_type="genomic DNA"
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Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2804
Db 1 AAAAAA 24
RESULT 586
AR168453
LOCUS AR168453 24 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 82 from patent US 6287854.
ACCESSION AR168453
VERSION AR168453.1 GI:17904379
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Spurr,N.K., Gray,I.C. and Stewart,L.M.
TITLE Diagnosis of susceptibility to cancer and treatment thereof
JOURNAL Patent: US 6287854-A 82 11-SEP-2001;
FEATURES
source 1. .24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2162 CTCCTTTT 2185
Db 1 CTCGAGTTT 24
RESULT 587
AR105982/C
LOCUS AR105982 25 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6103474.
ACCESSION AR105982
VERSION AR105982.1 GI:12820047
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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artificial sequences.
REFERENCE
1
AUTHORS Pease,J.S., Cromer,R., Patel,R., Kurn,N. and de Keczser,S.
TITLE Compositions for detection of multiple analytes
JOURNAL Patent: WO 0184157-A 1 08-NOV-2001;
Dade Behring Marburg GmbH (DE)
FEATURES
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1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthesized"

Query Match
Best Local Similarity 0.7%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804
Db 1 AAAAAA 24

RESULT 579
AX547294/c
LOCUS AX547294 24 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 433 from Patent WO02053141.
ACCESSION AX547294
VERSION AX547294.1 GI:25812438
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 433 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match
Best Local Similarity 0.7%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804
Db 24 AAAAAA 1

RESULT 580
AX547822/c
LOCUS AX547822 24 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 961 from Patent WO02053141.
ACCESSION AX547822
VERSION AX547822.1 GI:25812966
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 961 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
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/note="Synthetic Sequence"

Query Match
Best Local Similarity 0.7%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804
Db 24 AAAAAA 1

RESULT 581
AX547823
LOCUS AX547823 24 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 962 from Patent WO02053141.
ACCESSION AX547823
VERSION AX547823.1 GI:25812967
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 962 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match
Best Local Similarity 0.7%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804
Db 1 AAAAAA 24

RESULT 582
AX684290/c
LOCUS AX684290 24 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 13 from Patent WO02059609.
ACCESSION AX684290
VERSION AX684290.1 GI:29371160
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Mack,D.H., Gish,K.C. and Wilson,K.E.
TITLE Methods of diagnosing colorectal cancer and/or breast cancer,
compositions, and methods of screening for colorectal cancer and/or
breast cancer modulators
JOURNAL Patent: WO 02059609-A 13 01-AUG-2002;
EOS Biotechnology, Inc. (US)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7-(dT)-24 primer"

Query Match
Best Local Similarity 0.7%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804
Db 24 AAAAAA 1
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/db_xref="taxon:32630"

Query Match      0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2781 AATTGAAAAA...AAAAA 2804
Db      24  AAAAAA...AAAAA 1

RESULT 574
AX104770
LOCUS      AX104770          24 bp      DNA
DEFINITION Sequence 962 from Patent WO0122972.
ACCESSION  AX104770
VERSION     AX104770.1 GI:13920967
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE       Immunostimulatory nucleic acids
JOURNAL     Patent: WO 0122972-A 962 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES    Location/Qualifiers
            source
            1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2781 AATTGAAAAA...AAAAA 2804
Db      1  AAAAAA...AAAAA 24

RESULT 575
AX354553
LOCUS      AX354553          24 bp      DNA
DEFINITION Sequence 11 from Patent WO0173129.
ACCESSION  AX354553
VERSION     AX354553.1 GI:18619355
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Pollner,R.B.
TITLE       Real time monitoring of PCR using loci
JOURNAL     Patent: WO 0173129-A 11 04-OCT-2001;
            DADE BEHRING INC. (US)
FEATURES    Location/Qualifiers
            source
            1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide attached to beads"

Query Match      0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2781 AATTGAAAAA...AAAAA 2804
Db      1  AAAAAA...AAAAA 24
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RESULT 576
AX355813/c
LOCUS      AX355813          24 bp      DNA
DEFINITION Sequence 841 from Patent WO0197843.
ACCESSION  AX355813
VERSION     AX355813.1 GI:18620481
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Weiner,G. and Hartmann,G.
TITLE       Methods for enhancing antibody-induced cell lysis and treating
            cancer
JOURNAL     Patent: WO 0197843-A 841 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES    Location/Qualifiers
            source
            1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic oligonucleotide-phosphorothioate
            backbone"

Query Match      0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2781 AATTGAAAAA...AAAAA 2804
Db      24  AAAAAA...AAAAA 1

RESULT 577
AX427163/c
LOCUS      AX427163          24 bp      DNA
DEFINITION Sequence 12 from Patent WO0210374.
ACCESSION  AX427163
VERSION     AX427163.1 GI:21530544
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Lin,S.L., Chuong,C.M. and Widelitz,R.B.
TITLE       Gene silencing using mrna-cdna hybrids
JOURNAL     Patent: WO 0210374-A 12 07-FEB-2002;
            UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES    Location/Qualifiers
            source
            1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Poly(dT)24 primer"

Query Match      0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2781 AATTGAAAAA...AAAAA 2804
Db      24  AAAAAA...AAAAA 1

RESULT 578
AX428574
LOCUS      AX428574          24 bp      DNA
DEFINITION Sequence 1 from Patent WO0184157.
ACCESSION  AX428574
VERSION     AX428574.1 GI:21538485
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
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KEYWORDS		Unknown.	
SOURCE	ORGANISM	Unknown.	
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 24)		
TITLE	Su,X., Dong,H. and Ryder,T.B.		
JOURNAL	Amplification of nucleic acids		
FEATURES	Patent: US 6582938-A 1 24-JUN-2003;		
source	Location/Qualifiers		
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	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	0.7%;	Score 19.2;	DB 1;
Best Local Similarity	87.5%;	Pred. No. 7.3e+02;	Length 24;
Matches	21;	Conservative 0;	Mismatches 3;
		Indels 0;	Gaps 0;
QY	2781	AATTGAAAAA	2804
Db	1	AAAAA	24
RESULT 572	AX104241/c		
LOCUS	AX104241		
DEFINITION	Sequence 433 from Patent WO0122972.		
ACCESSION	AX104241		
VERSION	AX104241.1 GI:13920438		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Krieg,A.M., Schetter,C. and Vollmer,J.C.		
TITLE	Immunostimulatory nucleic acids		
JOURNAL	Patent: WO 0122972-A 433 05-APR-2001;		
FEATURES	UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)		
source	Location/Qualifiers		
	1..24		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
Query Match	0.7%;	Score 19.2;	DB 1;
Best Local Similarity	87.5%;	Pred. No. 7.3e+02;	Length 24;
Matches	21;	Conservative 0;	Mismatches 3;
		Indels 0;	Gaps 0;
QY	2781	AATTGAAAAA	2804
Db	24	AAAAA	1
RESULT 573	AX104769/c		
LOCUS	AX104769		
DEFINITION	Sequence 961 from Patent WO0122972.		
ACCESSION	AX104769		
VERSION	AX104769.1 GI:13920966		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Krieg,A.M., Schetter,C. and Vollmer,J.C.		
TITLE	Immunostimulatory nucleic acids		
JOURNAL	Patent: WO 0122972-A 961 05-APR-2001;		
FEATURES	UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)		
source	Location/Qualifiers		
	1..24		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		

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AR184443
LOCUS       AR184443          24 bp      DNA
DEFINITION  Sequence 11 from patent US 6346384.
ACCESSION   AR184443
VERSION     AR184443.1  GI:20230408
KEYWORDS    .
SOURCE      Unknown.
            ORGANISM      Unknown.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Pollner,R.B.
TITLE      Real-time monitoring of PCR using LOCI
JOURNAL    Patent: US 6346384-A 11 12-FEB-2002;
FEATURES    Location/Qualifiers
            source          1..24
                        /organism="unknown"
                        /mol_type="unassigned DNA"

Query Match      0.7%;      Score 19.2;      DB 1;      Length 24;
Best Local Similarity 87.5%;      Pred. No. 7.3e+02;
Matches 21;      Conservative 0;      Mismatches 3;      Indels 0;      Gaps 0;

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Qy	2781 AATTGAAAAAAAAAAAAA 2804
Dbb	 1 AAAAAAAAAAAAAAAAAA 24
RESULT 567	
AR202876	
LOCUS	AR202876 24 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 4 from patent US 6365346.
ACCESSION	AR202876
VERSION	AR202876.1 GI:21499117
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown. Unclassified.
REFERENCE	1 (bases 1 to 24)
AUTHORS	Patel,R. and Kurn,N.
TITLE	Quantitative determination of nucleic acid amplification products
JOURNAL	Patent: US 6365346-A 4 02-APR-2002;
FEATURES	Location/Qualifiers source 1..24

Query Match	0.7%;	Score 19.2;	DB 1;	Length 24;
Best Local Similarity	87.5%;	Pred. No. 7.3e+02;		
Matches 21:	Conservative	0;	Mismatches 3;	Indels 0;
	Gaps	0;		

Query Match	0.7%;	Score 19.2;	DB 1;	Length 24;
Best Local Similarity	87.5%;	Pred. No. 7.3e+02;		
Matches 21;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	2781	AATTGAAAAAAAAAAAAAAAAAAAA	2804
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	24

RESULT 568				
AR213697	AR213697	Sequence 4	24 bp	DNA
DEFINITION		from patent US 6406667.		
ACCESSION	AR213697			
VERSION	AR213697.1	GI:23310978		
KEYWORDS				
SOURCE		Unknown.		

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RESULT 568
AR213697
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AR213697
Sequence 4 from patent US 6406667.
AR213697
AR213697.1 GI:23310978
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Unknown.
Unknown.
Unclassified.
1 (bases 1 to 24)
Singh,S. and Ullman,E.F.
Chemiluminescent compositions for use in detection of multiple
analytes
Patent: US 6406667-A 4 18-JUN-2002;
Location/Qualifiers
1. .24
/organism="unknown"

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/organism="unknown"

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Best Local Similarity 95.0%; Pred. No. 7.3e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804
Db :|||||
24 BAAAAAAAAAAAAAAAAAAAAA 5

RESULT 559
AR010037
LOCUS AR010037 24 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 50 from patent US 5756684.
ACCESSION AR010037
VERSION AR010037.1 GI:3968842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Cloning and expression of PUR protein
JOURNAL Patent: US 5756684-A 50 26-MAY-1998;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db |||
1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 560
AR034772
LOCUS AR034772 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 50 from patent US 5869622.
ACCESSION AR034772
VERSION AR034772.1 GI:5950377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Monoclonal antibodies to the pur protein
JOURNAL Patent: US 5869622-A 50 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db |||
1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 561
AR068465
LOCUS AR068465 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5853993.
ACCESSION AR068465
VERSION AR068465.1 GI:6000672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dellinger,D.J., Dahm,S.C. and Troll,M.A.
TITLE Signal enhancement method and kit
JOURNAL Patent: US 5853993-A 1 29-DEC-1998;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db |||
1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 562
AR105984
LOCUS AR105984 24 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6103474.
ACCESSION AR105984
VERSION AR105984.1 GI:12820049
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
TITLE Hybridization assay signal enhancement
JOURNAL Patent: US 6103474-A 7 15-AUG-2000;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db |||
1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 563
AR107972
LOCUS AR107972 24 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6110682.
ACCESSION AR107972
VERSION AR107972.1 GI:12823459
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Dellinger,D.J., Dahm,S.C. and Troll,M.A.
TITLE Signal enhancement method and kit
JOURNAL Patent: US 6110682-A 1 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db |||
1 AAAAAAAAAAAAAAAAAAAAAA 24

	Matches	23; Conservative	0; Mismatches	6; Indels	0; Gaps	
Qy	2156	TTTTTCTCCTTTT	TTTTTTT	2184		
Db	1	TTTGCGGCGCTTTT	TTTTTTTTT	29		
RESULT 552						
AR409905						
LOCUS AR409905 29 bp RNA linear PAT 18-DEC-2003						
DEFINITION Sequence 18 from patent US 6635422.						
ACCESSION AR409905						
VERSION AR409905.1 GI:40161040						
KEYWORDS .						
SOURCE Unknown.						
ORGANISM Unknown.						
REFERENCE Unclassified.						
AUTHORS 1 (bases 1 to 29)						
TITLE Keene,J.D., Tenenbaum,S.A. and Carson,C.C.						
METHODS Methods for isolating and characterizing endogenous mRNA-protein (mRNP) complexes						
JOURNAL Patent: US 6635422-A 18 OCT-2003;						
FEATURES Location/Qualifiers						
source 1..29						
/organism="unknown"						
/mol_type="unassigned RNA"						
Query Match 0.7%; Score 19.4; DB 1; Length 29;						
Best Local Similarity 79.3%; Pred. No. 1.1e+03;						
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;						
Qy	2155	TTTTTCTCCTTTT	TTTTTTT	2183		
Db	1	TTTTTTAAATTTT	TATTTCCTTT	29		
RESULT 553						
AX181697/c						
LOCUS AX181697 29 bp DNA linear PAT 07-AUG-2001						
DEFINITION Sequence 54 from Patent WO0146231.						
ACCESSION AX181697						
VERSION AX181697.1 GI:15133035						
KEYWORDS .						
SOURCE Homo sapiens (human)						
ORGANISM Homo sapiens						
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS 1						
TITLE Novel proteins and nucleic acids encoding same						
JOURNAL Patent: WO 0146231-A 54 JUN-2001;						
Curagen Corporation (US)						
FEATURES Location/Qualifiers						
source 1..29						
/organism="Homo sapiens"						
/mol_type="unassigned DNA"						
/db_xref="taxon:9606"						
Query Match 0.7%; Score 19.4; DB 1; Length 29;						
Best Local Similarity 79.3%; Pred. No. 1.1e+03;						
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;						
Qy	2165	CTTTTCTTTT	TTTTTTTAACCTTG	2193		
Db	29	CTTTATTCCTTGT	TTTGTGTTTATTG	1		
RESULT 554						
AX394619/c						
LOCUS AX394619 29 bp DNA linear PAT 18-MAY-2002						
DEFINITION Sequence 17 from Patent EP1186673.						
ACCESSION AX394619						
VERSION AX394619.1 GI:21065732						

FEATURES	SOURCE
1. The first feature is the presence of a...	...
2. The second feature is the presence of a...	...
3. The third feature is the presence of a...	...
4. The fourth feature is the presence of a...	...
5. The fifth feature is the presence of a...	...
6. The sixth feature is the presence of a...	...
7. The seventh feature is the presence of a...	...
8. The eighth feature is the presence of a...	...
9. The ninth feature is the presence of a...	...
10. The tenth feature is the presence of a...	...

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RESULT 534
AX513052/c  AX513052          27 bp  DNA  linear  PAT 03-OCT-2002
LOCUS
DEFINITION  Sequence 42 from Patent WO02062135.
ACCESSION  AX513052
VERSION    AX513052.1  GI:23504143
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE  1
AUTHORS    Egelrud,T. and Hansson,L.
TITLE      Scce modified transgenic mammals and their use as models of human
           disease
JOURNAL
FEATURES   Patent: WO 02062135-A 42 15-AUG-2002;
           Egelrud, Torbjorn (SE) ; Hansson, Lennart (SE)
           Location/Qualifiers
           1..27
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="5 -RACE cDNA synthesis primer."

Query Match      0.7%;  Score 19.4;  DB 1;  Length 27;
Best Local Similarity 84.0%;  Pred. No. 9.3e+02;
Matches 21;  Conservative 1;  Mismatches 3;  Indels 0;  Gaps 0;

QY  2780 GAATTGAAAAAATAAAAAAAAAAAAAA 2804
Db  26 BAAAAAATAAAAAAAAAAAAAA 2

Query Match      0.7%;  Score 19.4;  DB 1;  Length 27;
Best Local Similarity 84.0%;  Pred. No. 9.3e+02;
Matches 21;  Conservative 1;  Mismatches 3;  Indels 0;  Gaps 0;

RESULT 535
AR022650
LOCUS
DEFINITION  Sequence 9 from patent US 5792931.
ACCESSION  AR022650
VERSION    AR022650.1  GI:3976712
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 28)
AUTHORS    Duwick,J., Rood,T., Maddox,J.R. and Wang,X.
TITLE      Fumonisin detoxification compositions and methods
JOURNAL    Patent: US 5792931-A 9 11-AUG-1998;
           Location/Qualifiers
           1..28
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.7%;  Score 19.4;  DB 1;  Length 28;
Best Local Similarity 95.2%;  Pred. No. 1e+03;
Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY  2163 TCCTTTTTCCTTTTTCCTTTTTCCTTTT 2183
Db  7 TCCGTTTTCCTTTTTCCTTTTTCCTTTT 27

RESULT 536
AR055108
LOCUS
DEFINITION  Sequence 13 from patent US 5837468.
ACCESSION  AR055108
VERSION    AR055108.1  GI:5980685
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 28)
AUTHORS    Wang,X., Duwick,J.P. and Briggs,S.P.
TITLE      PCR-based cDNA substructure cloning method
JOURNAL    Patent: US 5837468-A 15 17-NOV-1998;
           Location/Qualifiers
           1..28
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.7%;  Score 19.4;  DB 1;  Length 28;
Best Local Similarity 95.2%;  Pred. No. 1e+03;
Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY  2163 TCCTTTTTCCTTTTTCCTTTTTCCTTTT 2183
Db  7 TCCGTTTTCCTTTTTCCTTTTTCCTTTT 27
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AUTHORS    Wang,X., Duwick,J.P. and Briggs,S.P.
TITLE      PCR-based cDNA substructure cloning method
JOURNAL    Patent: US 5837468-A 13 17-NOV-1998;
           Location/Qualifiers
           1..28
           /organism="unknown"
           /mol_type="unassigned DNA"

FEATURES   source
           Query Match      0.7%;  Score 19.4;  DB 1;  Length 28;
           Best Local Similarity 95.2%;  Pred. No. 1e+03;
           Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY  2163 TCCTTTTTCCTTTTTCCTTTTTCCTTTT 2183
Db  7 TCCGTTTTCCTTTTTCCTTTTTCCTTTT 27

RESULT 537
AR055109
LOCUS
DEFINITION  Sequence 14 from patent US 5837468.
ACCESSION  AR055109
VERSION    AR055109.1  GI:5980686
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 28)
AUTHORS    Wang,X., Duwick,J.P. and Briggs,S.P.
TITLE      PCR-based cDNA substructure cloning method
JOURNAL    Patent: US 5837468-A 14 17-NOV-1998;
           Location/Qualifiers
           1..28
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.7%;  Score 19.4;  DB 1;  Length 28;
Best Local Similarity 95.2%;  Pred. No. 1e+03;
Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY  2163 TCCTTTTTCCTTTTTCCTTTTTCCTTTT 2183
Db  7 TCCGTTTTCCTTTTTCCTTTTTCCTTTT 27

RESULT 538
AR055110
LOCUS
DEFINITION  Sequence 15 from patent US 5837468.
ACCESSION  AR055110
VERSION    AR055110.1  GI:5980687
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 28)
AUTHORS    Wang,X., Duwick,J.P. and Briggs,S.P.
TITLE      PCR-based cDNA substructure cloning method
JOURNAL    Patent: US 5837468-A 15 17-NOV-1998;
           Location/Qualifiers
           1..28
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.7%;  Score 19.4;  DB 1;  Length 28;
Best Local Similarity 95.2%;  Pred. No. 1e+03;
Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY  2163 TCCTTTTTCCTTTTTCCTTTTTCCTTTT 2183
Db  7 TCCGTTTTCCTTTTTCCTTTTTCCTTTT 27

RESULT 539
AR055110
LOCUS
DEFINITION  Sequence 15 from patent US 5837468.
ACCESSION  AR055110
VERSION    AR055110.1  GI:5980687
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 28)
AUTHORS    Wang,X., Duwick,J.P. and Briggs,S.P.
TITLE      PCR-based cDNA substructure cloning method
JOURNAL    Patent: US 5837468-A 15 17-NOV-1998;
           Location/Qualifiers
           1..28
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.7%;  Score 19.4;  DB 1;  Length 28;
Best Local Similarity 95.2%;  Pred. No. 1e+03;
Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY  2163 TCCTTTTTCCTTTTTCCTTTTTCCTTTT 2183
Db  7 TCCGTTTTCCTTTTTCCTTTTTCCTTTT 27
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TITLE Genes and proteins predictive and therapeutic for stroke, hypertension, diabetes and obesity
JOURNAL Patent: US 6486299-A 43 26-NOV-2002;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19.4; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 8.4e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 BAAAAA 2

RESULT 530
AR263647/c
LOCUS AR263647 26 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 6 from patent US 6331413.
ACCESSION AR263647
VERSION AR263647.1 GI:28075580
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Adler,D.A. and Sheppard,P.O.
TITLE Secreted salivary ZSIG63 Polypeptide
JOURNAL Patent: US 6331413-A 6 18-DEC-2001;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19.4; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 8.4e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 BAAAAA 2

RESULT 531
AX814950/c
LOCUS AX814950 26 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 36 from Patent WO03064691.
ACCESSION AX814950
VERSION AX814950.1 GI:39104088
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnarsson,S., Ernfors,P., Bauren,P., Metsis,A., Pihlak,A. and Montelius,A.
TITLE Methods and means for manipulating nucleic acid
JOURNAL Patent: WO 03064691-A 36 07-AUG-2003;
FEATURES Location/Qualifiers
source
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
note="Description of Artificial Sequence: Primer"
misc_feature 26
/note="v is a, c or g"

Query Match 0.7%; Score 19.4; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 8.4e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 BAAAAA 2

RESULT 532
BD062456/c
LOCUS BD062456 26 bp DNA linear PAT 27-AUG-2002
DEFINITION A human 2-19 protein homologue, Z219A.
ACCESSION BD062456
VERSION BD062456.1 GI:22608059
KEYWORDS JP 2001507946-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 26)
AUTHORS Konklin,D.C. and Blumberg,H.
TITLE A human 2-19 protein homologue, Z219A
JOURNAL Patent: JP 2001507946-A 4 19-JUN-2001;
COMMENT ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2001507946-A/4
PD 19-JUN-2001
PF 06-OCT-1998 JP 1999522287
PR 06-OCT-1997 US 60/061712
PI DARRELL C KONKLIN,HAL BLUMBERG
PC C12N15/12,C12N15/62,C12N5/10,C07K14/47,C07K16/18,C12Q1/68, PC A01K67/027
CC Oligonucleotide primer ZC7231
FH Key Location/Qualifiers
1. .26
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19.4; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 8.4e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 BAAAAA 2

RESULT 533
AR013918
LOCUS AR013918 26 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5773223.
ACCESSION AR013918
VERSION AR013918.1 GI:3971372
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Shyamala,V. and Olson,P.Tekamp.
TITLE Endothelin B.sub.1, (ETB.sub.1) receptor polypeptide and its encoding nucleic acid methods, and uses thereof
JOURNAL Patent: US 5773223-A 3 30-JUN-1998;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19.4; DB 1; Length 26;
Best Local Similarity 95.2%; Pred. No. 8.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2163 TCCCTTTT 2183
Db 6 TACITTTT 26

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Best Local Similarity 87.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTTNTTTTATTTTATTTTAA 2188
Db 24 TTTNTTTTATTTTATTTTNC 2

RESULT 526
BD056964/c
LOCUS
DEFINITION
Sets of labeled energy transfer fluorescent primers and their use
in multi component analysis.
ACCESSION
BD056964
VERSION
BD056964.1 GI:22602570
KEYWORDS
JP 2001509271-A/1.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Ju,J.
TITLE
Sets of labeled energy transfer fluorescent primers and their use
in multi component analysis
JOURNAL
Patent: JP 2001509271-A 1 10-JUL-2001;
COMMENT
INCYTE PHARMACEUTICALS INC
PN JP 2001509271-A/1
PD 10-JUL-2001
PF 12-DEC-1997 JP 1998534358
PR 15-JAN-1997 US 08/784162
PI JINGYUE JU
PC G01N21/78,C12N15/09,C12Q1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
1..25
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

Query Match 0.7%; Score 19.4; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAAAAAA 2804
Db 24 TAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 527
AX708814
LOCUS
DEFINITION
Sequence 30 from Patent WO02095071.
ACCESSION
AX708814
VERSION
AX708814.1 GI:29564541
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Plasterk,R.H.
TITLE
Means and methods for identifying genes and proteins involved in
the prevention and/or repair of a replication error
JOURNAL
Patent: WO 02095071-A 30 28-NOV-2002;
Koninklijke Nederlandse Akademie van Wetenschappen (NL)
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="sequence to demonstrate the principle of how to
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detect somatic repeat instability~#N# stands for any
number of nucleotides selected from A, C, T or G#"

Query Match 0.7%; Score 19.4; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAAAAAAAAAAAAA 2804
Db 1 ATGNAAAAAAAAAAAAAAAAAA 23

RESULT 528
BD237566/c
LOCUS
DEFINITION
Genes and proteins predicting and treating fit, hypertension,
diabetes and obesity.
ACCESSION
BD237566
VERSION
BD237566.1 GI:33047336
KEYWORDS
JP 2002525115-A/1.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Shimkets,R.A.
TITLE
Genes and proteins predicting and treating fit, hypertension,
diabetes and obesity
JOURNAL
Patent: JP 2002525115-A 1 13-AUG-2002;
CURAGEN CORP
COMMENT
OS Artificial Sequence
PN JP 2002525115-A/1
PD 13-AUG-2002
PF 28-SEP-1999 JP 2000572365
PR 28-SEP-1998 US 09/161939
PI RICHARD A SHIMKETS
PC C12N15/09,A01K67/027,A61K31/7088,A61K38/00,A61K39/395,A61K39/
PC 395,
PC A61K39/395,A61K48/00,A61P3/04,A61P3/06,A61P9/10,A61P9/12, PC
A61P43/00,
PC C07K14/47,C07K16/18,C12N9/10,C12N9/88,C12Q1/25,C12Q1/52 PC
,C12Q1/68,G01N33/15,
PC G01N33/50,C12N15/00,A61K37/02
CC Description of Artificial Sequence: oligo(dT)<25>V FH Key
Location/Qualifiers
FT source 1..26
/organism='Artificial Sequence'.
FEATURES
source
1..26
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19.4; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 8.4e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAAAAAAAAAAAAAA 2804
Db 26 BAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 529
AR257336/c
LOCUS
DEFINITION
Sequence 43 from patent US 6486299.
ACCESSION
AR257336
VERSION
AR257336.1 GI:27307233
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Shimkets,R.A.
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QY      2784 TGAAAAAAAAAAAAAAAAAAAA 2804
Db      21  TCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 522
AX825158
LOCUS      AX825158                21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 56 from Patent WO03072818.
ACCESSION  AX825158
VERSION     AX825158.1  GI:39750887
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL    Patent: WO 03072818-A 56 04-SEP-2003;
           Degussa Bioactives GmbH (DE)
FEATURES   Location/Qualifiers
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               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz:Capture-Oligonukleotid"
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             6
               /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
           modified_base
             9
               /note="LNA-T (Locked Nucleic Acid)"
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Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2166 TTTTTTTTTTTTTTTTTTTT 2186
Db      1  TTTTTTTTTTTTTTTTTTTGT 21

RESULT 523
AR431308
LOCUS      AR431308                24 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6651008.
ACCESSION  AR431308
VERSION     AR431308.1  GI:40193276
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 24)
AUTHORS    Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
TITLE      Database system including computer code for predictive cellular
           bioinformatics
JOURNAL    Patent: US 6651008-A 2 18-NOV-2003;
           Location/Qualifiers
FEATURES
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source
1..24
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.7%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2166 TTTTTTTTTTTTTTTTTTTT 2186
Db      2  TTTTATTATTTTTTTTTTTT 22

RESULT 524
AX708815
LOCUS      AX708815                24 bp      DNA      linear      PAT 04-APR-2003
DEFINITION Sequence 31 from Patent WO02095071.
ACCESSION  AX708815
VERSION     AX708815.1  GI:29564542
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Plasterk,R.H.
TITLE      Means and methods for identifying genes and proteins involved in
           the prevention and/or repair of a replication error
JOURNAL    Patent: WO 02095071-A 31 28-NOV-2002;
           Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES   Location/Qualifiers
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="sequence to demonstrate the principle of how to
               detect somatic repeat instability-##N# stands for any
               number of nucleotides selected from A, C, T or G#"

Query Match      0.7%; Score 19.4; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2782 ATTGAAAAAAAAAAAAAAAAAAAA 2804
Db      1  ATGNAAAAAAAAAAAAAAAAAAANA 23

RESULT 525
AX708815/c
LOCUS      AX708815                24 bp      DNA      linear      PAT 04-APR-2003
DEFINITION Sequence 31 from Patent WO02095071.
ACCESSION  AX708815
VERSION     AX708815.1  GI:29564542
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Plasterk,R.H.
TITLE      Means and methods for identifying genes and proteins involved in
           the prevention and/or repair of a replication error
JOURNAL    Patent: WO 02095071-A 31 28-NOV-2002;
           Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES   Location/Qualifiers
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="sequence to demonstrate the principle of how to
               detect somatic repeat instability-##N# stands for any
               number of nucleotides selected from A, C, T or G#"

Query Match      0.7%; Score 19.4; DB 1; Length 24;
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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modified_base
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/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2783 TTGAAAAA 2803
Db 21 TGGAAAAA 1
RESULT 517
AX825147
LOCUS AX825147 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 45 from Patent WO03072818.
ACCESSION AX825147
VERSION AX825147.1 GI:39750876
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 45 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
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/mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
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modified_base
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/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2783 TTGAAAAA 2803
Db 21 TGGAAAAA 1
RESULT 517
AX825147
LOCUS AX825147 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 45 from Patent WO03072818.
ACCESSION AX825147
VERSION AX825147.1 GI:39750876
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 45 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
Location/Qualifiers
1. .21
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
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Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2167 TTTT 2187
Db 1 TTTT 21
RESULT 518
AX825147/c
LOCUS AX825147 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 45 from Patent WO03072818.
ACCESSION AX825147
VERSION AX825147.1 GI:39750876
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 45 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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Location/Qualifiers
1. .21
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
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modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
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modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
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modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
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Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2783 TTGAAAAA 2803
Db 21 TAGAAAAA 1
RESULT 519
AX825150
LOCUS AX825150 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 48 from Patent WO03072818.
ACCESSION AX825150


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modified_base      /mod_base=OTHER
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid)"
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Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2803
Db 21 TTCAAAAA 1

RESULT 511
AX825121
LOCUS AX825121 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 19 from Patent WO03072818.
ACCESSION AX825121
VERSION AX825121.1 GI:39750850
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 19 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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3
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/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid)"
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18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

misc_binding
1
/bound_moiety="Biotin"
3

modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
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/note="LNA-T (Locked Nucleic Acid)"
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Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2169 TTTT 2189
Db 1 TTTT 21

RESULT 512
AX825127/c
LOCUS AX825127 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 25 from Patent WO03072818.
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ACCESSION AX825127
VERSION AX825127.1 GI:39750856
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 25 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAAAAA 2804
Db 21 TGCAAAAA 1

RESULT 513
AX825131
LOCUS AX825131 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 29 from Patent WO03072818.
ACCESSION AX825131
VERSION AX825131.1 GI:39750860
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 29 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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1. .21
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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3

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3

modified_base
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 70-2986-100
 DATE: 10-2-55
 FILE NO: 70-2986


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modified_base     18 /note="LNA-T (Locked Nucleic Acid)"
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Query Match           0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY    2783 TTGAAAAAAAAAAAAAA 2803
Db    21 TTTAAAAAAAAAAAAAA 1

RESULT 498
AX825106/c
LOCUS       AX825106              21 bp DNA linear PAT 11-DEC-2003
DEFINITION   Sequence 4 from Patent WO03072818.
ACCESSION   AX825106
VERSION     AX825106.1 GI:39750835
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 Boekamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS      Method for sorting single-stranded nucleic acids
TITLE        Patent: WO 03072818-A 4 04-SEP-2003;
JOURNAL      Degussa Bioactives GmbH (DE)
FEATURES     Location/Qualifiers
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                  /mod_base=OTHER
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                  /mod_base=OTHER
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modified_base    15 /note="LNA-T (Locked Nucleic Acid)"
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modified_base    18 /note="LNA-T (Locked Nucleic Acid)"
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Query Match           0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY    2782 ATTGAAAAAAAAAAAAA 2802
Db    21 ATTAATAAAAAAAAAAAA 1

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Christensen,T.
TITLE Isolated transcription factor for an alpha-amylase promoter in filamentous fungi
JOURNAL Patent: US 655657-A 9 29-APR-2003;
FEATURES Location/Qualifiers
source 1..41
/organism="unknown"
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Query Match 0.7%; Score 19.6; DB 1; Length 41;
Best Local Similarity 84.6%; Pred. No. 2.1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 16
RESULT 492
AX225198/c 43 bp DNA linear PAT 10-SEP-2001
LOCUS AX225198
DEFINITION Sequence 7 from Patent WO0161033.
ACCESSION AX225198
VERSION AX225198.1 GI:15555219
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schouten,J.P.
TITLE Multiplex ligatable probe amplification
JOURNAL Patent: WO 0161033-A 7 23-AUG-2001;
Schouten, Johannes Petrus (NL)
FEATURES Location/Qualifiers
source 1..43
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/db_xref="taxon:32630"
/note="synthetic DNA"
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Best Local Similarity 84.6%; Pred. No. 2.2e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 18
RESULT 493
AX825135 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825135
DEFINITION Sequence 33 from Patent WO03072818.
ACCESSION AX825135
VERSION AX825135.1 GI:39750864
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 33 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers
source 1..21
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Best Local Similarity 84.6%; Pred. No. 1.9e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 13
RESULT 489
A48799 40 bp DNA linear PAT 07-MAR-1997
LOCUS A48799
DEFINITION Sequence 6 from Patent WO9603528.
ACCESSION A48799
VERSION A48799.1 GI:2302466
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 40)
AUTHORS Petrlik,J., Allain,J. and Pearson,G.J.
TITLE OLIGONUCLEOTIDES AND THEIR USE
JOURNAL Patent: WO 9603528-A 6 08-FEB-1996;
LYNXVALE LTD (GB)
COMMENT Other publication AU 3118395 960222.
FEATURES Location/Qualifiers
source 1..40
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.7%; Score 19.6; DB 1; Length 40;
Best Local Similarity 84.6%; Pred. No. 2.1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
RESULT 490
AR232955 40 bp DNA linear PAT 20-DEC-2002
LOCUS AR232955
DEFINITION Sequence 7 from patent US 6457426.
ACCESSION AR232955
VERSION AR232955.1 GI:27275302
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Cruson,I.
TITLE Front tube furrow opener attachment
JOURNAL Patent: US 6457426-A 7 01-OCT-2002;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
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Query Match 0.7%; Score 19.6; DB 1; Length 40;
Best Local Similarity 84.6%; Pred. No. 2.1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
RESULT 491
AR309630/c 41 bp DNA linear PAT 12-JUN-2003
LOCUS AR309630
DEFINITION Sequence 9 from patent US 6555657.
ACCESSION AR309630
VERSION AR309630.1 GI:31701680

AUTHORS Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
Grilley,M., Watkins,M. and Hillyard,D.R.
TITLE Contryphan peptides
JOURNAL Patent: US 6153738-A 26 28-NOV-2000;
FEATURES Location/Qualifiers
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1. .33
/organism="unknown"
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Query Match 0.7%; Score 19.6; DB 1; Length 33;
Best Local Similarity 84.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 33 AAAAAAAAAAAAAAAAAA 8

RESULT 485
A63578/c
LOCUS A63578 34 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 19 from Patent WO9720924.
ACCESSION A63578
VERSION A63578.1 GI:3717233
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Scaggiante,B. and Quadrioglio,F.
TITLE A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMORAL AGENTS
JOURNAL Patent: WO 9720924-A 19 12-JUN-1997;
COMMENT SAICOM S R L (IT)
Other publication IT MI952539 19970604
Other publication AU 1175497 19970627.
FEATURES Location/Qualifiers
source
1. .34
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 19.6; DB 1; Length 34;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 34 AAAAAAAAAAAAAAAAAA 9

RESULT 486
I29931
LOCUS I29931 37 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 44 from patent US 5578468.
ACCESSION I29931
VERSION I29931.1 GI:1820722
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 37)
AUTHORS Pickup,D.J., Patel,D. and Antczak,J.B.
TITLE Site-specific RNA cleavage
JOURNAL Patent: US 5578468-A 44 26-NOV-1996;
FEATURES Location/Qualifiers
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Query Match 0.7%; Score 19.6; DB 1; Length 37;
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Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 2 AAAAAAAAAAAAAAAAAA 27

RESULT 487
AX106972/c
LOCUS AX106972 37 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 25 from Patent WO0125442.
ACCESSION AX106972
VERSION AX106972.1 GI:13922521
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
TITLE Dna polymerase lambda and uses thereof
JOURNAL Patent: WO 0125442-A 25 12-APR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES Location/Qualifiers
source
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/organism="synthetic construct"
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/note="poly dT"

Query Match 0.7%; Score 19.6; DB 1; Length 37;
Best Local Similarity 84.6%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 37 AAAAAAAAAAAAAAAAAA 12

RESULT 488
E50766/c
LOCUS E50766 38 bp DNA linear PAT 31-JAN-2002
DEFINITION Vector expressing full-length gene of RNA virus and utilization thereof.
ACCESSION E50766
VERSION E50766.1 GI:18628191
KEYWORDS JP 2000152793-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 38)
AUTHORS Obara,M., Obara,K., Tabira,K., Matsuzaki,J. and Om,H.
TITLE Vector expressing full-length gene of RNA virus and utilization
JOURNAL Patent: JP 2000152793-A 19 06-JUN-2000;
TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, CHUGAI PHARMACEUT CO LTD
OS Artificial Sequence
PN JP 2000152793-A/19
PD 06-JUN-2000
PF 24-JUN-1999 JP 1999178347
PR
PI MICHINORI OBARA,KYOKO OBARA,KAZUNARI TABIRA,JUNICHI MATSUZAKI,
PI HIROSHI OMORI
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/70,C12N15/00,C12N5/00 CC

FH Key Location/Qualifiers
FT source 1. .38
/organism='Artificial Sequence'.
FEATURES Location/Qualifiers
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Query Match 0.7%; Score 19.6; DB 1; Length 38;

Sato,S.									
TITLE	Detection kit for SRSV								
JOURNAL	Patent: WO 0079280-A 13 28-DEC-2000; JAPAN AS REPRESENTED BY DIRECTOR GE YOSHIHIKO HIROSE, MITSUAKI MORIGUCHI, KIMIYASU ISOBE DISEASES, DENKA SEIKEN CO LTD, NAKAZAKU TAKEDA, KATSURO NATORI, TATSUO MIYAMURA, KUNIO KAMATA, TOSHINORI SATO, SEIYA SATO								
COMMENT	OS Artificial Sequence PN WO 0079280-A/13 PD 28-DEC-2000 PF 22-JUN-2000 WO 2000JP004095 PR 22-JUN-1999 JP 99P 175928 PI NAKAZU TAKEDA, KATSURO NATORI, TATSUO MIYAMURA, KUNIO PI KAMATA, TOSHINORI SATO, SEIYA SATO PC G01N33/569, C12N15/40 CC								
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Matches	22; Conservative 0; Mismatches 4; Indels 0; Gaps								
QY	2779 AGAATTGAAAAAAAAAAAAAAAAAAAAA 2804								
Db	33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8								
RESULT 483									
AR099615/c									
LOCUS	AR099615 33 bp DNA linear PAT 14-FEB-								
DEFINITION	Sequence 26 from patent US 6077934.								
ACCESSION	AR099615								
VERSION	AR099615.1 GI:12809381								
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 33) Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R., Grilley,M., Watkins,M. and Hillyard,D.R.								
TITLE	Contryphan peptides								
JOURNAL	Patent: US 6077934-A 26 20-JUN-2000;								
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Matches	22; Conservative 0; Mismatches 4; Indels 0; Gaps								
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Db	33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8								
RESULT 484									
AR120128/c									
LOCUS	AR120128 33 bp DNA linear PAT 16-MAR-								
DEFINITION	Sequence 26 from patent US 6153738.								
ACCESSION	AR120128								
VERSION	AR120128.1 GI:14102827								
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
	1 (bases 1 to 33)								

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RESULT 475
I59848/c
LOCUS I59848 30 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 85 from patent US 5654414.
ACCESSION I59848
VERSION I59848.1 GI:2478480
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 30)
AUTHORS Ryals,J.A., Beck,J.J. and Friedrich,L.B.
TITLE Chemically inducible promoter of a cucumber chitinase/lysozyme gene
JOURNAL Patent: US 5654414-A 85 05-AUG-1997;
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QY 2165 CTTTCTTTTTTTTTTTTTTTTAACT 2190
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Db 30 CTTATGTTTTTTTTTTTTTTTGAATT 5
RESULT 476
I75175/c
LOCUS I75175 30 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 85 from patent US 5689044.
ACCESSION I75175
VERSION I75175.1 GI:3011316
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 30)
AUTHORS Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
TITLE Chemically inducible promoter of a plant PR-1 gene
JOURNAL Patent: US 5689044-A 85.18-NOV-1997;
FEATURES Location/Qualifiers
source 1..30
/mol_type="unknown"
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Db 30 CTTATGTTTTTTTTTTTTTTTGAATT 5
RESULT 477
AR409723/c
LOCUS AR409723 30 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 85 from patent US 6632981.
ACCESSION AR409723
VERSION AR409723.1 GI:40160700
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 30)
AUTHORS Meins,F. Jr., Shinshi,H., Wenzler,H.C., Hofsteenge,J., Ryals,J.A.
and Sperisen,C.

TITLE DNA sequences encoding polypeptides having beta-1,3-glucanase activity
JOURNAL Patent: US 6632981-A 85 14-OCT-2003;
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RESULT 478
AR028195
LOCUS AR028195 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 44 from patent US 5858661.
ACCESSION AR028195
VERSION AR028195.1 GI:5940168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 30)
AUTHORS Shiloh,Y.
TITLE Ataxia-telangiectasia gene and its genomic organization
JOURNAL Patent: US 5858661-A 44 12-JAN-1999;
FEATURES Location/Qualifiers
source 1..30
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Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.1e+03;
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Db 5 GATTTTCTCTCTCTTTGTTTGTGTTT 30
RESULT 479
AR138598
LOCUS AR138598 30 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 123 from patent US 6200749.
ACCESSION AR138598
VERSION AR138598.1 GI:14480943
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 30)
AUTHORS Shiloh,Y.
TITLE Mutated forms of the ataxia-telangiectasia gene and method to screen for a partial A-T phenotype
JOURNAL Patent: US 6200749-A 123 13-MAR-2001;
FEATURES Location/Qualifiers
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Db					
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LOCUS BD132851 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods of nucleic acid detection.
ACCESSION BD132851
VERSION BD132851.1 GI:23227796
KEYWORDS JP 2002509443-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
TITLE Methods of nucleic acid detection
JOURNAL Patent: JP 2002509443-A 2 26-MAR-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002509443-A/2
PD 26-MAR-2002
PF 30-OCT-1998 JP 1999526687
PR 31-OCT-1997 US 60/063969
PI WILLIAM G WEISBURG, PAUL D STULL, MICHAEL R RESHATOFF PC
C12Q1/68
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
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Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5
RESULT 462
BD181358/C
LOCUS BD181358 30 bp DNA linear PAT 15-MAY-2003
DEFINITION Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION BD181358
VERSION BD181358.1 GI:30792276
KEYWORDS JP 2002327130-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Tokunaga,T., Ishiguro,T. and Horie,R.
TITLE Novel fluorescent colorant and method of assaying nucleic acid
JOURNAL Patent: JP 2002327130-A 1 15-NOV-2002;
TOSOH CORP
COMMENT OS Artificial Sequence
PN JP 2002327130-A/1
PD 15-NOV-2002
PF 11-JAN-2002 JP 2002005267
PI TAKUMI TOKUNAGA, TAKAHIKO ISHIGURO, RYUICHI HORIE PC
C09B23/00, C07D417/14, C09K11/06, C12N15/09, C12Q1/68, PC
G01N33/58.
PC C12N15/00
CC dt30mer
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Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5
RESULT 462
BD181358/C
LOCUS BD181358 30 bp DNA linear PAT 15-MAY-2003
DEFINITION Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION BD181358
VERSION BD181358.1 GI:30792276
KEYWORDS JP 2002327130-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
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REFERENCE 1 (bases 1 to 30)
AUTHORS Tokunaga,T., Ishiguro,T. and Horie,R.
TITLE Novel fluorescent colorant and method of assaying nucleic acid
JOURNAL Patent: JP 2002327130-A 1 15-NOV-2002;
TOSOH CORP
COMMENT OS Artificial Sequence
PN JP 2002327130-A/1
PD 15-NOV-2002
PF 11-JAN-2002 JP 2002005267
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C09B23/00, C07D417/14, C09K11/06, C12N15/09, C12Q1/68, PC
G01N33/58.
PC C12N15/00
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Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

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Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5
RESULT 463
BD181359
LOCUS BD181359 30 bp DNA linear PAT 15-MAY-2003
DEFINITION Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION BD181359
VERSION BD181359.1 GI:30792277
KEYWORDS JP 2002327130-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Tokunaga,T., Ishiguro,T. and Horie,R.
TITLE Novel fluorescent colorant and method of assaying nucleic acid
JOURNAL Patent: JP 2002327130-A 2 15-NOV-2002;
TOSOH CORP
COMMENT OS Artificial Sequence
PN JP 2002327130-A/2
PD 15-NOV-2002
PF 11-JAN-2002 JP 2002005267
PI TAKUMI TOKUNAGA, TAKAHIKO ISHIGURO, RYUICHI HORIE PC
C09B23/00, C07D417/14, C09K11/06, C12N15/09, C12Q1/68, PC
G01N33/58,
PC C12N15/00
CC da30mer
FH Key Location/Qualifiers
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Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
RESULT 464
AR051244
LOCUS AR051244 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5830658.
ACCESSION AR051244
VERSION AR051244.1 GI:5974608
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5830658-A 12 03-NOV-1998;
FEATURES
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Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.1e+03;
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8D132851/C

Query Match

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source
Aventis Research & Technologies GmbH & Co. KG (DE)
Location/Qualifiers
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/note="Linker"

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Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 444

AX052994
LOCUS AX052994 29 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 10 from Patent WO0071749.
ACCESSION AX052994
VERSION AX052994.1 GI:12227096
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Hoppe, H.U., Burgstaller, P., Konz, D., Woelk, U. and Pignot, M.
TITLE Detection system for analyzing molecular interactions, production and utilization thereof

JOURNAL Patent: WO 0071749-A 10 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)

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source
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/note="Beschreibung der kunstlichen Sequenz: Puromycin-Linker"

Query Match 0.7%; Score 19.6; DB 1; Length 29;
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QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 445

AX353685
LOCUS AX353685 29 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 5 from Patent WO0204656.
ACCESSION AX353685
VERSION AX353685.1 GI:18618749
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Wagner, P. and Polakowski, T.
TITLE Bio-probes and use thereof
JOURNAL Patent: WO 0204656-A 5 17-JAN-2002;
Xzillion GmbH & Co. KG (DE)

FEATURES
source
1. .29
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Linker mit Puromycin am 3'-Ende"

Query Match 0.7%; Score 19.6; DB 1; Length 29;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 446

AX662302
LOCUS AX662302 29 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 41 from Patent WO02059293.
ACCESSION AX662302
VERSION AX662302.1 GI:29163186
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Forster, A.C. and Blacklow, S.C.
TITLE Process and compositions for peptide, protein and peptidomimetic synthesis

JOURNAL Patent: WO 02059293-A 41 01-AUG-2002;
Forster, Anthony C. (US); Blacklow, Stephen C. (US)

FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Best Local Similarity 84.6%; Pred. No. 1e+03;
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 447

BD204968
LOCUS BD204968 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Protein array enabling site specification.
ACCESSION BD204968
VERSION BD204968.1 GI:33014738
KEYWORDS JP 2002510505-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 29)
AUTHORS Kuimelis, R.G. and Wagner, R.
TITLE Protein array enabling site specification
JOURNAL Patent: JP 2002510505-A 3 09-APR-2002;
PHYLOS INC

COMMENT OS Artificial Sequence
PN JP 2002510505-A/3
PD 09-APR-2002
PF 31-MAR-1999 JP 2000542484
PR 03-APR-1998 US 60/080686
PI ROBERT G KUIMELIS, RICHARD WAGNER
PC C12N15/09, C07H21/02, C07H21/04, C12M1/00, C12Q1/68, G01N33/566, PC

GO1N33/68,
C12N15/00
CC Oligonucleotide used for attaching puromycin
FH Key Location/Qualifiers
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FEATURES
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/mol_type="genomic DNA"


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DEFINITION Sorting of proteins using RNA-protein fused body.
ACCESSION  BD238387
VERSION    BD238387.1  GI:33048157
KEYWORDS   JP 2002536025-A/5.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 29)
AUTHORS    Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE      Sorting of proteins using RNA-protein fused body
JOURNAL    Patent: JP 2002536025-A 5 29-OCT-2002;
           THE GENERAL HOSPITAL CORP
COMMENT    OS Artificial Sequence
           PN JP 2002536025-A/5
           PD 29-OCT-2002
           PF 01-FEB-2000 JP 2000598669
           PR 09-FEB-1999 US 09/247190
           PI JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
           PC C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
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Best Local Similarity 84.6%; Pred. No. 1e+03;
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Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 440
AR279813
LOCUS      AR279813                29 bp    DNA        linear    PAT 10-APR-2003
DEFINITION Sequence 8 from patent US 6518018.
ACCESSION  AR279813
VERSION    AR279813.1  GI:29714958
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 29)
AUTHORS    Szostak,J.W. and Roberts,R.W.
TITLE      RNA-antibody fusions and their selection
JOURNAL    Patent: US 6518018-A 8 11-FEB-2003;
           Location/Qualifiers
FEATURES    source
            Location/Qualifiers
            1..29
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Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      2779 AGAATTGAAAAAAAAAAAAAAAAAAAA 2804
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Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 441
AR288232
LOCUS      AR288232                29 bp    DNA        linear    PAT 12-JAN-2001
DEFINITION Sequence 3 from patent US 6537749.
ACCESSION  AR288232
VERSION    AR288232.1  GI:31675516
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 29)
AUTHORS    Kuimelis,R.G. and Wagner,R.
TITLE      Addressable protein arrays
JOURNAL    Patent: US 6537749-A 3 25-MAR-2003;
           Location/Qualifiers
FEATURES    source
            Location/Qualifiers
            1..29
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match      0.7%; Score 19.6; DB 1; Length 29;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      2779 AGAATTGAAAAAAAAAAAAAAAAAAAA 2804
        ||| ||||| ||||| ||||| ||||| |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 442
AX048408/c
LOCUS      AX048408                29 bp    DNA        linear    PAT 12-JAN-2001
DEFINITION Sequence 7 from Patent WO0071747.
ACCESSION  AX048408
VERSION    AX048408.1  GI:12225572
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE      Detection system for separating constituents of a sample and
           production and use of the same
JOURNAL    Patent: WO 0071747-A 7 30-NOV-2000;
           Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES    Location/Qualifiers
            source
            1..29
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Region A"
Query Match      0.7%; Score 19.6; DB 1; Length 29;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      2779 AGAATTGAAAAAAAAAAAAAAAAAAAA 2804
        ||| ||||| ||||| ||||| ||||| |||||
Db      29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 443
AX048409
LOCUS      AX048409                29 bp    DNA        linear    PAT 12-JAN-2001
DEFINITION Sequence 8 from Patent WO0071747.
ACCESSION  AX048409
VERSION    AX048409.1  GI:12225573
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE      Detection system for separating constituents of a sample and
           production and use of the same
JOURNAL    Patent: WO 0071747-A 8 30-NOV-2000;
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DEFINITION Sequence 911 from Patent WO0122972.
ACCESSION AX104719
VERSION AX104719.1 GI:13920916
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 911 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
source
1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 8.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 435
AX355814/c
LOCUS AX355814 27 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 842 from Patent WO0197843.
ACCESSION AX355814
VERSION AX355814.1 GI:18620482
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL Patent: WO 0197843-A 842 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source
1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"
Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 8.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 436
AX547772/c
LOCUS AX547772 27 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 911 from Patent WO02053141.
ACCESSION AX547772
VERSION AX547772.1 GI:25812916
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.

TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 911 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source
1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 8.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 437
AR162080
LOCUS AR162080 29 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6258558.
ACCESSION AR162080
VERSION AR162080.1 GI:16229144
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Method for selection of proteins using RNA-protein fusions
JOURNAL Patent: US 6258558-A 8 10-JUL-2001;
FEATURES Location/Qualifiers
source
1. .29
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19.6; DB 1; Length 29;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26
RESULT 438
AR166605
LOCUS AR166605 29 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6281344.
ACCESSION AR166605
VERSION AR166605.1 GI:16241997
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Nucleic acid-protein fusion molecules and libraries
JOURNAL Patent: US 6281344-A 8 28-AUG-2001;
FEATURES Location/Qualifiers
source
1. .29
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 19.6; DB 1; Length 29;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 7.8e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 425
AX427154/c
LOCUS AX427154 26 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 3 from Patent WO0210374.
ACCESSION AX427154
VERSION AX427154.1 GI:21530535
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lin,S.L., Chuong,C.M. and Widelitz,R.B.
TITLE Gene silencing using mrna-cdna hybrids
JOURNAL Patent: WO 0210374-A 3 07-FEB-2002;
UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES
source
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Poly(dT) -26mer primer"

Query Match      0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 7.8e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 426
AX528804/c
LOCUS AX528804 26 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 53 from Patent WO02059357.
ACCESSION AX528804
VERSION AX528804.1 GI:25172859
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Pedersen,M.L.
TITLE Assay and kit for analyzing gene expression
JOURNAL Patent: WO 02059357-A 53 01-AUG-2002;
FEATURES
source
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic construct"

Query Match      0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 7.8e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 427
A63569
LOCUS A63569 26 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 10 from Patent WO9720924.
ACCESSION A63569
VERSION A63569.1 GI:3717224
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Scaggiante,B. and Quadrioglio,F.
TITLE A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMORAL AGENTS
JOURNAL Patent: WO 9720924-A 10 12-JUN-1997;
COMMENT SAICOM S R L (IT)
Other publication IT MI952539 19970604
Other publication AU 1175497 19970627.
FEATURES
source
1. .26
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 7.8e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2156 TTTTCTCCTTTT 2181
Db 1 TTTTCTCCTTTTGTGTTT 26

RESULT 428
AR010003
LOCUS AR010003 26 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 15 from patent US 5756684.
ACCESSION AR010003
VERSION AR010003.1 GI:39688808
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Cloning and expression of PUR protein
JOURNAL Patent: US 5756684-A 15 26-MAY-1998;
FEATURES
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 7.8e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2159 TTTCTCCTTTT 2184
Db 1 TATCTGCAGTTT 26

RESULT 429
AR034738
LOCUS AR034738 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5869622.
ACCESSION AR034738
VERSION AR034738.1 GI:5950343
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Johnson,E.M. and Bergemann,A.D.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.7%; Score 19.6; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 26 bp DNA PAT 10-JUN-1998
Db 26 TAAAAA 1

RESULT 420
I79494/c
LOCUS I79494 26 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5707807.
ACCESSION I79494
VERSION I79494.1 GI:3207784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 1 13-JAN-1998;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.7%; Score 19.6; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 26 bp DNA PAT 29-JAN-2003
Db 26 TAAAAA 1

RESULT 421
AR263648/c
LOCUS AR263648 26 bp DNA PAT 29-JAN-2003
DEFINITION Sequence 7 from patent US 6331413.
ACCESSION AR263648
VERSION AR263648.1 GI:28075581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Adler,D.A. and Sheppard,P.O.
TITLE Secreted salivary ZSIG63 Polypeptide
JOURNAL Patent: US 6331413-A 7 18-DEC-2001;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 19.6; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 26 bp DNA PAT 16-JUN-2001
Db 26 TAAAAA 1

RESULT 422
AR374073/c
LOCUS AR374073 26 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 38 from patent US 6605272.

AR374073
AR374073.1 GI:40076645
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE Methods of using zalphall ligand
JOURNAL Patent: US 6605272-A 38 12-AUG-2003;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 19.6; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 26 bp DNA PAT 30-APR-2001
Db 26 TAAAAA 1

RESULT 423
AX106717/c
LOCUS AX106717 26 bp DNA PAT 30-APR-2001
DEFINITION Sequence 9 from Patent WO0125444.
ACCESSION AX106717
VERSION AX106717.1 GI:13922378
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Presnell,S.R., Novak,J.E. and Gao,Z.
TITLE Human phosphodiesterase zcytor13
JOURNAL Patent: WO 0125444-A 9 12-APR-2001;
FEATURES Location/Qualifiers
source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer ZC7764b"

Query Match
Best Local Similarity 0.7%; Score 19.6; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 26 bp DNA PAT 16-JUN-2001
Db 26 TAAAAA 1

RESULT 424
AR137712/c
LOCUS AR137712 26 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6197554.
ACCESSION AR137712
VERSION AR137712.1 GI:14479221
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.
TITLE Method for generating full-length cDNA library from single cells
JOURNAL Patent: US 6197554-A 5 06-MAR-2001;
FEATURES Location/Qualifiers
source 1..26

probe with a target
CC acid.
FH Key
FT source
FT Location/Qualifiers
1. .30
/organism='Artificial Sequence'

FEATURES
source

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTT
Db 2 TATATATTTT

RESULT 409
BD166129
LOCUS

DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.
ACCESSION BD166129
VERSION BD166129.1 GI:27871941
KEYWORDS JP 2002191372-A/109.
SOURCE unidentified
ORGANISM unidentified

REFERENCE
1 (bases 1 to 30)

AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method
JOURNAL PATENT: JP 2002191372-A 109 09-JUL-2002;
COMMENT NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/109
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the decrease in fluorescence emission of a nucleic acid probe CC labeled with BODIBY FL/C6 upon the hybridization of the probe with a target
CC acid,
CC and the base sequence was used as that of the probe. FH Key
CC Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'

FEATURES
source

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTT
Db 2 TATATATTTT

RESULT 410
AR431313/c
LOCUS

DEFINITION Sequence 7 from patent US 6651008.
ACCESSION AR431313
VERSION AR431313.1 GI:40193281
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
TITLE Database system including computer code for predictive cellular bioinformatics
JOURNAL Patent: US 6651008-A 7 18-NOV-2003;
FEATURES Location/Qualifiers
source 1. .24
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA
Db 24 AATAGAAAAA

RESULT 411
AX338548
LOCUS

DEFINITION Sequence 4 from Patent WO0188192.
ACCESSION AX338548
VERSION AX338548.1 GI:18128948
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Nicolaides,N.C., Sass,P.M., Grasso,L., Vogelstein,B. and Kinzler,K.W.
TITLE A method for generating hypermutable organisms
JOURNAL Patent: WO 0188192-A 4 22-NOV-2001;
The Johns Hopkins University School of Medicine (US) ; Morphotek Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Sass, Philip, M. (US) ; Grasso, Luigi (US) ; Vogelstein, Bert (US)
FEATURES Location/Qualifiers
source 1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Recombinant DNA"

Query Match 0.7%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 6.4e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAA
Db 1 ATGGCAAAAAA

RESULT 412
BD244864/c
LOCUS

DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.
PAT 17-JUL-2003

ACCESSION BD145025
VERSION BD145025.1 GI:27850783
KEYWORDS JP 2002119291-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 6 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/6
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI TORIMURA,
SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53,
PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28,
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
/organism='Artificial Sequence'.
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTCTCCTTTTGTGTTTTTTT 2186
| | | | | | | | | | | | | | | | | | | | | |
2 TATATATTTTGTGTTTTTTT 29
RESULT 400
LOCUS BD145027
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD145027
VERSION BD145027.1 GI:27850785
KEYWORDS JP 2002119291-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 8 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/8
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI TORIMURA,
SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53,
PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28,
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
/organism='Artificial Sequence'.
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ACCESSION BD145026
VERSION BD145026.1 GI:27850784
KEYWORDS JP 2002119291-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 7 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/7
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI TORIMURA,
SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53,
PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28,
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
/organism='Artificial Sequence'.
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTCTCCTTTTGTGTTTTTTT 2186
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2 TATATATTTTGTGTTTTTTT 29
RESULT 399
LOCUS BD145026
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD145026
VERSION BD145026.1 GI:27850784
KEYWORDS JP 2002119291-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 7 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/7
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI TORIMURA,
SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53,
PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28,
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
/organism='Artificial Sequence'.
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTCTCCTTTTGTGTTTTTTTTTTT 2186
Db 2 TATATATTTTGTGTTTTTTTTTTT 29
RESULT 393
BD107494
LOCUS 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107494
VERSION BD107494.1 GI:23202312
KEYWORDS JP 2002000275-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 3 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/3
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTCTCCTTTTGTGTTTTTTTTTTT 2186
Db 2 TATATATTTTGTGTTTTTTTTTTT 29
RESULT 394
BD107495
LOCUS 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107495
VERSION BD107495.1 GI:23202313
KEYWORDS JP 2002000275-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 4 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/4
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTCTCCTTTTGTGTTTTTTTTTTT 2186
Db 2 TATATATTTTGTGTTTTTTTTTTT 29
RESULT 395
BD107496
LOCUS 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107496
VERSION BD107496.1 GI:23202314
KEYWORDS JP 2002000275-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.

KEYWORDS JP 2001286300-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 5 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/5
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC examining the
decrease in fluorescence emission of a nucleic acid probe CC
CC labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTTCTCCTTTTTTTTTTTTTTTTTTTTTTT 2186
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Db 2 TATATATTTTTTTTGTGTTTTTTTTT 29
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTTCTCCTTTTTTTTTTTTTTTTTTTTTTT 2186
||| ||||||| ||||||| |||||||
Db 2 TATATATTTTTTTTGTGTTTTTTTTT 29
RESULT 388
BD072868
LOCUS 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072868
VERSION 1 GI:22618471
KEYWORDS JP 2001286300-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 6 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/6
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097

PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC examining the
decrease in fluorescence emission of a nucleic acid probe CC
CC labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 9.8e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTTCTCCTTTTTTTTTTTTTTTTTTTTTTT 2186
||| ||||||| ||||||| |||||||
Db 2 TATATATTTTTTTTGTGTTTTTTTTT 29
RESULT 389
BD072869
LOCUS 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072869
VERSION 1 GI:22618472
KEYWORDS JP 2001286300-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 7 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/7
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC examining the
decrease in fluorescence emission of a nucleic acid probe CC
CC labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Qy	2159	TTTCTCC	TTTTTTTTTTTTTTTTTTTTTTTTTT	2186
Db	2	TATATAT	TTTTTTTGTTTTTTTTTTTTTT	29

RESULT	387
BD072867	
LOCUS	BD072867 30 bp DNA
DEFINITION	Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION	BD072867
VERSION	BD072867.1 GI:22618470


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Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 375
AX708814/c
LOCUS
DEFINITION
ACCESSION AX708814
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="sequence to demonstrate the principle of how to
detect somatic repeat instability-##N# stands for any
number of nucleotides selected from A, C, T or G#"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTNTTTTNTTTTNTTTTNTTTT 2186
Db 25 TTNTTTTNTTTTNTTTTNTTTT 5

RESULT 376
AR142409
LOCUS
DEFINITION
ACCESSION AR142409
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Ni, J., Yu, G.-L. and Gentz, R.
TITLE
Human endometrial specific steroid-binding factor I, II and III
JOURNAL
Patent: US 6174992-A 16 16-JAN-2001;
FEATURES
Location/Qualifiers
1. .27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTNTTTTNTTTTNTTTT 2183
Db 8 CCTTTTNTTTTNTTTTNTTTT 27
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 375
AX708814/c
LOCUS
DEFINITION
ACCESSION AX708814
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Ni, J., Yu, G.-L. and Gentz, R.
TITLE
Human endometrial specific steroid-binding factor I, II and III
JOURNAL
Patent: WO 02095071-A 30 28-NOV-2002;
FEATURES
Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="sequence to demonstrate the principle of how to
detect somatic repeat instability-##N# stands for any
number of nucleotides selected from A, C, T or G#"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTNTTTTNTTTTNTTTTNTTTT 2186
Db 25 TTNTTTTNTTTTNTTTTNTTTT 5

RESULT 376
AR142409
LOCUS
DEFINITION
ACCESSION AR142409
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Ni, J., Yu, G.-L. and Gentz, R.
TITLE
Human endometrial specific steroid-binding factor I, II and III
JOURNAL
Patent: US 6174992-A 16 16-JAN-2001;
FEATURES
Location/Qualifiers
1. .27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTNTTTTNTTTTNTTTT 2183
Db 8 CCTTTTNTTTTNTTTTNTTTT 27
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RESULT 377
AR182555
LOCUS
DEFINITION
ACCESSION AR182555
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Ni, J., Yu, G.-L. and Gentz, R.
TITLE
Human endometrial specific steroid-binding factor I, II and III
JOURNAL
Patent: US 6338948-A 16 15-JAN-2002;
FEATURES
Location/Qualifiers
1. .27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTNTTTTNTTTTNTTTT 2183
Db 8 CCTTTTNTTTTNTTTTNTTTT 27

RESULT 378
BD274321/c
LOCUS
DEFINITION
ACCESSION BD274321
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 29)
AUTHORS
Ecker, D.J., Sampath, R., Griffey, R. and Mcneil, J.
TITLE
Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL
Patent: JP 2002526030-A 288 20-AUG-2002;
COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/288
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL, PC
C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
1. .29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 29;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2169 TTTTNTTTTNTTTTNTTTTNTTTT 2196
Db 29 TTTTNTTTTNTTTTNTTTTNTTTT 2
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misc_binding /db_xref="taxon:32630"
modified_base /note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 21 GAAAAAAAAAAAAAAAAAAAAA 2

RESULT 372
BD087491/c
LOCUS BD087491 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis.
ACCESSION BD087491
VERSION BD087491.1 GI:22633101
KEYWORDS JP 2001525193-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 2 11-DEC-2001;
NANOGEN INC

COMMENT OS Artificial Sequence
PN JP 2001525193-A/2
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER,CARL F EDMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Synthesized with u at 3'
CC terminus to
CC provide ribonucleic acid base for reactivity; Poly A sequence
CC for reduced
CC secondary structure
CC Key Location/Qualifiers
FH source 1..21
FT Location/Qualifiers
FT 1..21
/organism="synthetic construct"

/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
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Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 373
AR241846/c
LOCUS AR241846 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 134 from patent US 6472154.
ACCESSION AR241846
VERSION AR241846.1 GI:27287658
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 134 29-OCT-2002;
FEATURES Location/Qualifiers
1..24
source /organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804
|||||
Db 24 GAAAAAAAAAAAAAAAAAAAAA 5

RESULT 374
E13209/c
LOCUS E13209 24 bp DNA linear PAT 27-APR-1998
DEFINITION DNA probe.
ACCESSION E13209
VERSION E13209.1 GI:3252014
KEYWORDS JP 1997149799-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kanbara,H., Okano,K. and Uematsu,K.
TITLE ANALYSIS OR DETECTION OF NUCLEIC ACID AND ANALYSER OR INSPECTION
JOURNAL DEVICE OF NUCLEIC ACID
Patent: JP 1997149799-A 1 10-JUN-1997;
HITACHI LTD

COMMENT OS None
OC Artificial sequences.
PN JP 1997149799-A/1
PD 10-JUN-1997
PF 30-NOV-1995 JP 1995311949
PI KANBARA HIDEKI, OKANO KAZUNOBU, UEMATSU KAZUMUNE PC
C12Q1/68,C07H21/04,C12M1/00,C12N15/09,C12Q1/44,C12Q1/48, PC
G01N27/447,
PC G01N27/447,G01N33/50;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..24
FT Location/Qualifiers
FT 1..24
/organism='Artificial sequences'.
FEATURES source


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/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid)"
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/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTTAA 2188
Db 1 TTTTTTTTTTTTTTTTAA 20

RESULT 358
AX825104
LOCUS AX825104 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 2 from Patent WO03072818.
ACCESSION AX825104
VERSION AX825104.1 GI:39750833
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 2 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

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modified_base
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Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTTAA 2188
Db 1 TTTTTTTTTTTTTTTTAA 20

RESULT 359
AX825106
LOCUS AX825106 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 4 from Patent WO03072818.
ACCESSION AX825106
VERSION AX825106.1 GI:39750835
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 4 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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Sequenz:Capture-Oligonukleotid"
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

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modified_base
modified_base
modified_base
modified_base

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Best Local Similarity 0.7%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTTAA 2188
Db 1 TTTTTTTTTTTTTTTTAA 20

RESULT 360
AX825136/c
LOCUS AX825136 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 34 from Patent WO03072818.
ACCESSION AX825136
VERSION AX825136.1 GI:39750865
KEYWORDS
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/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTTAA 2188
Db 1 TTTTTTTTTTTTTTTTAA 20

RESULT 359
AX825106
LOCUS AX825106 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 4 from Patent WO03072818.
ACCESSION AX825106
VERSION AX825106.1 GI:39750835
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 4 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid)"
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

misc_binding
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modified_base

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTTAA 2188
Db 1 TTTTTTTTTTTTTTTTAA 20

RESULT 360
AX825136/c
LOCUS AX825136 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 34 from Patent WO03072818.
ACCESSION AX825136
VERSION AX825136.1 GI:39750865
KEYWORDS
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CC Description of Artificial Sequence:primer
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 354
BD218101/c
LOCUS
DEFINITION Compositions derived from mycobacterium vaccae and methods for their use.
ACCESSION BD218101
VERSION BD218101.1 GI:33027871
KEYWORDS JP 2002514385-A/26.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Watson,J., Visser,E.S., Skinner,M.A. and Prestid,R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for their
JOURNAL Patent: JP 2002514385-A 26 21-MAY-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD
COMMENT OS Artificial Sequence
PN JP 2002514385-A/26
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624,11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
TAN,JAMES WATSON,ELIZABETH S VISSER,MARGOT A SKINNER,ROSS
PI L PRESTIDGE
PC C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
PC A61P17/00,
PC A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
PC C07K19/00,
PC C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
G01N33/68//
PC (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
CC Made in a lab
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
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Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 355
AR153849/c

LOCUS
DEFINITION Sequence 2 from patent US 6238624.
ACCESSION AR153849
VERSION AR153849.1 GI:15121902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
TITLE Methods for transport in molecular biological analysis and diagnostics
JOURNAL Patent: US 6238624-A 2 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
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Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 356
I36166/c
LOCUS
DEFINITION Sequence 2 from patent US 5605662.
ACCESSION I36166
VERSION I36166.1 GI:2086679
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Heller,M.J. and Tu,E.
TITLE Active programmable electronic devices for molecular biological analysis and diagnostics
JOURNAL Patent: US 5605662-A 2 25-FEB-1997;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 357
AX825103
LOCUS
DEFINITION Sequence 1 from Patent WO03072818.
ACCESSION AX825103
VERSION AX825103.1 GI:39750832
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 1 04-SEP-2003;
FEATURES Degussa Bioactives GmbH (DE)
source Location/Qualifiers
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Db      1 TTTT TTTT TTTT TTTT TTTT TTTT 20
/db_xref="taxon:32644"

RESULT 350
AX741052/c
LOCUS      AX741052      20 bp      DNA      linear      PAT 10-MAY-2003
DEFINITION Sequence 26 from Patent WO03027328.
ACCESSION  AX741052
VERSION     AX741052.1  GI:30523913
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE  1
AUTHORS    Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE      Methods, kits and compositions pertaining to the suppression of
            detectable probe binding to randomly distributed repeat sequences
            in genomic nucleic acid
JOURNAL    Patent: WO 03027328-A 26 03-APR-2003;
            Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
FEATURES   Location/Qualifiers
            1..20
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            /db_xref="taxon:32630"
            /note="Description of Combined DNA/RNA Molecule:Synthetic
            Oligomer Sequence-Synthetic Probe Sequence"
Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db      20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 351
BD008523/c
LOCUS      BD008523      20 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial
            infections.
ACCESSION  BD008523
VERSION     BD008523.1  GI:18636896
KEYWORDS    JP 2001503969-A/26.
SOURCE      unidentified
            unidentified
            unclassified.
            1 (bases 1 to 20)
            Tan,P., Hiyama,J., Visser,E.S., Skinner,M.A., Scott,L.M. and
            Prestidge,R.L.
            Compounds and methods for treatment and diagnosis of Mycobacterial
            infections
JOURNAL    Patent: JP 2001503969-A 26 27-MAR-2001;
            GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT    OS Unidentified
            PN JP 2001503969-A/26
            PD 27-MAR-2001
            PF 28-AUG-1997 JP 1998511516
            PR
            PI PAUL TAN,JUN HIYAMA,ELIZABETH S VISSER,MARGOT A SKINNER, PI
            LINDA M SCOTT,
            PI ROSS L PRESTIDGE
            PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
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            Location/Qualifiers
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FEATURES   source
            Location/Qualifiers
            1..20
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Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db      20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 352
BD080522
LOCUS      BD080522      20 bp      RNA      linear      PAT 27-AUG-2002
DEFINITION Ribonucleoside-derivative and method for preparing the same.
ACCESSION  BD080522
VERSION     BD080522.1  GI:22626125
KEYWORDS    JP 2001515087-A/1.
SOURCE      synthetic construct
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            artificial sequences.
            1 (bases 1 to 20)
            Pitsch,S., Weiss,P.A. and Jenny,L.
            Ribonucleoside-derivative and method for preparing the same
            Patent: JP 2001515087-A 1 18-SEP-2001;
            STEFAN PITTSCH,PATRICK A WEISS,LUZI JENNY
            OS Artificial Sequence
            PN JP 2001515087-A/1
            PD 18-SEP-2001
            PF 17-AUG-1998 JP 2000509723
            PR 18-AUG-1997 CH 1931/97
            PI STEFAN PITTSCH,PATRICK A WEISS,LUZI JENNY
            PC C07H19/06,C07F7/18,C07H19/16,C07H21/02,C07H23/00 CC
            Description of Artificial Sequence:synthetic polynucleotide FH
            Key Location/Qualifiers
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            Location/Qualifiers
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Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db      1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 353
BD107450
LOCUS      BD107450      20 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Method of detecting single base polymorphism.
ACCESSION  BD107450
VERSION     BD107450.1  GI:23202268
KEYWORDS    JP 2002034599-A/9.
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
            1 (bases 1 to 20)
            Segawa,M., Takarada,H., Aono,T. and Yoshiga,S.
            Method of detecting single base polymorphism
            Patent: JP 2002034599-A 9 05-FEB-2002;
            TOYOBO CO LTD
            OS Artificial Sequence
            PN JP 2002034599-A/9
            PD 05-FEB-2002
            PF 26-JUL-2000 JP 2000225354
            PI MASAYA SEGAWA,HIROSHI TAKARADA,TOSHIYA AONO,SATOKO YOSHIGA PC
            C12Q1/68,C12N15/09,C12N15/00
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Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A., Garimella, V., Li, Z. and Park, S.J. Nanoparticles having oligonucleotides attached thereto and uses therefor

LOCUS
DEFINITION
ACCESSION

CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="synthetic oligonucleotide"

misc_feature 1
/note="modified with digoxigenin"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 328
AX045787

LOCUS AX045787 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 17 from Patent WO0067023.
ACCESSION AX045787
VERSION AX045787.1 GI:11344154
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 17 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

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/db_xref="taxon:32630"
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/note="phosphorothioate backbone"
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/note="modified with digoxigenin"

misc_feature
misc_feature

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 329
AX045790

LOCUS AX045790 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 20 from Patent WO0067023.
ACCESSION AX045790
VERSION AX045790.1 GI:11344157
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 20 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
Location/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 330
AX104034

LOCUS AX104034 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 226 from Patent WO0122972.
ACCESSION AX104034
VERSION AX104034.1 GI:13920231
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 226 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)

FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 331
AX104364

LOCUS AX104364 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 556 from Patent WO0122972.
ACCESSION AX104364
VERSION AX104364.1 GI:13920561
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 556 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)

FEATURES
Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 325				
AR429653/c				
LOCUS	AR429653	20 bp	DNA	linear
				PAT 18-DEC-2003

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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 318
AR222466/c
LOCUS AR222466 26 from patent US 6429300. 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 26 from patent US 6429300.
ACCESSION AR222466
VERSION AR222466.1 GI:23329997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 26 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
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QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 319
AR236083
LOCUS AR236083 1 from patent US 6462184. 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6462184.
ACCESSION AR236083
VERSION AR236083.1 GI:27279782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 1 08-OCT-2002;
FEATURES Location/Qualifiers
source 1..20
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/mol_type="genomic DNA"

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Best Local Similarity 0.7%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
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RESULT 320
AR274394
LOCUS AR274394 55 from patent US 6506564. 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 55 from patent US 6506564.
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ACCESSION AR274394
VERSION AR274394.1 GI:29706840
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J., Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6506564-A 55 14-JAN-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 321
AR343047
LOCUS AR343047 10 from patent US 6576752. 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 10 from patent US 6576752.
ACCESSION AR343047
VERSION AR343047.1 GI:33738375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
TITLE Aminooxy functionalized oligomers
JOURNAL Patent: US 6576752-A 10 10-JUN-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 322
AR344936/c
LOCUS AR344936 55 from patent US 6582921. 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 55 from patent US 6582921.
ACCESSION AR344936
VERSION AR344936.1 GI:33741017
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J., Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6582921-A 55 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
```

PI	MIZUGUCHI MASATSUGU, KUROSAKI NAKO, MAKINO KEISUKE, PI									
KOYANAGI YOSHIO,										
PI	YAMAMOTO NAOKI									
PC	C07H21/04//A61K31/70;									
CC	strandedness: Single;									
CC	topology: Linear;									
CC	hypothetical: No;									
CC	anti-sense: Yes;									
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FT	Location/Qualifiers									
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;										
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LOCUS	I36180 20 bp DNA linear PAT 13-MAY-1997									
DEFINITION	Sequence 16 from patent US 5605662.									
ACCESSION	I36180									
VERSION	I36180.1 GI:2086693									
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 20)									
AUTHORS	Heller,M.J. and Tu,E.									
TITLE	Active programmable electronic devices for molecular biological analysis and diagnostics									
JOURNAL	Patent: US 5605662-A 16 25-FEB-1997;									
FEATURES	Location/Qualifiers									
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0										
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Db	1	TTTTTTTTTTTTTTTTTTTT 20								
RESULT 317										
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LOCUS	AR213738 20 bp DNA linear PAT 25-SEP-2000									
DEFINITION	Sequence 83 from patent US 6406704.									
ACCESSION	AR213738									
VERSION	AR213738.1 GI:23311025									
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 20)									
AUTHORS	Tan,P., Visser,E., Prestidge,R. and Watson,J.D.									
TITLE	Compounds and methods for treatment and diagnosis of mycobacterial infections									
JOURNAL	Patent: US 6406704-A 83 18-JUN-2002;									
FEATURES	Location/Qualifiers									
source	1. .20									

AUTHORS Watson, J.D. and Iwan, P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated psoriasis

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
TITLE Feline cytokine protein
JOURNAL Patent: US 6518045-A 23 11-FEB-2003;
FEATURES Location/Qualifiers
source 1..30
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/mol_type="mRNA"
Query Match 0.7%; Score 20.2; DB 1; Length 30;
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Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db
RESULT 299
AR322431
LOCUS AR322431 30 bp mRNA linear PAT 17-AUG-2003
DEFINITION Sequence 23 from patent US 6566097.
ACCESSION AR322431
VERSION AR322431.1 GI:33708184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
TITLE Feline cytokine protein
JOURNAL Patent: US 6566097-A 23 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="mRNA"
Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2161 TCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
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Db
RESULT 300
AR409723
LOCUS AR409723 30 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 85 from patent US 6632981.
ACCESSION AR409723
VERSION AR409723.1 GI:40160700
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Meins,F. Jr., Shinshi,H., Wenzler,H.C., Hofsteenge,J., Ryals,J.A.
TITLE DNA sequences encoding polypeptides having beta-1,3-glucanase
JOURNAL activity
FEATURES Patent: US 6632981-A 85 14-OCT-2003;
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA AAAAAA AAAAAA AAAAAA 2804
|||||
Db 4 GAATTCAAAAA AAAAAA AAAAAA AAAAAA 28
RESULT 301
AR222454
LOCUS AR222454 32 bp RNA linear PAT 26-SEP-2002
DEFINITION Sequence 14 from patent US 6429300.
ACCESSION AR222454
VERSION AR222454.1 GI:23329985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 14 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.7%; Score 20.2; DB 1; Length 32;
Best Local Similarity 88.0%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA AAAAAA AAAAAA AAAAAA 2804
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Db 5 GGATGCAAAAA AAAAAA AAAAAA AAAAAA 29
RESULT 302
BD238394/c
LOCUS BD238394 33 bp RNA linear PAT 17-JUL-2003
DEFINITION Sorting of proteins using RNA-protein fused body.
ACCESSION BD238394
VERSION BD238394.1 GI:33048164
KEYWORDS JP 2002536025-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 33)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Sorting of proteins using RNA-protein fused body
JOURNAL Patent: JP 2002536025-A 12 29-OCT-2002;
COMMENT THE GENERAL HOSPITAL CORP
OS Artificial Sequence
PN JP 2002536025-A/12
PD 29-OCT-2002
PF 01-FEB-2000 JP 2000598669
PR 09-FEB-1999 US 09/247190
PI JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
PC C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
Translation template
FH Key Location/Qualifiers
FT source 1..33
FT /organism='Artificial Sequence'.
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/db_xref="taxon:32630"
Query Match 0.7%; Score 20.2; DB 1; Length 33;
Best Local Similarity 88.0%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2169 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2193
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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
Friedrich,L.B., Harms,C., Meins,F. Jr., Montoya,A. deceased,
Moyer,M.B., Neuhaus,J.-M., Payne,G.B., Sperisen,C., Stinson,J.R.,
Uknes,S.J., Ward,E.R. and Williams,S.C.
TITLE Chemically regulatable and anti-pathogenic DNA sequences and uses
thereof
JOURNAL Patent: US 5614395-A 85 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAA 2804
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Db 4 GAATTCAAAAA 28

RESULT 294
I56982
LOCUS I56982 30 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 85 from patent US 5650505.
ACCESSION I56982
VERSION I56982.1 GI:2477395
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
Friedrich,L.B., Harms,C., Meins,F. Jr., Montoya,A. deceased,
Moyer,M.B., Neuhaus,J.-M., Payne,G.B., Sperisen,C., Stinson,J.R.,
Uknes,S.J., Ward,E.R. and Williams,S.C.
TITLE Chemically regulatable and anti-pathogenic DNA sequences and uses
thereof
JOURNAL Patent: US 5650505-A 85 22-JUL-1997;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
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Qy 2780 GAATTGAAAAA 2804
||||| ||||||| ||||||| |||
Db 4 GAATTCAAAAA 28

RESULT 295
I59848
LOCUS I59848 30 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 85 from patent US 5654414.
ACCESSION I59848
VERSION I59848.1 GI:2478480
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ryals,J.A., Beck,J.J. and Friedrich,L.B.
TITLE Chemically inducible promoter of a cucumber chitinase/lysozyme gene
JOURNAL Patent: US 5654414-A 85 05-AUG-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAA 2804
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Db 4 GAATTCAAAAA 28

RESULT 296
I75175
LOCUS I75175 30 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 85 from patent US 5689044.
ACCESSION I75175
VERSION I75175.1 GI:3011316
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
TITLE Chemically inducible promoter of a plant PR-1 gene
JOURNAL Patent: US 5689044-A 85 18-NOV-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAA 2804
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Db 4 GAATTCAAAAA 28

RESULT 297
AR242448
LOCUS AR242448 30 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 23 from patent US 6472509.
ACCESSION AR242448
VERSION AR242448.1 GI:27288865
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
TITLE Feline cytokine protein
JOURNAL Patent: US 6472509-A 23 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="mRNA"

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
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Qy 2161 TCTCCTTTTTTTT 2185
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Db 6 TCTCGAGTTTTTTT 30

RESULT 298
AR280216
LOCUS AR280216 30 bp mRNA linear PAT 10-APR-2003
DEFINITION Sequence 23 from patent US 6518045.
ACCESSION AR280216
VERSION AR280216.1 GI:29715606

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ACCESSION   AR020878
VERSION     AR020878.1  GI:3975493
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
TITLE       Method of inducing gene transcription in a plant
JOURNAL     Patent: US 5789214-A 85 04-AUG-1998;
FEATURES    Location/Qualifiers
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             /mol_type="unassigned DNA"

Query Match      0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 4 GAATTCAAAAA 28

RESULT 291
AR064630
LOCUS       AR064630          30 bp    DNA
DEFINITION  Sequence 85 from patent US 5847258.
ACCESSION   AR064630
VERSION     AR064630.1  GI:5993938
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Ryals,J.A., Moyer,M.B., Payne,G.B. and Ward,E.R.
TITLE       DNA encoding .beta.-1,3-glucanases
JOURNAL     Patent: US 5847258-A 85 08-DEC-1998;
FEATURES    Location/Qualifiers
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Query Match      0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 4 GAATTCAAAAA 28

RESULT 292
AR067555
LOCUS       AR067555          30 bp    DNA
DEFINITION  Sequence 85 from patent US 5851766.
ACCESSION   AR067555
VERSION     AR067555.1  GI:5998777
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Ryals,J.A. and Harms,C.
TITLE       Process for isolating chemically regulatable DNA sequences
JOURNAL     Patent: US 5851766-A 85 22-DEC-1998;
FEATURES    Location/Qualifiers
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             /mol_type="unassigned DNA"

Query Match      0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 4 GAATTCAAAAA 28

RESULT 293
AR067555
LOCUS       AR067555          30 bp    DNA
DEFINITION  Sequence 85 from patent US 5847258.
ACCESSION   AR067555
VERSION     AR067555.1  GI:5993938
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Ryals,J.A., Friedrich,L.B., Uknes,S.J., Ward,E.R.,
TITLE       Chemically regulatable and anti-pathogenic DNA sequences and uses
JOURNAL     Patent: US 5804693-A 85 08-SEP-1998;
FEATURES    Location/Qualifiers
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ACCESSION   AR020878
VERSION     AR020878.1  GI:3975493
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
TITLE       Method of inducing gene transcription in a plant
JOURNAL     Patent: US 5789214-A 85 04-AUG-1998;
FEATURES    Location/Qualifiers
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             /mol_type="unassigned DNA"

Query Match      0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 4 GAATTCAAAAA 28

RESULT 289
AR027201
LOCUS       AR027201          30 bp    DNA
DEFINITION  Sequence 85 from patent US 5856154.
ACCESSION   AR027201
VERSION     AR027201.1  GI:5938041
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Ryals,J.A., Alexander,D.C., Goodman,R.M. and Ward,E.R.
TITLE       Method of protecting plants from oomycete pathogens
JOURNAL     Patent: US 5856154-A 85 05-JAN-1999;
FEATURES    Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 4 GAATTCAAAAA 28

RESULT 290
AR038488
LOCUS       AR038488          30 bp    DNA
DEFINITION  Sequence 85 from patent US 5804693.
ACCESSION   AR038488
VERSION     AR038488.1  GI:5957205
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Gaffney,T.D., Ryals,J.A., Friedrich,L.B., Uknes,S.J., Ward,E.R.,
TITLE       Chemically regulatable and anti-pathogenic DNA sequences and uses
JOURNAL     Patent: US 5804693-A 85 08-SEP-1998;
FEATURES    Location/Qualifiers
             source
             1..30
             /organism="unknown"
             /mol_type="unassigned DNA"
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Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2161 TCCTCTTTTTTTTTTTTTTTTTTTTTTTT 2185
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Db 2 TCTCGAGTTTTTTTTTTTTTTTTTTTTTTT 26

RESULT 284
I06459
LOCUS I06459 28 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 2 from Patent WO 9001065.
ACCESSION I06459
VERSION I06459.1 GI:589700
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Fry,K., Larrick,J. and Tam,A.
TITLE RNA AND DNA AMPLIFICATION TECHNIQUES
JOURNAL Patent: WO 9001065-A 2 08-FEB-1990;
FEATURES
source
Location/Qualifiers
1..28
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/mol_type="unassigned DNA"

Query Match 0.7%; Score 20.2; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTTTTTTTTTTTTTTTTTTTTTT 2186
||| ||||||| ||||||| ||||||| |||||||
Db 3 CTCGAGTTTTTTTTTTTTTTTTTTTTTTT 27

RESULT 285
AX184127
LOCUS AX184127 28 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1880 from Patent WO0142511.
ACCESSION AX184127
VERSION AX184127.1 GI:15135467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1880 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
source
Location/Qualifiers
1..28
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 20.2; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2150 ATTGATTTTTTCTCCTTTTTTTTTTTT 2175
||| ||||||| ||||||| ||||||| |||||||
Db 3 ATTAATTTTTTCTTCCTCCTTTTTTTT 28

RESULT 286
BD183015/c
LOCUS BD183015 28 bp DNA linear PAT 17-JUN-2003
DEFINITION New functional nucleic acids targeting NS3 protease and helicase of
hepatitis C virus.
ACCESSION BD183015

VERSION BD183015.1 GI:31875215
KEYWORDS JP 2002345475-A/26.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 28)
AUTHORS Nishikawa,S., Fukuda,K., Funaji,K., Uragami,S. and Seki,S.
TITLE New functional nucleic acids targeting NS3 protease and helicase of
hepatitis C virus
JOURNAL Patent: JP 2002345475-A 26 03-DEC-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
MITSUBISHI GAS CHEMICAL CO INC
COMMENT OS Artificial Sequence
PN JP 2002345475-A/26
PD 03-DEC-2002
PF 25-MAY-2001 JP 2001156957
PI SATOSHI NISHIKAWA,KOTARO FUKUDA,KOHEI FUNAJI,SADAJI URAGAMI,
PC SATOSHI SEKIYA
PC C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K48/00,A61P1/16,
PC A61P31/14,
PC A61P43/00,C12N9/99,C12Q1/06,C12N15/00
CC Description of Artificial Sequence: Synthetic DNA FH Key
FT source
1..28
/organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..28
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 20.2; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2155 TTTTCTCTCCTTTTTTTTTTTTTTTT 2179
||| ||||||| ||||||| ||||||| |||||||
Db 25 TTCCTCTCTCCTTTTTTTTTTTTTTTT 1

RESULT 287
AR016852
LOCUS AR016852 30 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 85 from patent US 5777200.
ACCESSION AR016852
VERSION AR016852.1 GI:3973129
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ryals,J.A., Alexander,D.C., Goodman,R.M. and Stinson,J.R.
TITLE Chemically regulatable and anti-pathogenic DNA sequences and uses
thereof
JOURNAL Patent: US 5777200-A 85 07-JUL-1998;
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source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 9.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAAATAAAAAAAAAAAAAA 2804
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Db 4 GAATTCAAAAAATAAAAAAAAAAACATA 28

RESULT 288
AR020878
LOCUS AR020878 30 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 85 from patent US 5789214.


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source 1. .26
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 20.2; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 GAAAAA 2

RESULT 276
AR374074/c
LOCUS AR374074 26 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 39 from patent US 6605272.
ACCESSION AR374074
VERSION AR374074.1 GI:40076646
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .26
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/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 20.2; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 GAAAAA 2

RESULT 277
AR404597/c
LOCUS AR404597 26 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6627748.
ACCESSION AR404597
VERSION AR404597.1 GI:40153233
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .26
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/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 20.2; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 GAAAAA 2

RESULT 278
AR404597/c
LOCUS AR404597 26 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6627748.
ACCESSION AR404597
VERSION AR404597.1 GI:40153233
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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1. .26
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/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 20.2; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 GAAAAA 2

RESULT 279
AR144828
LOCUS AR144828 26 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 59 from patent US 6210942.
ACCESSION AR144828
VERSION AR144828.1 GI:15106695
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.7%; Score 20.2; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 GAAAAA 2

RESULT 280
E33560
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BD007174/c
LOCUS BD007174 26 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and composition for capturing multiple polynucleotide.
ACCESSION BD007174
VERSION BD007174.1 GI:18635545
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 2001503973-A/2
PD 27-MAR-2001
PF 02-OCT-1997 JP 1998516839
PR 04-OCT-1996 US 60/027832,12-JUN-1997 US 08/873437 PI
ROGER A O'NEILL, JAR CAIN CHEN, CLAUDIA CHIESA, GEORGE FRY PC
C12Q1/68, C12N15/09, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .26
FT /organism='Unidentified'.
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Query Match
Best Local Similarity 0.7%; Score 20.2; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 26 GAAAAA 2

RESULT 279
AR144828
LOCUS AR144828 26 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 59 from patent US 6210942.
ACCESSION AR144828
VERSION AR144828.1 GI:15106695
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.7%; Score 20.2; DB 1; Length 26;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2161 TCTCCTTTT 2185
Db 2 TCTCGAGTTT 26

RESULT 280
E33560
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ACCESSION AR261539
VERSION AR261539.1 GI:28072607
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Chetverin,A.B. and Kramer,F.R.
TITLE Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids
JOURNAL Patent: US 6322971-A 6 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 4.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2804
Db 1 TTTAAAAA 22

RESULT 261
AR431312
LOCUS AR431312 24 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6651008.
ACCESSION AR431312
VERSION AR431312.1 GI:40193280
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
TITLE Database system including computer code for predictive cellular bioinformatics
JOURNAL Patent: US 6651008-A 6 18-NOV-2003;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 4.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTT 2186
Db 1 CTTTTTTTTTTT 22

RESULT 262
A79651
LOCUS A79651 30 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 2 from Patent EP0780479.
ACCESSION A79651
VERSION A79651.1 GI:6092605
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 30)
AUTHORS Fritton,H.D. and Hinzpeter,M.D.
TITLE METHOD FOR QUANTITATIVE DETERMINATION OF SPECIFIC NUCLEIC ACID SEQUENCES
JOURNAL Patent: EP 0780479-A 2 25-JUN-1997;
FEATURES BOEHRINGER MANNHEIM GMBH (DE)
source Location/Qualifiers
1..30
/organism="unidentified"

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 8.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTT 2187
Db 1 TTTTTTTTTTTT 22

RESULT 263
AR264920
LOCUS AR264920 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 4 from patent US 6492121.
ACCESSION AR264920
VERSION AR264920.1 GI:29693307
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 4 10-DEC-2002;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2150 ATTGATTTTCTCCTTTT 2179
Db 1 ATATATATTTTGTGTTT 30

RESULT 264
AX394621/c
LOCUS AX394621 30 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 19 from Patent EP186673.
ACCESSION AX394621
VERSION AX394621.1 GI:21065734
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 19 13-MAR-2002;
FEATURES Agilent Technologies Inc (US)
source Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match 0.7%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2155 TTTTTCCTTTT 2184
Db 30 TTTTGGGAGATT 1

HSA241944/c
LOCUS HSA241944 29 bp DNA linear PRI 24-FEB-2000
DEFINITION Homo sapiens gpl30 gene, partial, intron 14 splice acceptor site.
ACCESSION AJ241944
VERSION AJ241944.1 GI:7105900
KEYWORDS gpl30 gene; splice acceptor site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szalai,C., Toth,S. and Falus,A.
TITLE Exon-intron organization of the human gpl30 gene
JOURNAL Gene 243 (1-2), 161-166 (2000)
MEDLINE 20156380
PUBMED 10675624
REFERENCE 2 (bases 1 to 29)
AUTHORS Szalai,C.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1999) Szalai C., Heim Pal Pediatric Hospital
Budapest, Budapest POBOX 66, H-1958 Hungary
COMMENT Related sequence M57230.
FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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/gene="gpl30"
1..24
/gene="gpl30"
/note="splice acceptor site"
/number=14
25..29
/gene="gpl30"
/number=15
Query Match 0.7%; Score 20.6; DB 1; Length 29;
Best Local Similarity 85.2%; Pred. No. 7.1e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2778 TAGAATTGAAAAA 2804
Db 29 TTGAGCTTAAAAA 3
RESULT 257
A08914
LOCUS A08914 31 bp DNA linear PAT 02-SEP-1993
DEFINITION H.sapiens (haplotype 3, allele MS32, isolate Mormon, serial number 2) minisatellite sequence.
ACCESSION A08914
VERSION A08914.1 GI:411836
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Jeffreys,A.J.
TITLE Extended nucleotide sequences
JOURNAL Patent: EP 0370719-A 97 30-MAY-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES
source
1..31
/organism="Homo sapiens"
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Query Match 0.7%; Score 20.6; DB 1; Length 31;
Best Local Similarity 85.2%; Pred. No. 8.5e+02;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2778 TAGAATTGAAAAA 2804
Db 1 TAAAAA 27
RESULT 258
AR365237
LOCUS AR365237 33 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 1 from patent US 5478746.
ACCESSION AR365237
VERSION AR365237.1 GI:34428753
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cohen,J.I., Purcell,R.H., Feinstone,S.M. and Ticehurst,J.R.
TITLE cDNA encoding attenuated cell culture adapted hepatitis A virus genome
JOURNAL Patent: US 5478746-A 1 26-DEC-1995;
FEATURES
source
1..33
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 20.6; DB 1; Length 33;
Best Local Similarity 85.2%; Pred. No. 1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2778 TAGAATTGAAAAA 2804
Db 2 TAAAAA 28
RESULT 259
AX495372
LOCUS AX495372 36 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1137 from Patent WO02059256.
ACCESSION AX495372
VERSION AX495372.1 GI:23340982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tuijnder,M., Telerman,A., Anson,R. and Susini,L.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 02059256-A 1137 01-AUG-2002;
MOLECULAR ENGINES LAB (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.7%; Score 20.6; DB 1; Length 36;
Best Local Similarity 85.2%; Pred. No. 1.2e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2778 TAGAATTGAAAAA 2804
Db 2 TACAGGTAAAAA 28
RESULT 260
AR261539
LOCUS AR261539 24 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 6 from patent US 6322971.

Query Match	0.7%; Score 21; DB 1; Length 25;				
Best Local Similarity	100.0%; Pred. No. 3.9e+02;				
Matches	21; Conservative	0; Mismatches	0; Indels	Gaps	0;
QY	2166	TTTTTTTTTTTTTTTTTTTTTTT	2186		
Db	2	TTTTTTTTTTTTTTTTTTTTTTT	22		
RESULT 212					
I58009					
LOCUS	I58009	25 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 2 from patent US 5610287.				
ACCESSION	I58009				
VERSION	I58009.1 GI:2483073				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 25)				
AUTHORS	Nikiforov, T. and Knapp, M.R.				
TITLE	Method for immobilizing nucleic acid molecules				
JOURNAL	Patent: US 5610287-A 2 11-MAR-1997;				
FEATURES	Location/Qualifiers				
source	1. .25				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.7%; Score 21; DB 1; Length 25;				
Best Local Similarity	100.0%; Pred. No. 3.9e+02;				
Matches	21; Conservative	0; Mismatches	0; Indels	Gaps	0;
QY	2166	TTTTTTTTTTTTTTTTTTTTTTT	2186		
Db	1	TTTTTTTTTTTTTTTTTTTTTTT	21		
RESULT 213					
I96072					
LOCUS	I96072	25 bp	DNA	linear	PAT 01-DEC-1998
DEFINITION	Sequence 2 from patent US 5734020.				
ACCESSION	I96072				
VERSION	I96072.1 GI:3940542				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 25)				
AUTHORS	Wong, Y.N.				
TITLE	Production and use of magnetic porous inorganic materials				
JOURNAL	Patent: US 5734020-A 2 31-MAR-1998;				
FEATURES	Location/Qualifiers				
source	1. .25				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.7%; Score 21; DB 1; Length 25;				
Best Local Similarity	100.0%; Pred. No. 3.9e+02;				
Matches	21; Conservative	0; Mismatches	0; Indels	Gaps	0;
QY	2166	TTTTTTTTTTTTTTTTTTTTTTT	2186		
Db	1	TTTTTTTTTTTTTTTTTTTTTTT	21		
RESULT 214					
AR288252					
LOCUS	AR288252	25 bp	DNA	linear	PAT 12-JUN-2000
DEFINITION	Sequence 23 from patent US 6537749.				
ACCESSION	AR288252				
VERSION	AR288252.1 GI:31675536				
KEYWORDS	Unknown.				

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Query Match
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 24 TTTT TTTT TTTT TTTT TTTT TTTT 4

RESULT 210
AR105982
LOCUS AR105982 25 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6103474.
ACCESSION AR105982
VERSION AR105982.1 GI:12820047
KEYWORDS
SOURCE
ORGANISM Unknown.
Unknwn.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
TITLE Hybridization assay signal enhancement
JOURNAL Patent: US 6103474-A 5 15-AUG-2000;
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1. .25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.7%; Score 21; DB 1; Length 25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 211
BD234336
LOCUS BD234336 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION BD234336
VERSION BD234336.1 GI:33044106
KEYWORDS JP 2002532085-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Romantchikov,Y.
TITLE Improved method for inserting nucleic acid into cyclic vector
JOURNAL Patent: JP 2002532085-A 9 02-OCT-2002;
COMMENT YURI ROMANTCHIKOV
OS Artificial Sequence
PN JP 2002532085-A/9
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588337
PR 17-DEC-1998 US 09/213834
PI YURI ROMANTCHIKOV
PC C12N15/09,C12N1/15,C12N1/21,C12N5/10,C12N15/00,C12N5/
PC 00
CC Cloning Vector
FH Key Location/Qualifiers
FT source 1. .25
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1. .25
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

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AUTHORS Mack, D. and Gish, K.C.
TITLE Methods of diagnosing breast cancer and screening for modulators

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/organism="synthetic construct"
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/note="Description of Artificial"

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/db_xref="taxon:32630"
/seq "Description of Artificial Sequence: T7-T24 oligo"

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
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Db 24 TTTTTTTTTTTTTTTTTTTT 4

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RESULT	194
AX104241	
LOCUS	AX104241
DEFINITION	Sequence 433 from Patent WO0122972.
ACCESSION	AX104241
VERSION	AX104241.1 GI:13920438
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct artificial sequences.

REFERENCE

1. Krieg, A.M., Schetter, C. and Vollmer, J.C.
AUTHORS
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 433 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

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FEATURES
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Query Match      0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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pb      1 TTTTTTTTTTTTTTTTTT 21
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RESULT	195
AX104769	
LOCUS	AX104769 24 bp DNA linear PAT 30-APR-2001
DEFINITION	Sequence 961 from Patent WO0122972.
ACCESSION	AX104769
VERSION	AX104769.1 GI:13920966
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct artificial sequences.

1
REFERENCE
AUTHORS
TITLE
JOURNAL
Krieg, A.M., Schetter, C. and Vollmer, J.C.
Immunostimulatory nucleic acids
Patent: WO 0122972-A 961 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

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FEATURES
  source
    1. .24
      Location/Qualifiers
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
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Query Match          0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy      2166 TTTTTTTTTTTTTTTTTT 2186
        |||||TTTTTTTTTTTTTTT
Db      1   TTTTTTTTTTTTTTTTTT 21
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RESULT 196					
AX104770/c					
LOCUS	AX104770	24 bp	DNA	linear	PAT 30-APR-2000
DEFINITION	Sequence 962 from Patent WO0122972.				

ACCESSION AX104770
VERSION AX104770.1 GI:13920967
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL

1
Krieg, A. M., Schetter, C. and Vollmer, J. C.
Immunostimulatory nucleic acids
patent: WO 0122972-A 962 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

```

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Query Match      0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 197	AX354553	Sequence 11 from Patent WO0173129.	DNA	linear	PAT 06-FEB-2002
LOCUS	AX354553/C				
DEFINITION	Sequence 11 from Patent WO0173129.				
ACCESSION	AX354553				
VERSION	AX354553.1	GI:18619355			

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

1
REFERENCE
AUTHORS Pollner, R.B.
TITLE Real time monitoring of PCR using loci
JOURNAL Patent: WO 0173129-A 11 04-OCT-2001;
DADE BEHRING INC. (US)

FEATURES	source
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Query Match      0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy			
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DEFINITION
Sequence 841 from Patent WO0197843.
AX355813
ACCESSION
AX355813.1 GI:18620481
VERSION
linear
DNA
24 bp
PAT 06-FEB-2000

KEYWORDS
SOURCE
ORGANISM
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synthetic construct
synthetic construct
artificial sequences.

REFERENCE	1	Weiner, G. and Hartmann, G.
AUTHORS		Methods for enhancing antibody-induced cell lysis and treating
TITLE		cancer
JOURNAL		Patent: WO 0197843-A 841 27-DEC-2001;

Query Match 0.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2784 TGAAAAA... 2804
Db 21 TGAAAAA... 1

RESULT 172
AX825163
LOCUS AX825163 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 61 from Patent WO03072818.
ACCESSION AX825163
VERSION AX825163.1 GI:39750892
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 61 04-SEP-2003;
Degussa Bioactives GmbH (DE)

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT... 2186
Db 1 TTTT... 21

RESULT 174
BD080832
LOCUS BD080832 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Mammaglobin, a secreted mammary specific breast cancer protein.
ACCESSION BD080832
VERSION BD080832.1 GI:22626435
KEYWORDS JP 2001516569-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mammaglobin, a secreted mammary specific breast cancer protein
JOURNAL Patent: JP 2001516569-A 10 02-OCT-2001;
WASHINGTON UNIVERSITY

COMMENT
OS Unidentified
PN JP 2001516569-A/10
PD 02-OCT-2001
PF 18-SEP-1998 JP 2000511779
PR 18-SEP-1997 US 08/933149
PI MARK A WATSON,TIMOTHY P FLEMING
PC C12N15/09,A61K35/26,A61K39/00,A61K39/395,A61K39/395,
A61P35/00,
PC C07K14/47,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Mammaglobin, a secreted mammary specific breast cancer protein
FH Key
FT source
FT Location/Qualifiers
1. .21
/organism='Unidentified'.
source

AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 64 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES
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/mol_type="unassigned DNA"
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT... 2186
Db 1 TTTT... 21

RESULT 174
BD080832
LOCUS BD080832 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Mammaglobin, a secreted mammary specific breast cancer protein.
ACCESSION BD080832
VERSION BD080832.1 GI:22626435
KEYWORDS JP 2001516569-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mammaglobin, a secreted mammary specific breast cancer protein
JOURNAL Patent: JP 2001516569-A 10 02-OCT-2001;
WASHINGTON UNIVERSITY

COMMENT
OS Unidentified
PN JP 2001516569-A/10
PD 02-OCT-2001
PF 18-SEP-1998 JP 2000511779
PR 18-SEP-1997 US 08/933149
PI MARK A WATSON,TIMOTHY P FLEMING
PC C12N15/09,A61K35/26,A61K39/00,A61K39/395,A61K39/395,
A61P35/00,
PC C07K14/47,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Mammaglobin, a secreted mammary specific breast cancer protein
FH Key
FT source
FT Location/Qualifiers
1. .21
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JOURNAL Patent: US 6004756-A 13 21-DEC-1999;
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Query Match      0.7%; Score 21; DB 1; Length 21;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT-----TTTTTTTTTTT 2186
Db 1 TTTT-----TTTTTTTTTTT 21

RESULT 163
I65744
LOCUS          21 bp DNA linear PAT 07-OCT-1997
DEFINITION     Sequence 13 from patent US 5668267.
ACCESSION      I65744
VERSION        I65744.1 GI:2482314
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
UNCLASSIFIED   Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS       Watson,M.A. and Fleming,T.P.
TITLE         Polynucleotides encoding mamaglobin, a mammary-specific breast cancer protein
JOURNAL       Patent: US 5668267-A 13 16-SEP-1997;
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source
    1. .21
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Query Match      0.7%; Score 21; DB 1; Length 21;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT-----TTTTTTTTTTT 2186
Db 1 TTTT-----TTTTTTTTTTT 21

RESULT 164
AR322245
LOCUS          21 bp DNA linear PAT 17-AUG-2003
DEFINITION     Sequence 13 from patent US 6566072.
ACCESSION      AR322245
VERSION        AR322245.1 GI:33707814
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
UNCLASSIFIED   Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS       Watson,M.A. and Fleming,T.P.
TITLE         Mamaglobin, a secreted mammary-specific breast cancer protein
JOURNAL       Patent: US 6566072-A 13 20-MAY-2003;
FEATURES
source
    1. .21
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Query Match      0.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT-----TTTTTTTTTTT 2186
Db 1 TTTT-----TTTTTTTTTTT 21

RESULT 165
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Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.
TITLE Method for generating full-length cDNA library from single cells
JOURNAL Patent: US 6197554-A 5 06-MAR-2001;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 4.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 TTTTTCCTCCTTTTCTTTTCTTTTCTTTT 26
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RESULT 143
BD237566
LOCUS 26 bp DNA linear PAT 17-JUL-2003
DEFINITION Genes and proteins predicting and treating fit, hypertension,
diabetes and obesity.
ACCESSION BD237566
VERSION BD237566.1 GI:33047336
KEYWORDS JP 2002525115-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Shimkets,R.A.
TITLE Genes and proteins predicting and treating fit, hypertension,
diabetes and obesity
JOURNAL Patent: JP 2002525115-A 1 13-AUG-2002;
COMMENT CURAGEN CORP
OS Artificial Sequence
PN JP 2002525115-A/1
PD 13-AUG-2002
PF 28-SEP-1999 JP 2000572365
PR 28-SEP-1998 US 09/161939
PI RICHARD A SHIMKETS
PC C12N15/09,A01K67/027,A61K31/7088,A61K38/00,A61K39/395,A61K39/
PC 395,
PC A61K39/395,A61K48/00,A61P3/04,A61P3/06,A61P9/10,A61P9/12, PC
A61P43/00,
PC C07K14/47,C07K16/18,C12N9/10,C12N9/88,C12Q1/25,C12Q1/52 PC
C12Q1/68,G01N33/15,
PC G01N33/50,C12N15/00,A61K37/02
CC Description of Artificial Sequence: oligo(dT)<25>V FH Key
Location/Qualifiers
FT source 1..26
FT /organism='Artificial Sequence'.
Location/Qualifiers
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Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 4.1e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TTTTTCCTCCTTTTCTTTTCTTTTCTTTT 26
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RESULT 144
I79496
LOCUS 26 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 3 from patent US 5707807.
ACCESSION I79496

VERSION I79496.1 GI:3207786
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 3 13-JAN-1998;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 4.1e+02;
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QY 2168 TTTTTCCTCCTTTTCTTTTCTTTTCTTTT 2193
Db 1 TTTTTCCTCCTTTTCTTTTCTTTTCTTTT 26
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RESULT 145
AR257336
LOCUS 26 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 43 from patent US 6486299.
ACCESSION AR257336
VERSION AR257336.1 GI:27307233
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Shimkets,R.A.
TITLE Genes and proteins predictive and therapeutic for stroke,
hypertension, diabetes and obesity
JOURNAL Patent: US 6486299-A 43 26-NOV-2002;
FEATURES Location/Qualifiers
source 1..26
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Query Match 0.8%; Score 21.2; DB 1; Length 26;
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Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTCCTCCTTTTCTTTTCTTTTCTTTT 2187
Db 5 TTTTTCCTCCTTTTCTTTTCTTTTCTTTT 26
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RESULT 146
AR263647
LOCUS 26 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 6 from patent US 6331413.
ACCESSION AR263647
VERSION AR263647.1 GI:28075580
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Adler,D.A. and Sheppard,P.O.
TITLE Secreted salivary ZSIG63 Polypeptide
JOURNAL Patent: US 6331413-A 6 18-DEC-2001;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 4.1e+02;

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REFERENCE	Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M., Sooter, L., Davidson, E., Cox, J.C. and Reidel, T.
AUTHORS	Regulatable, catalytically active nucleic acids
TITLE	Patent: WO 0196559-A 36 20-DEC-2001;
JOURNAL	Board of Regents, The University of Texas System (US)
FEATURES	Location/Qualifiers

DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107499
VERSION BD107499.1 GI:23202317
KEYWORDS JP 2002000275-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 8 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/8
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe
labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
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FEATURES
source Location/Qualifiers
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Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 129
BD145030 30 bp DNA linear PAT 17-JAN-2003
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145030
VERSION BD145030.1 GI:27850788
KEYWORDS JP 2002119291-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 11 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/11
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI TORIMURA,

DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107499
VERSION BD107499.1 GI:23202317
KEYWORDS JP 2002000275-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 8 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/8
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe
labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
/organism="synthetic construct"
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/db_xref="taxon:32630"

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source Location/Qualifiers
FT /organism='Artificial Sequence'.
Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2150 ATTGATTTTTTCTCCTTTTTTTTTTTT 2177
|| ||||| ||||| ||||| ||||| |||||
Db 3 ATATATTTTTTTTCTTTTTTTTTTTT 30

RESULT 129
BD145030 30 bp DNA linear PAT 17-JAN-2003
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145030
VERSION BD145030.1 GI:27850788
KEYWORDS JP 2002119291-A/11.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 11 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/11
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI TORIMURA,

PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
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PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
/organism='Artificial Sequence'.
FT Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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|| ||||| ||||| ||||| ||||| |||||
Db 3 ATATATTTTTTTTCTTTTTTTTTTTT 30

RESULT 130
BD145031 30 bp DNA linear PAT 17-JAN-2003
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145031
VERSION BD145031.1 GI:27850789
KEYWORDS JP 2002119291-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 12 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/12
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
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PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00, C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
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FT Location/Qualifiers
source 1. .30
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COMMENT OS Artificial Sequence
PN JP 2001286300-A/9
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU, OSAMU KOYAMA, KENTA FURUSHO
PC C12Q1/68, C12M1/00, C12N15/09, G01N31/22, G01N33/53, G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2150 ATTGATTTTTTCTCCTTTTTTTTTT 2177
|| ||||| ||||| ||||| ||||| |||||
Db 3 ATATATTTTTTTCTTTTTTTTTTTT 30
RESULT 126
BD072872
LOCUS 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072872
VERSION BD072872.1 GI:22618475
KEYWORDS JP 2001286300-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 10 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/10
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU, OSAMU KOYAMA, KENTA FURUSHO
PC C12Q1/68, C12M1/00, C12N15/09, G01N31/22, G01N33/53, G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic

CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2150 ATTGATTTTTTCTCCTTTTTTTTTT 2177
|| ||||| ||||| ||||| ||||| |||||
Db 3 ATATATTTTTTTCTTTTTTTTTTTT 30
RESULT 127
BD107498
LOCUS 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107498
VERSION BD107498.1 GI:23202316
KEYWORDS JP 2002000275-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 7 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/7
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2150 ATTGATTTTTTCTCCTTTTTTTTTT 2177
|| ||||| ||||| ||||| ||||| |||||
Db 3 ATATATTTTTTTCTTTTTTTTTTTT 30
RESULT 128
BD107499
LOCUS 30 bp DNA linear PAT 18-SEP-2002

Matches	24;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
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QY	2166	TTTTTTTTTTTTTTTTTTTTTAACTTTG	2193
Db	30	TTTTTTTTTTTTTTTTTTTTTTGTG	3

RESULT 121									
LOCUS	AR127791	30 bp	DNA	linear	PAT 16-MAY-2001				
DEFINITION	Sequence 12 from patent US 6180777.								
ACCESSION	AR127791								
VERSION	AR127791.1	GI:14114386							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 30)								
AUTHORS	Horn, T.								
TITLE	Synthesis of branched nucleic acids								
JOURNAL	Patent: US 6180777-A 12 30-JAN-2001;								
FEATURES	Location/Qualifiers								
source	1..30								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
Query Match	0.8%;	Score 21.6;	DB 1;	Length 30;					
Best Local Similarity	85.7%;	Pred. No. 5.2e+02;							
Matches	24;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;

QY	2166	TTTTTTTTTTTTTTTTTTTTTAACTTTG	2193
Db	30	TTTTTTTTTTTTTTTTTTTTTTGTG	3

RESULT 122									
LOCUS	I28373	30 bp	DNA	linear	PAT 06-FEB-1997				
DEFINITION	Sequence 12 from patent US 5571677.								
ACCESSION	I28373								
VERSION	I28373.1	GI:1819149							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 30)								
AUTHORS	Gryaznov, S.M.								
TITLE	Convergent synthesis of branched and multiply connected macromolecular structures								
JOURNAL	Patent: US 5571677-A 12 05-NOV-1996;								
FEATURES	Location/Qualifiers								
source	1..30								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
Query Match	0.8%;	Score 21.6;	DB 1;	Length 30;					
Best Local Similarity	85.7%;	Pred. No. 5.2e+02;							
Matches	24;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;

QY	2166	TTTTTTTTTTTTTTTTTTTTTAACTTTG	2193
Db	30	TTTTTTTTTTTTTTTTTTTTTTGTG	3

RESULT 123									
LOCUS	AR264926	30 bp	DNA	linear	PAT 10-APR-2003				
DEFINITION	Sequence 10 from patent US 6492121.								
ACCESSION	AR264926								
VERSION	AR264926.1	GI:29693313							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								


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TITLE      Dna detection by a strand reassociation complex
JOURNAL    Patent: EP 0962536-A 18 08-DEC-1999;
           ROCHE DIAGNOSTICS GMBH (DE)
FEATURES   Location/Qualifiers
            source             1..27
                                /organism="Mycobacterium tuberculosis"
                                /mol_type="unassigned DNA"
                                /db_xref="taxon:1773"
            misc_signal        1
                                /note="Phosphate linked to biotin via Aminolinker"
            misc_signal        27
                                /note="Y means incorporation of
                                Aminolinker-phosphoramidite subsequently esterified with 3-O
                                carboxymethyl digoxigenin"

Query Match      0.8%; Score 21.8; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 3.5e+02;
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2155 TTTTTTCTCCTTTTTTTTTTTTTTTTTT 2181
           ||||| | ||||| ||||| ||||| : ||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 27

RESULT 115
BD234335
LOCUS      BD234335                28 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION  BD234335
VERSION     BD234335.1 GI:33044105
KEYWORDS   JP 2002532085-A/8.
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 28)
AUTHORS   Romantchikov, Y.
TITLE     Improved method for inserting nucleic acid into cyclic vector
JOURNAL   Patent: JP 2002532085-A 8 02-OCT-2002;
           YURI ROMANTCHIKOV
COMMENT   OS Artificial Sequence
           PN JP 2002532085-A/8
           PD 02-OCT-2002
           PF 17-DEC-1999 JP 2000588337
           PR 17-DEC-1998 US 09/213834
           PI YURI ROMANTCHIKOV
           PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
           CC 00
           CC Cloning Vector
           FH Key
           FT source
           FT /organism='Artificial Sequence'.

FEATURES   Location/Qualifiers
            source             1..28
                                /organism="synthetic construct"
                                /mol_type="genomic DNA"
                                /db_xref="taxon:32630"

Query Match      0.8%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2162 CTCCTTTTTTTTTTTTTTTTTTTTTT 2186
           ||||| ||||| ||||| ||||| |||||
Db      1 CTAGTTTTTTTTTTTTTTTTTTTTTT 25

RESULT 116
BD234356
LOCUS      BD234356                32 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION  BD234356
VERSION     BD234356.1 GI:33044126
KEYWORDS   JP 2002532085-A/29.

```


RESULT 99
AX394514

1 (bases 1 to 26)

REFERENCE
AUTHORS
Novak, J. E., Presnell, S. R., Sprecher, C. A., Foster, D. C., Holly, R. D.,
Gross, J. A., Johnston, J. V., Nelson, A. J., Dillon, S. R. and
Hammond, A. K.

QY 2155 TTTTCTCCTTTT 2181
Db 1 TTTTCTCCTTTT 27

RESULT 92
AX355814
LOCUS AX355814 27 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 842 from Patent WO197843.
ACCESSION AX355814
VERSION AX355814.1 GI:18620482
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 842 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 0.8%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2155 TTTTCTCCTTTT 2181
Db 1 TTTTCTCCTTTT 27

RESULT 93
AX547772
LOCUS AX547772 27 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 911 from Patent WO02053141.
ACCESSION AX547772
VERSION AX547772.1 GI:25812916
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 911 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source 1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 0.8%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2155 TTTTCTCCTTTT 2181
Db 1 TTTTCTCCTTTT 27

RESULT 94
I32124
LOCUS I32124 32 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 14 from patent US 5585242.
ACCESSION I32124
VERSION I32124.1 GI:1822915
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Bouma, S.R., Khalil, O.S. and Pabich, E.K.
TITLE Method for detection of nucleic acid using total internal reflectance
JOURNAL Patent: US 5585242-A 14 17-DEC-1996;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 22.2; DB 1; Length 32;
Best Local Similarity 88.9%; Pred. No. 4.9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2159 TTTCTCCTTTT 2185
Db 6 TGTCCGCTTTT 32

RESULT 95
AR365237/c
LOCUS AR365237 33 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 1 from patent US 5478746.
ACCESSION AR365237
VERSION AR365237.1 GI:34428753
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cohen, J.I., Purcell, R.H., Feinstone, S.M. and Ticehurst, J.R.
TITLE cDNA encoding attenuated cell culture adapted hepatitis A virus genome
JOURNAL Patent: US 5478746-A 1 26-DEC-1995;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 22.2; DB 1; Length 33;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2161 TCTCCTTTT 2187
Db 28 TTTTCTCCTTTT 2

RESULT 96
AR431307
LOCUS AR431307 24 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6651008.
ACCESSION AR431307
VERSION AR431307.1 GI:40193275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Vaisberg, E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
TITLE Database system including computer code for predictive cellular bioinformatics
JOURNAL Patent: US 6651008-A 1 18-NOV-2003;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Szostak,J.W. and Roberts,R.W.
TITLE RNA-antibody fusions and their selection
JOURNAL Patent: US 6518018-A 15 11-FEB-2003;
FEATURES Location/Qualifiers
source 1. .33
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.8%; Score 22.4; DB 1; Length 33;
Best Local Similarity 95.8%; Pred. No. 5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA 2803
Db 8 GAAC TGA AAAAAA 31
RESULT 88
AR098680
LOCUS AR098680 34 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 38 from patent US 6077668.
ACCESSION AR098680
VERSION AR098680.1 GI:12808446
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 38 20-JUN-2000;
FEATURES Location/Qualifiers
source 1. .34
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 22.4; DB 1; Length 34;
Best Local Similarity 81.2%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2155 TTTTCTCCTTTT 2186
Db 2 TTCTTTCTCGATCTTTCTTTCTTTT 33
RESULT 89
AR204754
LOCUS AR204754 34 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 38 from patent US 6368802.
ACCESSION AR204754
VERSION AR204754.1 GI:21502161
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 38 09-APR-2002;
FEATURES Location/Qualifiers
source 1. .34
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 22.4; DB 1; Length 34;
Best Local Similarity 81.2%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2155 TTTTCTCCTTTT 2186
Db 2 TTCTTTCTCGATCTTTCTTTCTTTT 33
RESULT 90
E04985/c
LOCUS E04985 27 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence of 3'terminal fragment of ITR.
ACCESSION E04985
VERSION E04985.1 GI:2173180
KEYWORDS JP 1993103673-A/79.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 27)
AUTHORS Sengu,K.Y. and Ito,S.
TITLE REPLICATION OF DNA
JOURNAL Patent: JP 1993103673-A 79 27-APR-1993;
COMMENT ARIZONA BOARD OF REGENTS
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1993103673-A/79
PD 27-APR-1993
PF 26-AUG-1991 JP 1991240525
PI SENGU KUU YUU, ITO SUMIYOSHI
PC C12N15/10,C12N15/11//C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT misc_feature 1. .27
FT /note='3'terminal fragment of ITR'.
FEATURES
source Location/Qualifiers
1. .27
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2155 TTTTCTCCTTTT 2181
Db 27 TTTTCTTTT 1
RESULT 91
AX104719
LOCUS AX104719 27 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 911 from Patent WO0122972.
ACCESSION AX104719
VERSION AX104719.1 GI:13920916
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 911 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
source 1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


```

SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Forster,A.C. and Blacklow,S.C.
TITLE       Process and compositions for peptide, protein and peptidomimetic
            synthesis
JOURNAL     Patent: WO 02059293-A 41 01-AUG-2002;
            Forster, Anthony C. (US) ; Blacklow, Stephen C. (US)
FEATURES   source
            Location/Qualifiers
                1..29
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="FROM SYNTHETIC DNA"

Query Match          0.8%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 3.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2153 GATTTTTCCTCTTTTTTTTTTTTTTTT 2181
Db 29 GGTTTTTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 82
BD204968/c
LOCUS      BD204968              29 bp        DNA             linear           PAT 17-JUL-2003
DEFINITION Protein array enabling site specification.
ACCESSION  BD204968
VERSION    BD204968.1 GI:33014738
KEYWORDS   JP 2002510505-A/3.
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
           1 (bases 1 to 29)
REFERENCE  Kuimelis,R.G. and Wagner,R.
AUTHORS    Protein array enabling site specification
TITLE      Patent: JP 2002510505-A 3 09-APR-2002;
JOURNAL    PHYLLOS INC

COMMENT    OS Artificial Sequence
PN         JP 2002510505-A/3
PD         09-APR-2002
PF         31-MAR-1999 JP 2000542484
PR         03-APR-1998 US 60/080686
PI         ROBERT G KUIMELIS,RICHARD WAGNER
PC         C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
           G01N33/68,
PC         C12N15/00
CC         Oligonucleotide used for attaching puromycin
FH         Key Location/Qualifiers
FT         FT source 1..29
           /organism='Artificial Sequence'.

FEATURES   source
            Location/Qualifiers
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

Query Match          0.8%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 3.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2153 GATTTTTCCTCTTTTTTTTTTTTTTTT 2181
Db 29 GGTTTTTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 83
AX351711/c
LOCUS      AX351711              30 bp        DNA             linear           PAT 06-FEB-2002
DEFINITION Sequence 7 from Patent WO0193902.
ACCESSION  AX351711
```


[illegible]

RESULT	60
BD234339	
LOCUS	28 bp DNA linear PAT 17-JUL-2003
DEFINITION	Improved method for inserting nucleic acid into cyclic vector.
ACCESSION	BD234339
VERSION	BD234339.1 GI:33044109
KEYWORDS	JP 2002532085-A/12.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1 (bases 1 to 28)
AUTHORS	Romantchikov,Y.
TITLE	Improved method for inserting nucleic acid into cyclic vector
JOURNAL	Patent: JP 2002532085-A 12 OCT-2002;
	YURI ROMANTCHIKOV
COMMENT	OS Artificial Sequence
	PN JP 2002532085-A/12
	PD 02-OCT-2002
	PF 17-DEC-1999 JP 2000588337
	PR 17-DEC-1998 US 09/213834
	PI YURI ROMANTCHIKOV
	PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/00,C12N5/10
	PP 00
	CC Cloning Vector

DEFINITION Sorting of proteins using RNA-protein fused body.
ACCESSION BD238393
VERSION BD238393.1 GI:33048163
KEYWORDS JP 2002536025-A/11.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 36)
AUTHORS Szostak, J.W., Roberts, R.W. and Liu, R.
TITLE Sorting of proteins using RNA-protein fused body
JOURNAL Patent: JP 2002536025-A 11 29-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002536025-A/11
PD 29-OCT-2002
PF 01-FEB-2000 JP 2000598669
PR 09-FEB-1999 US 09/247190
PI JACK W SZOSTAK, RICHARD W ROBERTS, RIHE LIU
PC C12N15/09, C07K7/00, C07K14/00, C12Q1/68, C12N15/00 CC
Translation template
FH Key Location/Qualifiers
FT source 1..36
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
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/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
Query Match 0.8%; Score 23.4; DB 1; Length 36;
Best Local Similarity 96.0%; Pred. No. 4.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA AAAAAAAAAA AAAAAA 2804
|||||
Db 8 GAAC TGAAAAA AAAAAAAAAA AAAAAA 32
RESULT 53
AR279819
LOCUS AR279819 36 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 14 from patent US 6518018.
ACCESSION AR279819
VERSION AR279819.1 GI:29714964
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS Szostak, J.W. and Roberts, R.W.
TITLE RNA-antibody fusions and their selection
JOURNAL Patent: US 6518018-A 14 11-FEB-2003;
FEATURES
source Location/Qualifiers
1..36
/organism='unknown'
/mol_type='unassigned RNA'
Query Match 0.8%; Score 23.4; DB 1; Length 36;
Best Local Similarity 96.0%; Pred. No. 4.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA AAAAAAAAAA AAAAAA 2804
|||||
Db 8 GAAC TGAAAAA AAAAAAAAAA AAAAAA 32
RESULT 54
AX430216/c
LOCUS AX430216 29 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 7 from Patent EP1207210.
ACCESSION AX430216
VERSION AX430216.1 GI:21655581
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dietmaier, W.
TITLE Method for melting curve analysis of repetitive pcr products
JOURNAL Patent: EP 1207210-A 7 22-MAY-2002;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
source Location/Qualifiers
1..29
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
Query Match 0.8%; Score 23.2; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 2.4e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2152 TGATTTTTCCTCTTTT TTTT TTTT TTTT 2179
|||||
Db 29 TGATTTTTCCTCTTTT TTTT TTTT TTTT 2
RESULT 55
BD165919/c
LOCUS BD165919 29 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for melting curve analysis of repetitive PCR products.
ACCESSION BD165919
VERSION BD165919.1 GI:27871731
KEYWORDS JP 2002191384-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 29)
AUTHORS Dietmaier, W.
TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: JP 2002191384-A 7 09-JUL-2002;
F HOFFMANN LA ROCHE AG
COMMENT OS Homo sapiens (human)
PN JP 2002191384-A/7
PD 09-JUL-2002
PF 13-NOV-2001 JP 2001348017
PR 15-NOV-2000 EP 00124897.0
PI WOLFGANG DIETMAIER
PC C12N15/09, C12Q1/68, C12N15/00
CC Method for melting curve analysis of repetitive PCR products
FH Key Location/Qualifiers
FT source 1..29
FT /organism='Homo sapiens (human)'.
FEATURES
source Location/Qualifiers
1..29
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.8%; Score 23.2; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 2.4e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2152 TGATTTTTCCTCTTTT TTTT TTTT TTTT 2179
|||||
Db 29 TGATTTTTCCTCTTTT TTTT TTTT TTTT 2
RESULT 56
BD238393/c
LOCUS BD238393 36 bp RNA linear PAT 17-JUL-2003
DEFINITION Sorting of proteins using RNA-protein fused body.
ACCESSION BD238393
VERSION BD238393.1 GI:33048163
KEYWORDS JP 2002536025-A/11.
SOURCE synthetic construct

		/db_xref="taxon:32644"			
Query Match		0.8%; Score 23.6; DB 1; Length 32;			
Best Local Similarity		86.7%; Pred. No. 2.8e+02;			
Matches		26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
Qy	2161	TCTCCTTTT	30 bp	DNA	linear
	2190	TTTAACT			
Db	2161	TCTCCTTTT	30 bp	DNA	linear
	2190	TTTAACT			
RESULT 48					
AX196237/c					
LOCUS					
DEFINITION		Sequence 68 from Patent WO0151665.			
ACCESSION		AX196237			
VERSION		AX196237.1 GI:15386440			
KEYWORDS					
SOURCE		synthetic construct			
ORGANISM		synthetic construct			
REFERENCE		artificial sequences.			
AUTHORS		1			
TITLE		Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,			
JOURNAL		Elghanian,R., Taton,T.A. and Li,Z.			
FEATURES		Nanoparticles having oligonucleotides attached thereto and uses			
source		therefor			
Patent: WO 0151665-A 68 19-JUL-2001;					
Nanosphere, Inc. (US)					
Location/Qualifiers					
1. .30					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="random synthetic sequence"					
Query Match		0.8%; Score 23.4; DB 1; Length 30;			
Best Local Similarity		96.0%; Pred. No. 2.5e+02;			
Matches		24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	2161	TCTCCTTTT	30 bp	DNA	linear
	2185	TTT			
Db	2161	TCTCCTTTT	30 bp	DNA	linear
	2185	TTT			
RESULT 49					
AX440138/c					
LOCUS					
DEFINITION		Sequence 68 from Patent WO0173123.			
ACCESSION		AX440138			
VERSION		AX440138.1 GI:21664949			
KEYWORDS					
SOURCE		synthetic construct			
ORGANISM		synthetic construct			
REFERENCE		artificial sequences.			
AUTHORS		1			
TITLE		Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,			
JOURNAL		Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.			
FEATURES		Nanoparticles having oligonucleotides attached thereto and uses			
source		therefor			
Patent: WO 0173123-A 68 04-OCT-2001;					
Nanosphere, Inc. (US)					
Location/Qualifiers					
1. .30					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="random synthetic sequence"					
Query Match		0.8%; Score 23.4; DB 1; Length 30;			
Best Local Similarity		96.0%; Pred. No. 2.5e+02;			
Matches		24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	2161	TCTCCTTTT	30 bp	DNA	linear
	2185	TTT			
Db	2161	TCTCCTTTT	30 bp	DNA	linear
	2185	TTT			
RESULT 50					
AX465324/c					
LOCUS					
DEFINITION		Sequence 68 from Patent WO0218643.			
ACCESSION		AX465324			
VERSION		AX465324.1 GI:21899687			
KEYWORDS					
SOURCE		synthetic construct			
ORGANISM		synthetic construct			
REFERENCE		artificial sequences.			
AUTHORS		1			
TITLE		Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,			
JOURNAL		Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.			
FEATURES		Nanoparticles having oligonucleotides attached thereto and uses			
source		therefor			
Patent: WO 0218643-A 68 07-MAR-2002;					
Nanosphere, Inc. (US)					
Location/Qualifiers					
1. .30					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="random synthetic sequence"					
Query Match		0.8%; Score 23.4; DB 1; Length 30;			
Best Local Similarity		96.0%; Pred. No. 2.5e+02;			
Matches		24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	2161	TCTCCTTTT	30 bp	DNA	linear
	2185	TTT			
Db	2161	TCTCCTTTT	30 bp	DNA	linear
	2185	TTT			
RESULT 51					
AX556137/c					
LOCUS					
DEFINITION		Sequence 68 from Patent WO0246472.			
ACCESSION		AX556137			
VERSION		AX556137.1 GI:25899519			
KEYWORDS					
SOURCE		synthetic construct			
ORGANISM		synthetic construct			
REFERENCE		artificial sequences.			
AUTHORS		1			
TITLE		Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,			
JOURNAL		Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.			
FEATURES		Nanoparticles having oligonucleotides attached thereto and uses			
source		therefor			
Patent: WO 0246472-A 68 13-JUN-2002;					
Nanosphere, Inc. (US)					
Location/Qualifiers					
1. .30					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="random synthetic sequence"					
Query Match		0.8%; Score 23.4; DB 1; Length 30;			
Best Local Similarity		96.0%; Pred. No. 2.5e+02;			
Matches		24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	2161	TCTCCTTTT	30 bp	DNA	linear
	2185	TTT			
Db	2161	TCTCCTTTT	30 bp	DNA	linear
	2185	TTT			
RESULT 52					
BD238393					
LOCUS					
BD238393					
PAT 17-JUL-2003					

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 23.6; DB 1; Length 31;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2154 ATTTTCTCCTTTTTTTTTTTTTTTTTTTT 2183
Db 31 ATATTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 46
AX430213/c
LOCUS AX430213 32 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 4 from Patent EPI207210.
ACCESSION AX430213
VERSION AX430213.1 GI:21655578
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive pcr products
JOURNAL Patent: EP 1207210-A 4 22-MAY-2002;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
source
1..32
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 23.6; DB 1; Length 32;
Best Local Similarity 86.7%; Pred. No. 2.8e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2161 TCCTCTTTTTTTTTTTTTTTTTTTTAACT 2190
Db 32 TTTTCTTTTTTTTTTTTTTTTTTTTACCT 3

RESULT 47
BD165916/c
LOCUS BD165916 32 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for melting curve analysis of repetitive PCR products.
ACCESSION BD165916
VERSION BD165916.1 GI:27871728
KEYWORDS JP 2002191384-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 32)
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: JP 2002191384-A 4 09-JUL-2002;
F HOFFMANN LA ROCHE AG
COMMENT OS Homo sapiens (human)
PN JP 2002191384-A/4
PD 09-JUL-2002
PE 13-NOV-2001 JP 2001348017
PR 15-NOV-2000 EP 00124897.0
PI WOLFGANG DIETMAIER
PC C12N15/09,C12Q1/68,C12N15/00
CC Method for melting curve analysis of repetitive PCR products
FH Key Location/Qualifiers
FT source 1..30
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
FT Location/Qualifiers
1..32
/mol_type="unidentified"
/mol_type="genomic DNA"

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1. .29
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

source
1. .29
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 24.4; DB 1; Length 29;
Best Local Similarity 96.2%; Pred. No. 1.5e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 2803
Db 4 TAGAACTGAAAAA 29

RESULT 38
AX079109 30 bp DNA linear PAT 22-FEB-2001
LOCUS
DEFINITION Sequence 7 from Patent WO0106226.
ACCESSION AX079109
VERSION AX079109.1 GI:13158683
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"

Query Match 0.9%; Score 24; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2163 TCCTTTT 2186
Db 3 TCCTTTT 26

RESULT 39
BD171339 33 bp DNA linear PAT 18-FEB-2003
LOCUS
DEFINITION Production method of cytochrome c.
ACCESSION BD171339
VERSION BD171339.1 GI:28412629
KEYWORDS JP 2002218979-A/2.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Artificial Sequence
PN JP 2002218979-A/2
PD 06-AUG-2002
PF 23-JAN-2001 JP 2001014510
PI TADATAKE OKU, TOSHIOYUKI NISHIO, TADASHI SATO
PC C12N15/09, C12N1/21, C12P21/02, (C12N15/09, C12R1:91), (C12N1/21,
PC C12R1:01),
PC (C12P21/02, C12R1:01), C12N15/00, (C12N15/00, C12R1:91) CC
Production method of cytochrome c
FH Key Location/Qualifiers
FT source 1. .33
/organism="Artificial Sequence".
FEATURES
Location/Qualifiers
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29 bp DNA linear PAT 17-JUL-2003
BD274321
IDENTIFICATION OF MOLECULAR INTERACTION SITES IN RNA FOR NOVEL DRUG
DISCOVERY.
ACCESSION BD274321
VERSION BD274321.1 GI:33084089
KEYWORDS JP 2002526030-A/288.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
PN JP 2002526030-A/288
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1. .29
/organism="Artificial Sequence".
FEATURES
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1. .29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 24.4; DB 1; Length 29;
Best Local Similarity 96.2%; Pred. No. 1.5e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 2803
Db 4 TAGAACTGAAAAA 29

RESULT 37
BD274339 29 bp RNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274339
VERSION BD274339.1 GI:33084107
KEYWORDS JP 2002526030-A/306.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Artificial Sequence
PN JP 2002526030-A/306
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1. .29
/organism="Artificial Sequence".
FEATURES
Location/Qualifiers
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ORGANISM unidentified
REFERENCE 1 unclassified.
AUTHORS Oerum,H. and Seeger,C.
TITLE METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
JOURNAL Patent: WO 9720068-A 7 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE)
FEATURES
  source 1. .30
    Location/Qualifiers
      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"
Query Match 0.9%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2155 TTTTCTCCTTTT 2184
Db 30 TTTTCTCCTTTT 1

RESULT 20
AR179066
LOCUS AR179066 30 bp DNA linear PAT 16-MAY-2002
DEFINITION Sequence 3 from patent US 6326143.
ACCESSION AR179066
VERSION AR179066.1 GI:20220621
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Oerum,H. and Seeger,C.
TITLE Method for generating multiple double stranded nucleic acids
JOURNAL Patent: US 6326143-A 3 04-DEC-2001;
FEATURES
  source 1. .30
    Location/Qualifiers
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 0.9%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2155 TTTTCTCCTTTT 2184
Db 1 TTTTCTCCTTTT 30

RESULT 21
AR179070/c
LOCUS AR179070 30 bp DNA linear PAT 16-MAY-2002
DEFINITION Sequence 7 from patent US 6326143.
ACCESSION AR179070
VERSION AR179070.1 GI:20220625
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Oerum,H. and Seeger,C.
TITLE Method for generating multiple double stranded nucleic acids
JOURNAL Patent: US 6326143-A 7 04-DEC-2001;
FEATURES
  source 1. .30
    Location/Qualifiers
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 0.9%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2155 TTTTCTCCTTTT 2184
Db 30 TTTTCTCCTTTT 1

RESULT 22
E04638
LOCUS E04638 30 bp RNA linear PAT 29-SEP-1997
DEFINITION Synthesized Oligoribonucleotides of more than 20 mers.
ACCESSION E04638
VERSION E04638.1 GI:5708508
KEYWORDS JP 1992330093-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Tanimura,H. and Imada,M.
TITLE PRODUCTION OF OLIGORIBONUCLEOTIDE
JOURNAL Patent: JP 1992330093-A 2 18-NOV-1992;
TAKEDA CHEM IND LTD
COMMENT OS Artificial gene
OS Artificial sequence; Genes.
PN JP 1992330093-A/2
PD 18-NOV-1992
PF 07-JUN-1991 JP 1991136086
PR 20-JUL-1990 JP 90P 190762
PI TANIMURA HIROSHI, IMADA MICHIO
PC C07H21/02;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH misc_feature 1. .30
FT /note='suitably selected protection of RNA FT
FT units
FT Location/Qualifiers
  source 1. .30
    /organism="synthetic construct"
    /mol_type="genomic RNA"
    /db_xref="taxon:32630"
Query Match 0.9%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2155 TTTTCTCCTTTT 2184
Db 1 TTTTCTCCTTTT 30

RESULT 23
I84450/c
LOCUS I84450 30 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 9 from patent US 5695936.
ACCESSION I84450
VERSION I84450.1 GI:3021970
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Mandrand,B., Cros,P., Delair,T., Charles,M.-H., Erout,M.-N. and
Pichot,C.
TITLE Reagent and method for the detection of a nucleotide sequence with
signal amplification
JOURNAL Patent: US 5695936-A 9 09-DEC-1997;
FEATURES
  source 1. .30
    Location/Qualifiers
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 0.9%; Score 25.2; DB 1; Length 30;
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REFERENCE 1 (bases 1 to 37)
AUTHORS Pickup,D.J., Patel,D. and Antczak,J.B.
TITLE Site-specific RNA cleavage
JOURNAL Patent: US 5578468-A 44 26-NOV-1996;
FEATURES Location/Qualifiers
source 1..37
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 28; DB 1; Length 37;
Best Local Similarity 86.1%; Pred. No. 67;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2151 TTGATTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTTT 2186
|| ||||| | ||||| ||||| ||||| ||||| |||||
Db 37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 7
AX106972
LOCUS AX106972 37 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 25 from Patent WO0125442.
ACCESSION AX106972
VERSION AX106972.1 GI:13922521
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
TITLE Dna polymerase lambda and uses thereof
JOURNAL Patent: WO 0125442-A 25 12-APR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES Location/Qualifiers
source 1..37
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="poly dT"

Query Match 1.0%; Score 28; DB 1; Length 37;
Best Local Similarity 86.1%; Pred. No. 67;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2151 TTGATTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTTT 2186
|| ||||| | ||||| ||||| ||||| ||||| |||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36

RESULT 8
E50766
LOCUS E50766 38 bp DNA linear PAT 31-JAN-2002
DEFINITION Vector expressing full-length gene of RNA virus and utilization thereof.
ACCESSION E50766
VERSION E50766.1 GI:18628191
KEYWORDS JP 2000152793-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Obara,M., Obara,K., Tabira,K., Matsuzaki,J. and Om,H.
TITLE Vector expressing full-length gene of RNA virus and utilization
JOURNAL Patent: JP 2000152793-A 19 06-JUN-2000;
TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, CHUGAI PHARMACEUT CO LTD
COMMENT OS Artificial Sequence
PN JP 2000152793-A/19
PD 06-JUN-2000
PF 24-JUN-1999 JP 1999178347
PR
PI MICHINORI OBARA,KYOKO OBARA,KAZUNARI TABIRA,JUNICHI MATSUZAKI,HIROSHI OMORI

PC C12N15/09,A01K67/027,C12N5/10,C12Q1/70,C12N15/00,C12N5/00 CC
FH Key Location/Qualifiers
FT source 1..38
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..38
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 27.4; DB 1; Length 38;
Best Local Similarity 83.8%; Pred. No. 94;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2150 ATTGATTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
|| ||||| | ||||| ||||| ||||| ||||| |||||
Db 2 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38

RESULT 9
BD011883
LOCUS BD011883 33 bp DNA linear PAT 02-AUG-2002
DEFINITION Detection kit for SRSV.
ACCESSION BD011883
VERSION BD011883.1 GI:22092072
KEYWORDS WO 0079280-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Takeda,N., Natori,K., Miyamura,T., Kunio, Kamata, Sato,T. and Sato,S.
TITLE Detection kit for SRSV
JOURNAL Patent: WO 0079280-A 13 28-DEC-2000;
JAPAN AS REPRESENTED BY DIRECTOR GE YOSHIHIKO HIROSE,MITSUAKI MORIGUCHI,KIMIYASU ISOBE DISEASES, DENKA SEIKEN CO LTD,NAOKAZU TAKEDA,KATSURO NATORI,TATSUO MIYAMURA, KUNIO KAMATA,TOSHINORI SATO,SEIYA SATO
COMMENT OS Artificial Sequence
PN WO 0079280-A/13
PD 28-DEC-2000
PF 22-JUN-2000 WO 2000JP004095
PR 22-JUN-1999 JP. 99P 175928
PI NAOKAZU TAKEDA,KATSURO NATORI,TATSUO MIYAMURA,KUNIO PI KAMATA,TOSHINORI SATO,
PI SEIYA SATO
PC G01N33/569,C12N15/40
CC
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1..33
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 27.2; DB 1; Length 33;
Best Local Similarity 90.6%; Pred. No. 66;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2155 TTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTTT 2186
||||| | ||||| ||||| ||||| ||||| |||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 10
BD170449/c
LOCUS BD170449 40 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of detecting DNA polymorphism using mass spectrometry.
ACCESSION BD170449
VERSION BD170449.1 GI:27876261
KEYWORDS WO 0250307-A/4.
SOURCE synthetic construct

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ALIGNMENTS

RESULT 1	AX287571	AX287571	Sequence 14	45 bp	DNA	linear	PAT 21-NOV-2001
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DEFINITION	AX287571	AX287571					
ACCESSION	AX287571	AX287571.1	GI:17049337				
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							

synthetic construct
synthetic construct
artificial sequences.
1
abarz A, P.
Process for allele discrimination utilizing primer extension
Patent: WO 0177390-A 14 18-OCT-2001;
Molecular Staging, Inc. (US)
Location/Qualifiers

4341	13.2	0.5	20	1	AX804495	ACCESSION:AX804495	C4414	13	0.5	24	1	AX043137	ACCESSION:AX043137
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C4361	13.2	0.5	20	1	BD178842	ACCESSION:BD178842	C4434	12.8	0.5	20	1	AX354981	ACCESSION:AX354981
C4362	13.2	0.5	20	1	BD179443	ACCESSION:BD179443	C4435	12.8	0.5	20	1	AX547637	ACCESSION:AX547637
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C4372	13.2	0.5	21	1	AR342463	ACCESSION:AR342463	4445	12.6	0.4	20	1	AR360428	ACCESSION:AR360428
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C4375	13.2	0.5	22	1	AR003281	ACCESSION:AR003281	4448	12.6	0.4	20	1	AR360398	ACCESSION:AR360398
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C4381	13.2	0.5	22	1	BD206194	ACCESSION:BD206194	4454	12.6	0.4	20	1	AX462490	ACCESSION:AX462490
C4382	13.2	0.5	22	1	A63568	ACCESSION:A63568	4455	12.6	0.4	20	1	A88305	ACCESSION:A88305
C4383	13.2	0.5	23	1	AX084400	ACCESSION:AX084400	4456	12.6	0.4	20	1	A90272	ACCESSION:A90272
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4390	13	0.5	14	1	BD176797	ACCESSION:BD176797	C4463	12.6	0.4	20	1	AR360394	ACCESSION:AR360394
C4391	13	0.5	14	1	BD176801	ACCESSION:BD176801	C4464	12.6	0.4	20	1	AR360395	ACCESSION:AR360395
4392	13	0.5	14	1	BD176802	ACCESSION:BD176802	C4465	12.6	0.4	20	1	AR360396	ACCESSION:AR360396
C4393	13	0.5	17	1	AR187059	ACCESSION:AR187059	4466	12.6	0.4	20	1	AR360397	ACCESSION:AR360397
C4394	13	0.5	17	1	AR323669	ACCESSION:AR323669	4467	12.6	0.4	20	1	AR360399	ACCESSION:AR360399
C4395	13	0.5	18	1	BD096968	ACCESSION:BD096968	4468	12.6	0.4	20	1	AR360402	ACCESSION:AR360402
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4400	13	0.5	18	1	BD166064	ACCESSION:BD166064	4473	12.6	0.4	20	1	AR360424	ACCESSION:AR360424
4401	13	0.5	20	1	A17773	ACCESSION:A17773	4474	12.6	0.4	20	1	AR360426	ACCESSION:AR360426
4402	13	0.5	20	1	A29944	ACCESSION:A29944	4475	12.6	0.4	20	1	AR360429	ACCESSION:AR360429
4403	13	0.5	20	1	AR094462	ACCESSION:AR094462	C4476	12.6	0.4	20	1	AR382158	ACCESSION:AR382158
4404	13	0.5	20	1	AR164799	ACCESSION:AR164799	4477	12.6	0.4	20	1	AR382159	ACCESSION:AR382159
4405	13	0.5	20	1	I58491	ACCESSION:I58491	C4478	12.6	0.4	20	1	AX136904	ACCESSION:AX136904
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c3919	13.2	0.5	18	1	A63086	c3992	13.2	0.5	19	1	AR030972	ACCESSION:AR030972
c3920	13.2	0.5	18	1	A87862	c3993	13.2	0.5	19	1	AR030974	ACCESSION:AR030974
c3921	13.2	0.5	18	1	A87864	c3994	13.2	0.5	19	1	AR030975	ACCESSION:AR030975
3922	13.2	0.5	18	1	A87993	c3995	13.2	0.5	19	1	AR030976	ACCESSION:AR030976
c3923	13.2	0.5	18	1	A89829	c3996	13.2	0.5	19	1	AR030977	ACCESSION:AR030977
c3924	13.2	0.5	18	1	A89831	c3997	13.2	0.5	19	1	AR030978	ACCESSION:AR030978
3925	13.2	0.5	18	1	A89960	c3998	13.2	0.5	19	1	AR030981	ACCESSION:AR030981
c3926	13.2	0.5	18	1	AR019212	c3999	13.2	0.5	19	1	AR030982	ACCESSION:AR030982
c3927	13.2	0.5	18	1	AR019245	c4000	13.2	0.5	19	1	AR030983	ACCESSION:AR030983
c3928	13.2	0.5	18	1	AR042299	c4001	13.2	0.5	19	1	AR030984	ACCESSION:AR030984
c3929	13.2	0.5	18	1	AR055425	c4002	13.2	0.5	19	1	AR108814	ACCESSION:AR108814
c3930	13.2	0.5	18	1	AR076325	c4003	13.2	0.5	19	1	AR108817	ACCESSION:AR108817
c3931	13.2	0.5	18	1	AR092808	c4004	13.2	0.5	19	1	AR108819	ACCESSION:AR108819
3932	13.2	0.5	18	1	AR092813	c4005	13.2	0.5	19	1	AR108820	ACCESSION:AR108820
c3933	13.2	0.5	18	1	AR098789	c4006	13.2	0.5	19	1	AR108821	ACCESSION:AR108821
c3934	13.2	0.5	18	1	AR098791	c4007	13.2	0.5	19	1	AR108822	ACCESSION:AR108822
3935	13.2	0.5	18	1	AR101834	c4008	13.2	0.5	19	1	AR108823	ACCESSION:AR108823
c3936	13.2	0.5	18	1	AR101834	c4009	13.2	0.5	19	1	AR108826	ACCESSION:AR108826
3937	13.2	0.5	18	1	AR144877	c4010	13.2	0.5	19	1	AR108827	ACCESSION:AR108827
c3938	13.2	0.5	18	1	AR160886	c4011	13.2	0.5	19	1	AR108828	ACCESSION:AR108828
c3939	13.2	0.5	18	1	BD234557	c4012	13.2	0.5	19	1	AR108829	ACCESSION:AR108829
c3940	13.2	0.5	18	1	BD250635	c4013	13.2	0.5	19	1	I62823	ACCESSION:I62823
c3941	13.2	0.5	18	1	I12014	c4014	13.2	0.5	19	1	AR205763	ACCESSION:AR205763
3942	13.2	0.5	18	1	I83492	c4015	13.2	0.5	19	1	AR205766	ACCESSION:AR205766
c3943	13.2	0.5	18	1	AR196142	c4016	13.2	0.5	19	1	AR205768	ACCESSION:AR205768
c3944	13.2	0.5	18	1	AR196694	c4017	13.2	0.5	19	1	AR205769	ACCESSION:AR205769
3945	13.2	0.5	18	1	AR211267	c4018	13.2	0.5	19	1	AR205770	ACCESSION:AR205770
3946	13.2	0.5	18	1	AR264964	c4019	13.2	0.5	19	1	AR205771	ACCESSION:AR205771
c3947	13.2	0.5	18	1	AR268663	c4020	13.2	0.5	19	1	AR205772	ACCESSION:AR205772
c3948	13.2	0.5	18	1	AR294187	c4021	13.2	0.5	19	1	AR205775	ACCESSION:AR205775
3949	13.2	0.5	18	1	AR295456	c4022	13.2	0.5	19	1	AR205776	ACCESSION:AR205776
c3950	13.2	0.5	18	1	AR305637	c4023	13.2	0.5	19	1	AR205777	ACCESSION:AR205777
c3951	13.2	0.5	18	1	AR305637	c4024	13.2	0.5	19	1	AR205778	ACCESSION:AR205778
3952	13.2	0.5	18	1	AR351522	c4025	13.2	0.5	19	1	A37094	ACCESSION:A37094
c3953	13.2	0.5	18	1	AR351534	4026	13.2	0.5	19	1	A39742	ACCESSION:A39742
3954	13.2	0.5	18	1	AR410329	c4027	13.2	0.5	19	1	A41231	ACCESSION:A41231
3955	13.2	0.5	18	1	AR437532	c4028	13.2	0.5	19	1	A91188	ACCESSION:A91188
c3956	13.2	0.5	18	1	AX098985	c4029	13.2	0.5	19	1	AR002990	ACCESSION:AR002990
c3957	13.2	0.5	18	1	AX137004	4030	13.2	0.5	19	1	AR007260	ACCESSION:AR007260
3958	13.2	0.5	18	1	AX191970	c4031	13.2	0.5	19	1	AR007261	ACCESSION:AR007261
c3959	13.2	0.5	18	1	AX469443	c4032	13.2	0.5	19	1	AR019659	ACCESSION:AR019659
3960	13.2	0.5	18	1	AX473186	4033	13.2	0.5	19	1	AR067985	ACCESSION:AR067985
3961	13.2	0.5	18	1	AX572835	c4034	13.2	0.5	19	1	AR067986	ACCESSION:AR067986
3962	13.2	0.5	18	1	AX595553	4035	13.2	0.5	19	1	AR069633	ACCESSION:AR069633
c3963	13.2	0.5	18	1	AX599628	c4036	13.2	0.5	19	1	AR074187	ACCESSION:AR074187
3964	13.2	0.5	18	1	AX600742	4037	13.2	0.5	19	1	AR082444	ACCESSION:AR082444
c3965	13.2	0.5	18	1	AX637756	4038	13.2	0.5	19	1	AR084247	ACCESSION:AR084247
3966	13.2	0.5	18	1	AX705457	c4039	13.2	0.5	19	1	AR084248	ACCESSION:AR084248
c3967	13.2	0.5	18	1	AX705459	4040	13.2	0.5	19	1	AR097619	ACCESSION:AR097619
3968	13.2	0.5	18	1	AX708192	c4041	13.2	0.5	19	1	AR097620	ACCESSION:AR097620
c3969	13.2	0.5	18	1	AX767877	4042	13.2	0.5	19	1	AR110289	ACCESSION:AR110289
3970	13.2	0.5	18	1	AX796513	4043	13.2	0.5	19	1	AR139000	ACCESSION:AR139000
3971	13.2	0.5	18	1	AX796532	c4044	13.2	0.5	19	1	AR162033	ACCESSION:AR162033
3972	13.2	0.5	18	1	AX822178	4045	13.2	0.5	19	1	BD252160	ACCESSION:BD252160
3973	13.2	0.5	18	1	AX822998	4046	13.2	0.5	19	1	BD262907	ACCESSION:BD262907
3974	13.2	0.5	18	1	AX823077	4047	13.2	0.5	19	1	I73729	ACCESSION:I73729
3975	13.2	0.5	18	1	AX825818	c4048	13.2	0.5	19	1	AR209033	ACCESSION:AR209033

ACCESSION:A52265	3976	13.2	0.5	18	1	AX826638	ACCESSION:AX826638
ACCESSION:E13665	3977	13.2	0.5	18	1	AX826717	ACCESSION:AX826717
ACCESSION:E13665	c3978	13.2	0.5	18	1	BD065375	ACCESSION:BD065375
ACCESSION:E13670	c3979	13.2	0.5	18	1	BD065377	ACCESSION:BD065377
ACCESSION:E13670	3980	13.2	0.5	18	1	BD065506	ACCESSION:BD065506
ACCESSION:AR266627	c3981	13.2	0.5	18	1	BD072905	ACCESSION:BD072905
ACCESSION:AR266627	3982	13.2	0.5	18	1	BD081036	ACCESSION:BD081036
ACCESSION:AR084213	c3983	13.2	0.5	18	1	BD089313	ACCESSION:BD089313
ACCESSION:AR264960	c3984	13.2	0.5	18	1	BD089762	ACCESSION:BD089762
ACCESSION:AR008470	3985	13.2	0.5	18	1	BD104961	ACCESSION:BD104961
ACCESSION:AR008471	c3986	13.2	0.5	18	1	BD107532	ACCESSION:BD107532
ACCESSION:AR009718	c3987	13.2	0.5	18	1	BD145064	ACCESSION:BD145064
ACCESSION:AR009719	c3988	13.2	0.5	18	1	BD166064	ACCESSION:BD166064
ACCESSION:AR063241	3989	13.2	0.5	18	1	BD225045	ACCESSION:BD225045
ACCESSION:AR063243	3990	13.2	0.5	18	1	AJ589110	ACCESSION:AJ589110
ACCESSION:AX662307	c3991	13.2	0.5	19	1	AR030969	ACCESSION:AR030969
ACCESSION:A63086	c3992	13.2	0.5	19	1	AR030972	ACCESSION:AR030972
ACCESSION:A87862	c3993	13.2	0.5	19	1	AR030974	ACCESSION:AR030974
ACCESSION:A87864	c3994	13.2	0.5	19	1	AR030975	ACCESSION:AR030975
ACCESSION:A87993	c3995	13.2	0.5	19	1	AR030976	ACCESSION:AR030976
ACCESSION:A89829	c3996	13.2	0.5	19	1	AR030977	ACCESSION:AR030977
ACCESSION:A89831	c3997	13.2	0.5	19	1	AR030978	ACCESSION:AR030978
ACCESSION:A89960	c3998	13.2	0.5	19	1	AR030981	ACCESSION:AR030981
ACCESSION:AR019212	c3999	13.2	0.5	19	1	AR030982	ACCESSION:AR030982
ACCESSION:AR019245	c4000	13.2	0.5	19	1	AR030983	ACCESSION:AR030983
ACCESSION:AR042299	c4001	13.2	0.5	19	1	AR030984	ACCESSION:AR030984
ACCESSION:AR055425	c4002	13.2	0.5	19	1	AR108814	ACCESSION:AR108814
ACCESSION:AR076325	c4003	13.2	0.5	19	1	AR108817	ACCESSION:AR108817
ACCESSION:AR092808	c4004	13.2	0.5	19	1	AR108819	ACCESSION:AR108819
ACCESSION:AR092813	c4005	13.2	0.5	19	1	AR108820	ACCESSION:AR108820
ACCESSION:AR098789	c4006	13.2	0.5	19	1	AR108821	ACCESSION:AR108821
ACCESSION:AR098791	c4007	13.2	0.5	19	1	AR108822	ACCESSION:AR108822
ACCESSION:AR101834	c4008	13.2	0.5	19	1	AR108823	ACCESSION:AR108823
ACCESSION:AR101834	c4009	13.2	0.5	19	1	AR108826	ACCESSION:AR108826
ACCESSION:AR144877	c4010	13.2	0.5	19	1	AR108827	ACCESSION:AR108827
ACCESSION:AR160886	c4011	13.2	0.5	19	1	AR108828	ACCESSION:AR108828
ACCESSION:BD234557	c4012	13.2	0.5	19	1	AR108829	ACCESSION:AR108829
ACCESSION:BD250635	c4013	13.2	0.5	19	1	I62823	ACCESSION:I62823
ACCESSION:I12014	c4014	13.2	0.5	19	1	AR205763	ACCESSION:AR205763
ACCESSION:I83492	c4015	13.2	0.5	19	1	AR205766	ACCESSION:AR205766
ACCESSION:AR196142	c4016	13.2	0.5	19	1	AR205768	ACCESSION:AR205768
ACCESSION:AR196694	c4017	13.2	0.5	19	1	AR205769	ACCESSION:AR205769
ACCESSION:AR211267	c4018	13.2	0.5	19	1	AR205770	ACCESSION:AR205770
ACCESSION:AR264964	c4019	13.2	0.5	19	1	AR205771	ACCESSION:AR205771
ACCESSION:AR268663	c4020	13.2	0.5	19	1	AR205772	ACCESSION:AR205772
ACCESSION:AR294187	c4021	13.2	0.5	19	1	AR205775	ACCESSION:AR205775
ACCESSION:AR295456	c4022	13.2	0.5	19	1	AR205776	ACCESSION:AR205776
ACCESSION:AR305637	c4023	13.2	0.5	19	1	AR205777	ACCESSION:AR205777
ACCESSION:AR305637	c4024	13.2	0.5	19	1	AR205778	ACCESSION:AR205778
ACCESSION:AR351522	c4025	13.2	0.5	19	1	A37094	ACCESSION:A37094
ACCESSION:AR351534	4026	13.2	0.5	19	1	A39742	ACCESSION:A39742
ACCESSION:AR410329	c4027	13.2	0.5	19	1	A41231	ACCESSION:A41231
ACCESSION:AR437532	c4028	13.2	0.5	19	1	A91188	ACCESSION:A91188
ACCESSION:AX098985	c4029	13.2	0.5	19	1	AR002990	ACCESSION:AR002990
ACCESSION:AX137004	4030	13.2	0.5	19	1	AR007260	ACCESSION:AR007260
ACCESSION:AX191970	c4031	13.2	0.5	19	1	AR007261	ACCESSION:AR007261
ACCESSION:AX469443	c4032	13.2	0.5	19	1	AR019659	ACCESSION:AR019659
ACCESSION:AX473186	4033	13.2	0.5	19	1	AR067985	ACCESSION:AR067985
ACCESSION:AX572835	c4034	13.2	0.5	19	1	AR067986	ACCESSION:AR067986
ACCESSION:AX599553	4035	13.2	0.5	19	1	AR069633	ACCESSION:AR069633
ACCESSION:AX599628	c4036	13.2	0.5	19	1	AR074187	ACCESSION:AR074187
ACCESSION:AX600742	4037	13.2	0.5	19	1	AR082444	ACCESSION:AR082444
ACCESSION:AX637756	4038	13.2	0.5	19	1	AR084247	ACCESSION:AR084247
ACCESSION:AX705457	c4039	13.2	0.5	19	1	AR084248	ACCESSION:AR084248
ACCESSION:AX705459	4040	13.2	0.5	19	1	AR097619	ACCESSION:AR097619
ACCESSION:AX708192	c4041	13.2	0.5	19	1	AR097620	ACCESSION:AR097620
ACCESSION:AX767877	4042	13.2	0.5	19	1	AR110289	ACCESSION:AR110289
ACCESSION:AX796513	4043	13.2	0.5	19	1	AR139000	ACCESSION:AR139000
ACCESSION:AX796532	c4044	13.2	0.5	19	1	AR162033	ACCESSION:AR162033
ACCESSION:AX822178	4045	13.2	0.5	19	1	BD252160	ACCESSION:BD252160
ACCESSION:AX822998	4046	13.2	0.5	19	1	BD262907	ACCESSION:BD262907
ACCESSION:AX823077	4047	13.2	0.5	19	1	I73729	ACCESSION:I73729
ACCESSION:AX825818	c4048	13.2	0.5	19	1	AR209033	ACCESSION:AR209033

3757	13.4	0.5	18	1	AR229573	ACCESSION:AR229573	C3830	13.4	0.5	20	1	AR100054	ACCESSION:AR100054
C3758	13.4	0.5	18	1	AR292914	ACCESSION:AR292914	C3831	13.4	0.5	20	1	AR100185	ACCESSION:AR100185
3759	13.4	0.5	18	1	AR295535	ACCESSION:AR295535	3832	13.4	0.5	20	1	AR107217	ACCESSION:AR107217
C3760	13.4	0.5	18	1	AR324012	ACCESSION:AR324012	C3833	13.4	0.5	20	1	AR112276	ACCESSION:AR112276
3761	13.4	0.5	18	1	AR324101	ACCESSION:AR324101	C3834	13.4	0.5	20	1	AR120878	ACCESSION:AR120878
C3762	13.4	0.5	18	1	AR431658	ACCESSION:AR431658	C3835	13.4	0.5	20	1	AR121079	ACCESSION:AR121079
C3763	13.4	0.5	18	1	AX078831	ACCESSION:AX078831	C3836	13.4	0.5	20	1	AR124966	ACCESSION:AR124966
C3764	13.4	0.5	18	1	AX078842	ACCESSION:AX078842	3837	13.4	0.5	20	1	AR130110	ACCESSION:AR130110
C3765	13.4	0.5	18	1	AX078848	ACCESSION:AX078848	C3838	13.4	0.5	20	1	AR137875	ACCESSION:AR137875
C3766	13.4	0.5	18	1	AX078859	ACCESSION:AX078859	3839	13.4	0.5	20	1	AR143184	ACCESSION:AR143184
C3767	13.4	0.5	18	1	AX268173	ACCESSION:AX268173	C3840	13.4	0.5	20	1	AR149869	ACCESSION:AR149869
3768	13.4	0.5	18	1	AX557193	ACCESSION:AX557193	C3841	13.4	0.5	20	1	AR150391	ACCESSION:AR150391
C3769	13.4	0.5	18	1	AX599315	ACCESSION:AX599315	3842	13.4	0.5	20	1	AR153754	ACCESSION:AR153754
C3770	13.4	0.5	18	1	AX599746	ACCESSION:AX599746	C3843	13.4	0.5	20	1	AR153754	ACCESSION:AR153754
C3771	13.4	0.5	18	1	AX601190	ACCESSION:AX601190	3844	13.4	0.5	20	1	AR158931	ACCESSION:AR158931
C3772	13.4	0.5	18	1	AX685128	ACCESSION:AX685128	3845	13.4	0.5	20	1	AR163732	ACCESSION:AR163732
C3773	13.4	0.5	18	1	AX767735	ACCESSION:AX767735	C3846	13.4	0.5	20	1	BD228264	ACCESSION:BD228264
C3774	13.4	0.5	18	1	AX796171	ACCESSION:AX796171	C3847	13.4	0.5	20	1	BD243056	ACCESSION:BD243056
3775	13.4	0.5	18	1	AX822843	ACCESSION:AX822843	3848	13.4	0.5	20	1	BD249359	ACCESSION:BD249359
C3776	13.4	0.5	18	1	AX826483	ACCESSION:AX826483	C3849	13.4	0.5	20	1	BD272700	ACCESSION:BD272700
3777	13.4	0.5	18	1	AX837788	ACCESSION:AX837788	C3850	13.4	0.5	20	1	E11827	ACCESSION:E11827
C3778	13.4	0.5	18	1	BD065376	ACCESSION:BD065376	3851	13.4	0.5	20	1	E11838	ACCESSION:E11838
C3779	13.4	0.5	18	1	BD065659	ACCESSION:BD065659	3852	13.4	0.5	20	1	E35764	ACCESSION:E35764
3780	13.4	0.5	18	1	BD089867	ACCESSION:BD089867	3853	13.4	0.5	20	1	I51693	ACCESSION:I51693
C3781	13.4	0.5	18	1	BD103917	ACCESSION:BD103917	C3854	13.4	0.5	20	1	I51693	ACCESSION:I51693
C3782	13.4	0.5	18	1	BD104957	ACCESSION:BD104957	C3855	13.4	0.5	20	1	I77271	ACCESSION:I77271
C3783	13.4	0.5	18	1	BD217399	ACCESSION:BD217399	C3856	13.4	0.5	20	1	I78382	ACCESSION:I78382
3784	13.4	0.5	18	1	AB068476	ACCESSION:AB068476	C3857	13.4	0.5	20	1	AR220978	ACCESSION:AR220978
C3785	13.4	0.5	19	1	A51090	ACCESSION:A51090	3858	13.4	0.5	20	1	AR229050	ACCESSION:AR229050
3786	13.4	0.5	19	1	AR029157	ACCESSION:AR029157	C3859	13.4	0.5	20	1	AR234664	ACCESSION:AR234664
C3787	13.4	0.5	19	1	AR029157	ACCESSION:AR029157	C3860	13.4	0.5	20	1	AR305210	ACCESSION:AR305210
3788	13.4	0.5	19	1	AR036541	ACCESSION:AR036541	C3861	13.4	0.5	20	1	AR309314	ACCESSION:AR309314
C3789	13.4	0.5	19	1	AR036541	ACCESSION:AR036541	3862	13.4	0.5	20	1	AR311840	ACCESSION:AR311840
3790	13.4	0.5	19	1	AR096074	ACCESSION:AR096074	C3863	13.4	0.5	20	1	AR312330	ACCESSION:AR312330
C3791	13.4	0.5	19	1	AR096074	ACCESSION:AR096074	3864	13.4	0.5	20	1	AR312943	ACCESSION:AR312943
3792	13.4	0.5	19	1	AR097400	ACCESSION:AR097400	C3865	13.4	0.5	20	1	AR312983	ACCESSION:AR312983
C3793	13.4	0.5	19	1	AR111930	ACCESSION:AR111930	C3866	13.4	0.5	20	1	AR313616	ACCESSION:AR313616
C3794	13.4	0.5	19	1	AR111930	ACCESSION:AR111930	3867	13.4	0.5	20	1	AR314827	ACCESSION:AR314827
3795	13.4	0.5	19	1	AR124827	ACCESSION:AR124827	C3868	13.4	0.5	20	1	AR315171	ACCESSION:AR315171
C3796	13.4	0.5	19	1	AR124827	ACCESSION:AR124827	C3869	13.4	0.5	20	1	AR315937	ACCESSION:AR315937
3797	13.4	0.5	19	1	AR135275	ACCESSION:AR135275	C3870	13.4	0.5	20	1	AR373738	ACCESSION:AR373738
C3798	13.4	0.5	19	1	AR135275	ACCESSION:AR135275	C3871	13.4	0.5	20	1	AR373818	ACCESSION:AR373818
3799	13.4	0.5	19	1	AR137398	ACCESSION:AR137398	3872	13.4	0.5	20	1	AR432278	ACCESSION:AR432278
C3800	13.4	0.5	19	1	AR137402	ACCESSION:AR137402	3873	13.4	0.5	20	1	AX099164	ACCESSION:AX099164
3801	13.4	0.5	19	1	AR141345	ACCESSION:AR141345	3874	13.4	0.5	20	1	AX148814	ACCESSION:AX148814
C3802	13.4	0.5	19	1	AR141345	ACCESSION:AR141345	3875	13.4	0.5	20	1	AX149017	ACCESSION:AX149017
C3803	13.4	0.5	19	1	AR160892	ACCESSION:AR160892	3876	13.4	0.5	20	1	AX149191	ACCESSION:AX149191
3804	13.4	0.5	19	1	AR179524	ACCESSION:AR179524	C3877	13.4	0.5	20	1	AX201485	ACCESSION:AX201485
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3806	13.4	0.5	19	1	I25705	ACCESSION:I25705	3879	13.4	0.5	20	1	AX418735	ACCESSION:AX418735
3807	13.4	0.5	19	1	AR212307	ACCESSION:AR212307	C3880	13.4	0.5	20	1	AX418815	ACCESSION:AX418815
C3808	13.4	0.5	19	1	AR212307	ACCESSION:AR212307	C3881	13.4	0.5	20	1	AX462751	ACCESSION:AX462751
3809	13.4	0.5	19	1	AR231437	ACCESSION:AR231437	3882	13.4	0.5	20	1	AX477137	ACCESSION:AX477137
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3811	13.4	0.5	19	1	AR412353	ACCESSION:AR412353	3884	13.4	0.5	20	1	AX613548	ACCESSION:AX613548
C3812	13.4	0.5	19	1	AX115855	ACCESSION:AX115855	C3885	13.4	0.5	20	1	AX697401	ACCESSION:AX697401
C3813	13.4	0.5	19	1	AX115855	ACCESSION:AX115855	3886	13.4	0.5	20	1	AX753521	ACCESSION:AX753521
3814	13.4	0.5	19	1	AX132036	ACCESSION:AX132036	3887	13.4	0.5	20	1	AX753625	ACCESSION:AX753625
3815	13.4	0.5	19	1	AX192337	ACCESSION:AX192337	C3888	13.4	0.5	20	1	BD023379	ACCESSION:BD023379
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C3817	13.4	0.5	19	1	AX535777	ACCESSION:AX535777	C3890	13.4	0.5	20	1	BD106121	ACCESSION:BD106121
C3818	13.4	0.5	19	1	AX539268	ACCESSION:AX539268	3891	13.4	0.5	20	1	BD128192	ACCESSION:BD128192
C3819	13.4	0.5	19	1	AX815849	ACCESSION:AX815849	C3892	13.4	0.5	20	1	BD134696	ACCESSION:BD134696
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3822	13.4	0.5	19	1	BD222586	ACCESSION:BD222586	C3895	13.4	0.5	20	1	AB069398	ACCESSION:AB069398
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C3825	13.4	0.5	20	1	A91597	ACCESSION:A91597	3898	13.4	0.5	21	1	I24714	ACCESSION:I24714
3826	13.4	0.5	20	1	AR051133	ACCESSION:AR051133	C3899	13.4	0.5	24	1	AR364668	ACCESSION:AR364668
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3613	13.4	0.5	15	1	AR084519	ACCESSION:AR084519	C3686	13.4	0.5	17	1	AX500255	ACCESSION:AX500255
3614	13.4	0.5	15	1	AR127784	ACCESSION:AR127784	C3687	13.4	0.5	17	1	AX500256	ACCESSION:AX500256
3615	13.4	0.5	15	1	I16031	ACCESSION:I16031	3688	13.4	0.5	17	1	AX600667	ACCESSION:AX600667
3616	13.4	0.5	15	1	I28366	ACCESSION:I28366	3689	13.4	0.5	17	1	AX672113	ACCESSION:AX672113
3617	13.4	0.5	15	1	A15242	ACCESSION:A15242	3690	13.4	0.5	17	1	AX673606	ACCESSION:AX673606
3618	13.4	0.5	15	1	A16457	ACCESSION:A16457	3691	13.4	0.5	17	1	AX674437	ACCESSION:AX674437
3619	13.4	0.5	15	1	AR084518	ACCESSION:AR084518	C3692	13.4	0.5	17	1	AX674708	ACCESSION:AX674708
3620	13.4	0.5	15	1	AR084518	ACCESSION:AR084518	3693	13.4	0.5	17	1	AX688047	ACCESSION:AX688047
3621	13.4	0.5	15	1	AR084532	ACCESSION:AR084532	3694	13.4	0.5	17	1	AX688048	ACCESSION:AX688048
3622	13.4	0.5	15	1	BD244856	ACCESSION:BD244856	3695	13.4	0.5	17	1	AX692521	ACCESSION:AX692521
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3625	13.4	0.5	15	1	AR241876	ACCESSION:AR241876	C3698	13.4	0.5	17	1	AX692529	ACCESSION:AX692529
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C3629	13.4	0.5	16	1	BD233092	ACCESSION:BD233092	C3702	13.4	0.5	17	1	AX723265	ACCESSION:AX723265
C3630	13.4	0.5	16	1	E33197	ACCESSION:E33197	3703	13.4	0.5	17	1	AX724168	ACCESSION:AX724168
C3631	13.4	0.5	16	1	AR328462	ACCESSION:AR328462	C3704	13.4	0.5	17	1	AX725075	ACCESSION:AX725075
C3632	13.4	0.5	16	1	AX007646	ACCESSION:AX007646	3705	13.4	0.5	17	1	AX725350	ACCESSION:AX725350
C3633	13.4	0.5	17	1	BD255422	ACCESSION:BD255422	C3706	13.4	0.5	17	1	AX729187	ACCESSION:AX729187
C3634	13.4	0.5	17	1	BD255423	ACCESSION:BD255423	3707	13.4	0.5	17	1	AX729876	ACCESSION:AX729876
C3635	13.4	0.5	17	1	BD255424	ACCESSION:BD255424	C3708	13.4	0.5	17	1	AX732099	ACCESSION:AX732099
C3636	13.4	0.5	17	1	AX738493	ACCESSION:AX738493	C3709	13.4	0.5	17	1	AX732979	ACCESSION:AX732979
C3637	13.4	0.5	17	1	AX757892	ACCESSION:AX757892	C3710	13.4	0.5	17	1	AX737962	ACCESSION:AX737962
C3638	13.4	0.5	17	1	A05414	ACCESSION:A05414	C3711	13.4	0.5	17	1	AX738283	ACCESSION:AX738283
C3639	13.4	0.5	17	1	A09621	ACCESSION:A09621	3712	13.4	0.5	17	1	AX744261	ACCESSION:AX744261
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3641	13.4	0.5	17	1	AR047114	ACCESSION:AR047114	C3714	13.4	0.5	17	1	AX751000	ACCESSION:AX751000
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3643	13.4	0.5	17	1	AR158488	ACCESSION:AR158488	C3716	13.4	0.5	17	1	AX758401	ACCESSION:AX758401
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3645	13.4	0.5	17	1	AR158490	ACCESSION:AR158490	3718	13.4	0.5	17	1	AX758703	ACCESSION:AX758703
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3655	13.4	0.5	17	1	I54166	ACCESSION:I54166	C3728	13.4	0.5	17	1	BD105064	ACCESSION:BD105064
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3670	13.4	0.5	17	1	AR434234	ACCESSION:AR434234	C3743	13.4	0.5	18	1	AR162696	ACCESSION:AR162696
3671	13.4	0.5	17	1	AX099948	ACCESSION:AX099948	C3744	13.4	0.5	18	1	AR163233	ACCESSION:AR163233
3672	13.4	0.5	17	1	AX214956	ACCESSION:AX214956	C3745	13.4	0.5	18	1	AR165895	ACCESSION:AR165895
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3435	13.6	0.5	20	1	AR136423
3436	13.6	0.5	20	1	AR143173
3437	13.6	0.5	20	1	AR150141
c3438	13.6	0.5	20	1	AR153094
c3439	13.6	0.5	20	1	AR158732
3440	13.6	0.5	20	1	AR158929
c3441	13.6	0.5	20	1	AR159152
c3442	13.6	0.5	20	1	AR159153
c3443	13.6	0.5	20	1	AR159154
c3444	13.6	0.5	20	1	AR163820
3445	13.6	0.5	20	1	AR163962
c3446	13.6	0.5	20	1	AR164029
3447	13.6	0.5	20	1	AR173039
3448	13.6	0.5	20	1	AR176812
3449	13.6	0.5	20	1	BD228014
3450	13.6	0.5	20	1	BD249348
3451	13.6	0.5	20	1	BD251480
c3452	13.6	0.5	20	1	BD269458
3453	13.6	0.5	20	1	BD269459
3454	13.6	0.5	20	1	BD272643
c3455	13.6	0.5	20	1	E16129
c3456	13.6	0.5	20	1	E29890
3457	13.6	0.5	20	1	E29952
3458	13.6	0.5	20	1	E39288
3459	13.6	0.5	20	1	E39963
3460	13.6	0.5	20	1	E58734
c3461	13.6	0.5	20	1	I19926
c3462	13.6	0.5	20	1	I72480
c3463	13.6	0.5	20	1	I88040
3464	13.6	0.5	20	1	AR199794

ACCESSION:BD056555
ACCESSION:BD089006
ACCESSION:BD134288
ACCESSION:BD140134
ACCESSION:BD161939
ACCESSION:AB069141
ACCESSION:AR066407
ACCESSION:AX011524
ACCESSION:BD226411
ACCESSION:AX042978
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ACCESSION:AR102419
ACCESSION:AR103803
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ACCESSION:AR116415
ACCESSION:AR121022
ACCESSION:AR121320
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ACCESSION:AR124459
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ACCESSION:E39963
ACCESSION:E58734
ACCESSION:I19926
ACCESSION:I72480
ACCESSION:I88040
ACCESSION:AR199794

c3173	13.8	0.5	18	1	AX207025	ACCESSION:AX207025	3246	13.8	0.5	20	1	AR040612	ACCESSION:AR040612
3174	13.8	0.5	18	1	AX298581	ACCESSION:AX298581	c3247	13.8	0.5	20	1	AR052440	ACCESSION:AR052440
3175	13.8	0.5	18	1	AX301867	ACCESSION:AX301867	3248	13.8	0.5	20	1	AR068795	ACCESSION:AR068795
c3176	13.8	0.5	18	1	AX327038	ACCESSION:AX327038	3249	13.8	0.5	20	1	AR075147	ACCESSION:AR075147
3177	13.8	0.5	18	1	AX404240	ACCESSION:AX404240	c3250	13.8	0.5	20	1	AR082428	ACCESSION:AR082428
c3178	13.8	0.5	18	1	AX662307	ACCESSION:AX662307	3251	13.8	0.5	20	1	AR089233	ACCESSION:AR089233
3179	13.8	0.5	18	1	BD089251	ACCESSION:BD089251	3252	13.8	0.5	20	1	AR092669	ACCESSION:AR092669
3180	13.8	0.5	19	1	A25084	ACCESSION:A25084	c3253	13.8	0.5	20	1	AR100377	ACCESSION:AR100377
3181	13.8	0.5	19	1	A85285	ACCESSION:A85285	3254	13.8	0.5	20	1	AR103911	ACCESSION:AR103911
3182	13.8	0.5	19	1	AR030969	ACCESSION:AR030969	c3255	13.8	0.5	20	1	AR107643	ACCESSION:AR107643
3183	13.8	0.5	19	1	AR030972	ACCESSION:AR030972	3256	13.8	0.5	20	1	AR108815	ACCESSION:AR108815
3184	13.8	0.5	19	1	AR030974	ACCESSION:AR030974	c3257	13.8	0.5	20	1	AR109207	ACCESSION:AR109207
3185	13.8	0.5	19	1	AR030975	ACCESSION:AR030975	3258	13.8	0.5	20	1	AR116574	ACCESSION:AR116574
3186	13.8	0.5	19	1	AR030976	ACCESSION:AR030976	c3259	13.8	0.5	20	1	AR124483	ACCESSION:AR124483
3187	13.8	0.5	19	1	AR030977	ACCESSION:AR030977	3260	13.8	0.5	20	1	AR126737	ACCESSION:AR126737
3188	13.8	0.5	19	1	AR030978	ACCESSION:AR030978	3261	13.8	0.5	20	1	AR130999	ACCESSION:AR130999
3189	13.8	0.5	19	1	AR030981	ACCESSION:AR030981	c3262	13.8	0.5	20	1	AR150032	ACCESSION:AR150032
3190	13.8	0.5	19	1	AR030982	ACCESSION:AR030982	3263	13.8	0.5	20	1	AR158377	ACCESSION:AR158377
3191	13.8	0.5	19	1	AR030983	ACCESSION:AR030983	3264	13.8	0.5	20	1	AR163975	ACCESSION:AR163975
3192	13.8	0.5	19	1	AR030984	ACCESSION:AR030984	c3265	13.8	0.5	20	1	AR174366	ACCESSION:AR174366
3193	13.8	0.5	19	1	AR108814	ACCESSION:AR108814	c3266	13.8	0.5	20	1	BD227905	ACCESSION:BD227905
3194	13.8	0.5	19	1	AR108817	ACCESSION:AR108817	c3267	13.8	0.5	20	1	BD241888	ACCESSION:BD241888
3195	13.8	0.5	19	1	AR108819	ACCESSION:AR108819	c3268	13.8	0.5	20	1	E08391	ACCESSION:E08391
3196	13.8	0.5	19	1	AR108820	ACCESSION:AR108820	c3269	13.8	0.5	20	1	E39195	ACCESSION:E39195
3197	13.8	0.5	19	1	AR108821	ACCESSION:AR108821	c3270	13.8	0.5	20	1	I12653	ACCESSION:I12653
3198	13.8	0.5	19	1	AR108822	ACCESSION:AR108822	3271	13.8	0.5	20	1	I19623	ACCESSION:I19623
3199	13.8	0.5	19	1	AR108823	ACCESSION:AR108823	c3272	13.8	0.5	20	1	I43323	ACCESSION:I43323
3200	13.8	0.5	19	1	AR108826	ACCESSION:AR108826	c3273	13.8	0.5	20	1	I46642	ACCESSION:I46642
3201	13.8	0.5	19	1	AR108827	ACCESSION:AR108827	c3274	13.8	0.5	20	1	I95826	ACCESSION:I95826
3202	13.8	0.5	19	1	AR108828	ACCESSION:AR108828	3275	13.8	0.5	20	1	AR182905	ACCESSION:AR182905
3203	13.8	0.5	19	1	AR108829	ACCESSION:AR108829	c3276	13.8	0.5	20	1	AR182905	ACCESSION:AR182905
3204	13.8	0.5	19	1	BD242593	ACCESSION:BD242593	3277	13.8	0.5	20	1	AR205764	ACCESSION:AR205764
3205	13.8	0.5	19	1	BD269034	ACCESSION:BD269034	3278	13.8	0.5	20	1	AR207166	ACCESSION:AR207166
3206	13.8	0.5	19	1	I38722	ACCESSION:I38722	c3279	13.8	0.5	20	1	AR208724	ACCESSION:AR208724
3207	13.8	0.5	19	1	I62823	ACCESSION:I62823	c3280	13.8	0.5	20	1	AR228938	ACCESSION:AR228938
3208	13.8	0.5	19	1	I81331	ACCESSION:I81331	c3281	13.8	0.5	20	1	AR230963	ACCESSION:AR230963
3209	13.8	0.5	19	1	I88034	ACCESSION:I88034	3282	13.8	0.5	20	1	AR231782	ACCESSION:AR231782
3210	13.8	0.5	19	1	AR202164	ACCESSION:AR202164	3283	13.8	0.5	20	1	AR235921	ACCESSION:AR235921
3211	13.8	0.5	19	1	AR205763	ACCESSION:AR205763	c3284	13.8	0.5	20	1	AR264956	ACCESSION:AR264956
3212	13.8	0.5	19	1	AR205766	ACCESSION:AR205766	c3285	13.8	0.5	20	1	AR264957	ACCESSION:AR264957
3213	13.8	0.5	19	1	AR205768	ACCESSION:AR205768	c3286	13.8	0.5	20	1	AR264958	ACCESSION:AR264958
3214	13.8	0.5	19	1	AR205769	ACCESSION:AR205769	3287	13.8	0.5	20	1	AR268790	ACCESSION:AR268790
3215	13.8	0.5	19	1	AR205770	ACCESSION:AR205770	3288	13.8	0.5	20	1	AR271203	ACCESSION:AR271203
3216	13.8	0.5	19	1	AR205771	ACCESSION:AR205771	c3289	13.8	0.5	20	1	AR274662	ACCESSION:AR274662
3217	13.8	0.5	19	1	AR205772	ACCESSION:AR205772	c3290	13.8	0.5	20	1	AR275179	ACCESSION:AR275179
3218	13.8	0.5	19	1	AR205775	ACCESSION:AR205775	3291	13.8	0.5	20	1	AR278913	ACCESSION:AR278913
3219	13.8	0.5	19	1	AR205776	ACCESSION:AR205776	c3292	13.8	0.5	20	1	AR312181	ACCESSION:AR312181
3220	13.8	0.5	19	1	AR205777	ACCESSION:AR205777	3293	13.8	0.5	20	1	AR313789	ACCESSION:AR313789
3221	13.8	0.5	19	1	AR205778	ACCESSION:AR205778	3294	13.8	0.5	20	1	AR337182	ACCESSION:AR337182
3222	13.8	0.5	19	1	AR280183	ACCESSION:AR280183	c3295	13.8	0.5	20	1	AR344858	ACCESSION:AR344858
3223	13.8	0.5	19	1	AR293201	ACCESSION:AR293201	c3296	13.8	0.5	20	1	AR373535	ACCESSION:AR373535
3224	13.8	0.5	19	1	AR296121	ACCESSION:AR296121	3297	13.8	0.5	20	1	AR438112	ACCESSION:AR438112
3225	13.8	0.5	19	1	AR307194	ACCESSION:AR307194	3298	13.8	0.5	20	1	AX003426	ACCESSION:AX003426
3226	13.8	0.5	19	1	AX011598	ACCESSION:AX011598	c3299	13.8	0.5	20	1	AX008654	ACCESSION:AX008654
c3227	13.8	0.5	19	1	AX130773	ACCESSION:AX130773	c3300	13.8	0.5	20	1	AX046104	ACCESSION:AX046104
c3228	13.8	0.5	19	1	AX131091	ACCESSION:AX131091	3301	13.8	0.5	20	1	AX103947	ACCESSION:AX103947
c3229	13.8	0.5	19	1	AX132837	ACCESSION:AX132837	c3302	13.8	0.5	20	1	AX103947	ACCESSION:AX103947
c3230	13.8	0.5	19	1	AX132840	ACCESSION:AX132840	3303	13.8	0.5	20	1	AX117022	ACCESSION:AX117022
3231	13.8	0.5	19	1	AX378760	ACCESSION:AX378760	c3304	13.8	0.5	20	1	AX117942	ACCESSION:AX117942
3232	13.8	0.5	19	1	AX803976	ACCESSION:AX803976	3305	13.8	0.5	20	1	AX149223	ACCESSION:AX149223
3233	13.8	0.5	19	1	BD103645	ACCESSION:BD103645	c3306	13.8	0.5	20	1	AX166722	ACCESSION:AX166722
3234	13.8	0.5	19	1	BD107601	ACCESSION:BD107601	3307	13.8	0.5	20	1	AX214231	ACCESSION:AX214231
3235	13.8	0.5	19	1	BD196445	ACCESSION:BD196445	c3308	13.8	0.5	20	1	AX294287	ACCESSION:AX294287
3236	13.8	0.5	19	1	BD196765	ACCESSION:BD196765	3309	13.8	0.5	20	1	AX295071	ACCESSION:AX295071
c3237	13.8	0.5	20	1	AR107647	ACCESSION:AR107647	3310	13.8	0.5	20	1	AX295402	ACCESSION:AX295402
c3238	13.8	0.5	20	1	AX048444	ACCESSION:AX048444	c3311	13.8	0.5	20	1	AX298595	ACCESSION:AX298595
3239	13.8	0.5	20	1	AR107644	ACCESSION:AR107644	3312	13.8	0.5	20	1	AX355150	ACCESSION:AX355150
3240	13.8	0.5	20	1	A40401	ACCESSION:A40401	c3313	13.8	0.5	20	1	AX355150	ACCESSION:AX355150
c3241	13.8	0.5	20	1	AR010207	ACCESSION:AR010207	3314	13.8	0.5	20	1	AX356992	ACCESSION:AX356992
3242	13.8	0.5	20	1	AR011627	ACCESSION:AR011627	3315	13.8	0.5	20	1	AX376964	ACCESSION:AX376964
3243	13.8	0.5	20	1	AR030970	ACCESSION:AR030970	c3316	13.8	0.5	20	1	AX397813	ACCESSION:AX397813
c3244	13.8	0.5	20	1	AR031542	ACCESSION:AR031542	3317	13.8	0.5	20	1	AX449244	ACCESSION:AX449244
3245	13.8	0.5	20	1	AR037329	ACCESSION:AR037329	c3318	13.8	0.5	20	1	AX452338	ACCESSION:AX452338

C2735	14.4	0.5	25	1	AX0433367	ACCESSION:AX0433367
2736	14.4	0.5	28	1	BD183015	ACCESSION:BD183015
C2737	14.2	0.5	19	1	I31281	ACCESSION:I31281
C2738	14.2	0.5	19	1	AR211892	ACCESSION:AR211892
C2739	14.2	0.5	19	1	AR294493	ACCESSION:AR294493
2740	14.2	0.5	19	1	AX019945	ACCESSION:AX019945
2741	14.2	0.5	19	1	AX039843	ACCESSION:AX039843
C2742	14.2	0.5	19	1	AX131090	ACCESSION:AX131090
C2743	14.2	0.5	19	1	AX132096	ACCESSION:AX132096
C2744	14.2	0.5	19	1	AX132836	ACCESSION:AX132836
C2745	14.2	0.5	19	1	AX132839	ACCESSION:AX132839
C2746	14.2	0.5	19	1	BD221962	ACCESSION:BD221962
2747	14.2	0.5	20	1	AR118884	ACCESSION:AR118884
C2748	14.2	0.5	20	1	E59334	ACCESSION:E59334
2749	14.2	0.5	20	1	AR360403	ACCESSION:AR360403
2750	14.2	0.5	20	1	AR360430	ACCESSION:AR360430
2751	14.2	0.5	20	1	AX441514	ACCESSION:AX441514
C2752	14.2	0.5	20	1	AX594032	ACCESSION:AX594032
2753	14.2	0.5	20	1	S58563	ACCESSION:S58563
2754	14.2	0.5	20	1	A10280	ACCESSION:A10280
2755	14.2	0.5	20	1	AR026579	ACCESSION:AR026579
C2756	14.2	0.5	20	1	AR036620	ACCESSION:AR036620
C2757	14.2	0.5	20	1	AR079640	ACCESSION:AR079640
C2758	14.2	0.5	20	1	AR085554	ACCESSION:AR085554
2759	14.2	0.5	20	1	AR086217	ACCESSION:AR086217
C2760	14.2	0.5	20	1	AR102403	ACCESSION:AR102403
2761	14.2	0.5	20	1	AR116439	ACCESSION:AR116439
2762	14.2	0.5	20	1	AR122372	ACCESSION:AR122372
C2763	14.2	0.5	20	1	AR123087	ACCESSION:AR123087
2764	14.2	0.5	20	1	AR123336	ACCESSION:AR123336
C2765	14.2	0.5	20	1	AR123336	ACCESSION:AR123336
C2766	14.2	0.5	20	1	AR129678	ACCESSION:AR129678
2767	14.2	0.5	20	1	AR130151	ACCESSION:AR130151
2768	14.2	0.5	20	1	AR158937	ACCESSION:AR158937
2769	14.2	0.5	20	1	AR176783	ACCESSION:AR176783
C2770	14.2	0.5	20	1	E05742	ACCESSION:E05742
2771	14.2	0.5	20	1	E30155	ACCESSION:E30155
2772	14.2	0.5	20	1	E30160	ACCESSION:E30160
2773	14.2	0.5	20	1	E41503	ACCESSION:E41503
C2774	14.2	0.5	20	1	AR201438	ACCESSION:AR201438
2775	14.2	0.5	20	1	AR212010	ACCESSION:AR212010
C2776	14.2	0.5	20	1	AR216074	ACCESSION:AR216074
2777	14.2	0.5	20	1	AR224560	ACCESSION:AR224560
C2778	14.2	0.5	20	1	AR229041	ACCESSION:AR229041
C2779	14.2	0.5	20	1	AR229057	ACCESSION:AR229057
2780	14.2	0.5	20	1	AR230940	ACCESSION:AR230940
C2781	14.2	0.5	20	1	AR241068	ACCESSION:AR241068
C2782	14.2	0.5	20	1	AR264950	ACCESSION:AR264950
C2783	14.2	0.5	20	1	AR264952	ACCESSION:AR264952
C2784	14.2	0.5	20	1	AR293466	ACCESSION:AR293466
2785	14.2	0.5	20	1	AR294519	ACCESSION:AR294519
2786	14.2	0.5	20	1	AR298863	ACCESSION:AR298863
2787	14.2	0.5	20	1	AR311200	ACCESSION:AR311200
C2788	14.2	0.5	20	1	AR314483	ACCESSION:AR314483
C2789	14.2	0.5	20	1	AR342466	ACCESSION:AR342466
2790	14.2	0.5	20	1	AX020020	ACCESSION:AX020020
2791	14.2	0.5	20	1	AX094814	ACCESSION:AX094814
2792	14.2	0.5	20	1	AX109872	ACCESSION:AX109872
2793	14.2	0.5	20	1	AX241251	ACCESSION:AX241251
C2794	14.2	0.5	20	1	AX294679	ACCESSION:AX294679
C2795	14.2	0.5	20	1	AX316300	ACCESSION:AX316300
2796	14.2	0.5	20	1	AX394084	ACCESSION:AX394084
2797	14.2	0.5	20	1	AX487419	ACCESSION:AX487419
2798	14.2	0.5	20	1	AX487788	ACCESSION:AX487788
2799	14.2	0.5	20	1	AX662813	ACCESSION:AX662813
2800	14.2	0.5	20	1	AX708914	ACCESSION:AX708914
2801	14.2	0.5	20	1	AX716655	ACCESSION:AX716655
C2802	14.2	0.5	20	1	AX787157	ACCESSION:AX787157
C2803	14.2	0.5	20	1	BD006253	ACCESSION:BD006253
2804	14.2	0.5	20	1	BD073147	ACCESSION:BD073147
2805	14.2	0.5	20	1	BD074596	ACCESSION:BD074596
2806	14.2	0.5	20	1	BD090423	ACCESSION:BD090423
2807	14.2	0.5	20	1	BD094674	ACCESSION:BD094674
C2808	14.2	0.5	20	1	C2808	ACCESSION:AX0433367
2809	14.2	0.5	20	1	2809	ACCESSION:BD183015
2810	14.2	0.5	20	1	2810	ACCESSION:I31281
C2811	14.2	0.5	20	1	C2811	ACCESSION:AR211892
C2812	14.2	0.5	20	1	C2812	ACCESSION:AR294493
C2813	14.2	0.5	20	1	C2813	ACCESSION:AX019945
2814	14.2	0.5	20	1	2814	ACCESSION:AX039843
C2815	14.2	0.5	20	1	C2815	ACCESSION:AX131090
C2816	14.2	0.5	21	1	C2816	ACCESSION:AX132096
2817	14.2	0.5	21	1	2817	ACCESSION:AX132836
2818	14.2	0.5	21	1	2818	ACCESSION:AX132839
C2819	14.2	0.5	21	1	C2819	ACCESSION:BD221962
C2820	14.2	0.5	21	1	C2820	ACCESSION:AR118884
C2821	14.2	0.5	21	1	C2821	ACCESSION:E59334
2822	14.2	0.5	21	1	2822	ACCESSION:AR360403
2823	14.2	0.5	21	1	2823	ACCESSION:AR360430
C2824	14.2	0.5	21	1	C2824	ACCESSION:AX441514
2825	14.2	0.5	21	1	2825	ACCESSION:AX594032
C2826	14.2	0.5	21	1	C2826	ACCESSION:S58563
C2827	14.2	0.5	21	1	C2827	ACCESSION:A10280
2828	14.2	0.5	21	1	2828	ACCESSION:AR026579
2829	14.2	0.5	21	1	2829	ACCESSION:AR036620
2830	14.2	0.5	21	1	2830	ACCESSION:AR079640
C2831	14.2	0.5	21	1	C2831	ACCESSION:AR085554
C2832	14.2	0.5	21	1	C2832	ACCESSION:AR086217
2833	14.2	0.5	21	1	2833	ACCESSION:AR102403
2834	14.2	0.5	21	1	2834	ACCESSION:AR116439
C2835	14.2	0.5	21	1	C2835	ACCESSION:AR122372
C2836	14.2	0.5	21	1	C2836	ACCESSION:AR123087
2837	14.2	0.5	21	1	2837	ACCESSION:AR123336
C2838	14.2	0.5	21	1	C2838	ACCESSION:AR123336
2839	14.2	0.5	21	1	2839	ACCESSION:AR129678
2840	14.2	0.5	21	1	2840	ACCESSION:AR130151
2841	14.2	0.5	21	1	2841	ACCESSION:AR158937
2842	14.2	0.5	21	1	2842	ACCESSION:AR176783
2843	14.2	0.5	21	1	2843	ACCESSION:E05742
2844	14.2	0.5	21	1	2844	ACCESSION:E30155
2845	14.2	0.5	21	1	2845	ACCESSION:E30160
2846	14.2	0.5	21	1	2846	ACCESSION:E41503
C2847	14.2	0.5	21	1	C2847	ACCESSION:AR201438
2848	14.2	0.5	21	1	2848	ACCESSION:AR212010
C2849	14.2	0.5	21	1	C2849	ACCESSION:AR216074
C2850	14.2	0.5	21	1	C2850	ACCESSION:AR224560
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2852	14.2	0.5	21	1	2852	ACCESSION:AR229057
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C2857	14.2	0.5	21	1	C2857	ACCESSION:AR293466
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2860	14.2	0.5	21	1	2860	ACCESSION:AR311200
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C2867	14.2	0.5	22	1	C2867	ACCESSION:AX294679
C2868	14.2	0.5	23	1	C2868	ACCESSION:AX316300
2869	14.2	0.5	25	1	2869	ACCESSION:AX394084
2870	14.2	0.5	28	1	2870	ACCESSION:AX487419
2871	14	0.5	14	1	2871	ACCESSION:AX487788
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2873	14	0.5	14	1	2873	ACCESSION:AX708914
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2875	14	0.5	14	1	2875	ACCESSION:AX787157
C2876	14	0.5	14	1	C2876	ACCESSION:BD006253
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2879	14	0.5	14	1	2879	ACCESSION:BD090423
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C2882	14.2	0.5	14	1	C2882	ACCESSION:BD183015
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C2890	14.2	0.5	14	1	C2890	ACCESSION:AX132836
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C2591	14.6	0.5	22	1	BD133307	ACCESSION:BD133307
C2592	14.6	0.5	24	1	AX803836	ACCESSION:AX803836
C2593	14.6	0.5	25	1	AX043563	ACCESSION:AX043563
C2594	14.6	0.5	25	1	AX042571	ACCESSION:AX042571
C2595	14.6	0.5	25	1	AX042652	ACCESSION:AX042652
C2596	14.6	0.5	25	1	AX043295	ACCESSION:AX043295
C2597	14.6	0.5	25	1	AX043259	ACCESSION:AX043259
C2598	14.6	0.5	26	1	BD082357	ACCESSION:BD082357
C2599	14.4	0.5	16	1	AX053187	ACCESSION:AX053187
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C2601	14.4	0.5	16	1	AX059786	ACCESSION:AX059786
C2602	14.4	0.5	16	1	AX059827	ACCESSION:AX059827
C2603	14.4	0.5	16	1	AX201949	ACCESSION:AX201949
C2604	14.4	0.5	16	1	AX201990	ACCESSION:AX201990
C2605	14.4	0.5	16	1	AX202013	ACCESSION:AX202013
C2606	14.4	0.5	17	1	AR029854	ACCESSION:AR029854
C2607	14.4	0.5	17	1	AR029855	ACCESSION:AR029855
C2608	14.4	0.5	17	1	BD254621	ACCESSION:BD254621
C2609	14.4	0.5	17	1	BD254815	ACCESSION:BD254815
C2610	14.4	0.5	17	1	BD258525	ACCESSION:BD258525
C2611	14.4	0.5	17	1	BD258578	ACCESSION:BD258578
C2612	14.4	0.5	17	1	BD258579	ACCESSION:BD258579
C2613	14.4	0.5	17	1	AR187057	ACCESSION:AR187057
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C2616	14.4	0.5	17	1	AR286101	ACCESSION:AR286101
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C2619	14.4	0.5	17	1	AR324345	ACCESSION:AR324345
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C2622	14.4	0.5	17	1	AR402072	ACCESSION:AR402072
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2449	14.8	0.5	18	1	AB069627
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2491	14.8	0.5	20	1	AR231311
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2514	14.8	0.5	21	1	AX095108
2515	14.8	0.5	21	1	AX096473

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2517	14.8	0.5	22	1	A83654
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C2520	14.8	0.5	22	1	AX599143
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C2522	14.8	0.5	22	1	AX767637
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c2186	15	0.5	15	1	15	1	AX696087	2259	15	0.5	16	1	1	BD073878	ACCESSION:AX696087
2187	15	0.5	15	1	15	1	AX696087	c2260	15	0.5	17	1	1	BD073879	ACCESSION:AX696087
c2188	15	0.5	15	1	15	1	AX711176	2261	15	0.5	17	1	1	E34258	ACCESSION:AX711176
2189	15	0.5	15	1	15	1	AX711176	c2262	15	0.5	17	1	1	E34259	ACCESSION:AX711176
c2190	15	0.5	15	1	15	1	BD074424	2263	15	0.5	17	1	1	AR187061	ACCESSION:BD074424
2191	15	0.5	15	1	15	1	BD074424	c2264	15	0.5	17	1	1	AR187064	ACCESSION:BD074424
c2192	15	0.5	15	1	15	1	BD084687	2265	15	0.5	17	1	1	AR241830	ACCESSION:BD084687
2193	15	0.5	15	1	15	1	BD084687	c2266	15	0.5	17	1	1	AR266625	ACCESSION:BD084687
c2194	15	0.5	15	1	15	1	BD184668	2267	15	0.5	17	1	1	AR323671	ACCESSION:BD184668
2195	15	0.5	15	1	15	1	BD184668	c2268	15	0.5	17	1	1	AR323674	ACCESSION:BD184668
c2196	15	0.5	15	1	15	1	BD206432	2269	15	0.5	17	1	1	BD011730	ACCESSION:BD206432
2197	15	0.5	15	1	15	1	BD206432	c2270	15	0.5	17	1	1	BD011731	ACCESSION:BD206432
c2198	15	0.5	15	1	15	1	BD209488	2271	15	0.5	17	1	1	BD091742	ACCESSION:BD209488
2199	15	0.5	15	1	15	1	BD209488	c2272	15	0.5	17	1	1	BD091743	ACCESSION:BD209488
c2200	15	0.5	15	1	15	1	AR002257	2273	15	0.5	17	1	1	BD091750	ACCESSION:AR002257
2201	15	0.5	15	1	15	1	AR045207	c2274	15	0.5	17	1	1	BD091751	ACCESSION:AR045207
c2202	15	0.5	15	1	15	1	AR051238	2275	15	0.5	17	1	1	BD091773	ACCESSION:AR051238
2203	15	0.5	15	1	15	1	BD268990	c2276	15	0.5	17	1	1	BD091774	ACCESSION:BD268990
c2204	15	0.5	15	1	15	1	BD268991	2277	15	0.5	17	1	1	BD097334	ACCESSION:BD268991
2205	15	0.5	15	1	15	1	BD274864	c2278	15	0.5	17	1	1	BD097335	ACCESSION:BD274864
c2206	15	0.5	15	1	15	1	I16032	2279	15	0.5	17	1	1	BD142808	ACCESSION:I16032
2207	15	0.5	15	1	15	1	I28367	c2280	15	0.5	17	1	1	BD142809	ACCESSION:I28367
c2208	15	0.5	15	1	15	1	AR221693	2281	15	0.5	17	1	1	BD143834	ACCESSION:AR221693
2209	15	0.5	15	1	15	1	AR221693	c2282	15	0.5	17	1	1	BD143835	ACCESSION:AR221693
c2210	15	0.5	15	1	15	1	AR221694	2283	15	0.5	17	1	1	BD167835	ACCESSION:AR221694
2211	15	0.5	15	1	15	1	AR221694	c2284	15	0.5	17	1	1	BD167836	ACCESSION:AR221694
c2212	15	0.5	15	1	15	1	AR221695	2285	15	0.5	17	1	1	BD167907	ACCESSION:AR221695
2213	15	0.5	15	1	15	1	AR221695	c2286	15	0.5	17	1	1	BD167908	ACCESSION:AR221695
c2214	15	0.5	15	1	15	1	AR221696	2287	15	0.5	17	1	1	BD168111	ACCESSION:AR221696
2215	15	0.5	15	1	15	1	AR221696	c2288	15	0.5	17	1	1	BD168112	ACCESSION:AR221696
c2216	15	0.5	15	1	15	1	AR221697	2289	15	0.5	17	1	1	BD171177	ACCESSION:AR221697
2217	15	0.5	15	1	15	1	AR221697	c2290	15	0.5	17	1	1	BD171178	ACCESSION:AR221697
c2218	15	0.5	15	1	15	1	AR221698	2291	15	0.5	17	1	1	BD217905	ACCESSION:AR221698
2219	15	0.5	15	1	15	1	AR221698	c2292	15	0.5	17	1	1	E34260	ACCESSION:AR221698
c2220	15	0.5	15	1	15	1	AR221992	2293	15	0.5	17	1	1	E34260	ACCESSION:AR221992
2221	15	0.5	15	1	15	1	AR232210	c2294	15	0.5	17	1	1	E59657	ACCESSION:AR232210
c2222	15	0.5	15	1	15	1	AR257438	2295	15	0.5	17	1	1	AR186697	ACCESSION:AR257438
2223	15	0.5	15	1	15	1	AR257438	c2296	15	0.5	17	1	1	AR186698	ACCESSION:AR257438
							AR257439							AR186699	ACCESSION:AR257439

2005	15.4	0.5	22	1	BD206198	ACCESSION:BD206198	c2078	15.2	0.5	22	1	AR152265	ACCESSION:AR152265
2006	15.4	0.5	22	1	BD206199	ACCESSION:BD206199	c2079	15.2	0.5	22	1	AR157803	ACCESSION:AR157803
2007	15.4	0.5	22	1	BD206200	ACCESSION:BD206200	c2080	15.2	0.5	22	1	AX593265	ACCESSION:AX593265
c2008	15.4	0.5	23	1	AX052993	ACCESSION:AX052993	c2081	15.2	0.5	22	1	AX751620	ACCESSION:AX751620
c2009	15.4	0.5	23	1	AX053002	ACCESSION:AX053002	2082	15.2	0.5	22	1	AX817759	ACCESSION:AX817759
c2010	15.4	0.5	23	1	AX038544	ACCESSION:AX038544	2083	15.2	0.5	22	1	BD089101	ACCESSION:BD089101
2011	15.4	0.5	23	1	AX468432	ACCESSION:AX468432	c2084	15.2	0.5	22	1	BD191561	ACCESSION:BD191561
2012	15.4	0.5	24	1	AX498250	ACCESSION:AX498250	2085	15.2	0.5	22	1	AB067984	ACCESSION:AB067984
2013	15.4	0.5	24	1	BD229208	ACCESSION:BD229208	2086	15.2	0.5	23	1	AX164418	ACCESSION:AX164418
2014	15.4	0.5	24	1	AR349460	ACCESSION:AR349460	2087	15.2	0.5	23	1	AX698793	ACCESSION:AX698793
c2015	15.4	0.5	25	1	AX043281	ACCESSION:AX043281	2088	15.2	0.5	23	1	AX771993	ACCESSION:AX771993
2016	15.4	0.5	25	1	AX043100	ACCESSION:AX043100	c2089	15.2	0.5	25	1	I20186	ACCESSION:I20186
c2017	15.4	0.5	25	1	AX043038	ACCESSION:AX043038	c2090	15.2	0.5	25	1	AX042938	ACCESSION:AX042938
c2018	15.4	0.5	25	1	AX042684	ACCESSION:AX042684	2091	15.2	0.5	25	1	AX043680	ACCESSION:AX043680
c2019	15.4	0.5	25	1	AX043487	ACCESSION:AX043487	c2092	15.2	0.5	25	1	AX043297	ACCESSION:AX043297
2020	15.4	0.5	25	1	AX042585	ACCESSION:AX042585	c2093	15.2	0.5	25	1	AX043310	ACCESSION:AX043310
2021	15.4	0.5	25	1	AX043287	ACCESSION:AX043287	c2094	15.2	0.5	25	1	AX043311	ACCESSION:AX043311
2022	15.4	0.5	25	1	AX498245	ACCESSION:AX498245	c2095	15.2	0.5	25	1	AX042593	ACCESSION:AX042593
c2023	15.4	0.5	25	1	AR409905	ACCESSION:AR409905	c2096	15.2	0.5	25	1	AX043312	ACCESSION:AX043312
2024	15.2	0.5	16	1	E52143	ACCESSION:E52143	c2097	15.2	0.5	26	1	AR172578	ACCESSION:AR172578
c2025	15.2	0.5	16	1	E52143	ACCESSION:E52143	c2098	15.2	0.5	26	1	AR430169	ACCESSION:AR430169
2026	15.2	0.5	16	1	E53842	ACCESSION:E53842	2099	15	0.5	15	1	AR029402	ACCESSION:AR029402
c2027	15.2	0.5	16	1	E53842	ACCESSION:E53842	c2100	15	0.5	15	1	AR029402	ACCESSION:AR029402
2028	15.2	0.5	17	1	AR183909	ACCESSION:AR183909	2101	15	0.5	15	1	AR029403	ACCESSION:AR029403
c2029	15.2	0.5	17	1	AR183909	ACCESSION:AR183909	c2102	15	0.5	15	1	AR029403	ACCESSION:AR029403
2030	15.2	0.5	17	1	AR429726	ACCESSION:AR429726	2103	15	0.5	15	1	AR034895	ACCESSION:AR034895
c2031	15.2	0.5	17	1	AR429726	ACCESSION:AR429726	c2104	15	0.5	15	1	AR034895	ACCESSION:AR034895
c2032	15.2	0.5	20	1	AX048436	ACCESSION:AX048436	2105	15	0.5	15	1	AR034898	ACCESSION:AR034898
2033	15.2	0.5	20	1	DOGP34201	ACCESSION:L24226	c2106	15	0.5	15	1	AR034898	ACCESSION:AR034898
c2034	15.2	0.5	20	1	AR099507	ACCESSION:AR099507	2107	15	0.5	15	1	AR048768	ACCESSION:AR048768
c2035	15.2	0.5	20	1	AR118884	ACCESSION:AR118884	c2108	15	0.5	15	1	AR048768	ACCESSION:AR048768
2036	15.2	0.5	20	1	AR137400	ACCESSION:AR137400	2109	15	0.5	15	1	AR049970	ACCESSION:AR049970
2037	15.2	0.5	20	1	AR158936	ACCESSION:AR158936	c2110	15	0.5	15	1	AR049970	ACCESSION:AR049970
c2038	15.2	0.5	20	1	AR163830	ACCESSION:AR163830	2111	15	0.5	15	1	AR049971	ACCESSION:AR049971
c2039	15.2	0.5	20	1	AR174362	ACCESSION:AR174362	c2112	15	0.5	15	1	AR049971	ACCESSION:AR049971
c2040	15.2	0.5	20	1	AR178788	ACCESSION:AR178788	2113	15	0.5	15	1	AR056157	ACCESSION:AR056157
c2041	15.2	0.5	20	1	AR178895	ACCESSION:AR178895	c2114	15	0.5	15	1	AR056157	ACCESSION:AR056157
2042	15.2	0.5	20	1	E59334	ACCESSION:E59334	2115	15	0.5	15	1	AR056158	ACCESSION:AR056158
c2043	15.2	0.5	20	1	I88036	ACCESSION:I88036	c2116	15	0.5	15	1	AR056158	ACCESSION:AR056158
c2044	15.2	0.5	20	1	AR315615	ACCESSION:AR315615	c2117	15	0.5	15	1	AR056159	ACCESSION:AR056159
c2045	15.2	0.5	20	1	AR360398	ACCESSION:AR360398	c2118	15	0.5	15	1	AR056160	ACCESSION:AR056160
c2046	15.2	0.5	20	1	AR360400	ACCESSION:AR360400	2119	15	0.5	15	1	AR080676	ACCESSION:AR080676
c2047	15.2	0.5	20	1	AR360403	ACCESSION:AR360403	c2120	15	0.5	15	1	AR080676	ACCESSION:AR080676
c2048	15.2	0.5	20	1	AR360425	ACCESSION:AR360425	2121	15	0.5	15	1	AR084516	ACCESSION:AR084516
c2049	15.2	0.5	20	1	AR360427	ACCESSION:AR360427	c2122	15	0.5	15	1	AR084516	ACCESSION:AR084516
c2050	15.2	0.5	20	1	AR360430	ACCESSION:AR360430	2123	15	0.5	15	1	AR084520	ACCESSION:AR084520
2051	15.2	0.5	20	1	AR429749	ACCESSION:AR429749	c2124	15	0.5	15	1	AR084520	ACCESSION:AR084520
2052	15.2	0.5	20	1	AX004425	ACCESSION:AX004425	2125	15	0.5	15	1	AR105981	ACCESSION:AR105981
2053	15.2	0.5	20	1	AX048432	ACCESSION:AX048432	c2126	15	0.5	15	1	AR105981	ACCESSION:AR105981
c2054	15.2	0.5	20	1	AX048433	ACCESSION:AX048433	2127	15	0.5	15	1	AR113915	ACCESSION:AR113915
2055	15.2	0.5	20	1	AX048437	ACCESSION:AX048437	c2128	15	0.5	15	1	AR113915	ACCESSION:AR113915
c2056	15.2	0.5	20	1	AX057494	ACCESSION:AX057494	2129	15	0.5	15	1	AR113916	ACCESSION:AR113916
c2057	15.2	0.5	20	1	AX441509	ACCESSION:AX441509	c2130	15	0.5	15	1	AR113916	ACCESSION:AR113916
c2058	15.2	0.5	20	1	AX441511	ACCESSION:AX441511	c2131	15	0.5	15	1	AR113917	ACCESSION:AR113917
c2059	15.2	0.5	20	1	AX441514	ACCESSION:AX441514	c2132	15	0.5	15	1	AR113918	ACCESSION:AR113918
2060	15.2	0.5	20	1	AX594032	ACCESSION:AX594032	2133	15	0.5	15	1	AR170375	ACCESSION:AR170375
c2061	15.2	0.5	20	1	AX786006	ACCESSION:AX786006	c2134	15	0.5	15	1	AR170375	ACCESSION:AR170375
c2062	15.2	0.5	20	1	BD090422	ACCESSION:BD090422	2135	15	0.5	15	1	E08522	ACCESSION:E08522
2063	15.2	0.5	20	1	BD138163	ACCESSION:BD138163	c2136	15	0.5	15	1	E08522	ACCESSION:E08522
c2064	15.2	0.5	20	1	BD176500	ACCESSION:BD176500	2137	15	0.5	15	1	E12591	ACCESSION:E12591
c2065	15.2	0.5	21	1	AX356851	ACCESSION:AX356851	c2138	15	0.5	15	1	E12591	ACCESSION:E12591
2066	15.2	0.5	21	1	AR029929	ACCESSION:AR029929	2139	15	0.5	15	1	I29068	ACCESSION:I29068
c2067	15.2	0.5	21	1	I49863	ACCESSION:I49863	c2140	15	0.5	15	1	I29068	ACCESSION:I29068
2068	15.2	0.5	21	1	AR297993	ACCESSION:AR297993	2141	15	0.5	15	1	I38641	ACCESSION:I38641
c2069	15.2	0.5	21	1	AR298358	ACCESSION:AR298358	c2142	15	0.5	15	1	I38641	ACCESSION:I38641
c2070	15.2	0.5	21	1	AX000973	ACCESSION:AX000973	2143	15	0.5	15	1	AR200476	ACCESSION:AR200476
c2071	15.2	0.5	21	1	AX146093	ACCESSION:AX146093	c2144	15	0.5	15	1	AR200476	ACCESSION:AR200476
2072	15.2	0.5	21	1	AX268236	ACCESSION:AX268236	2145	15	0.5	15	1	AR200477	ACCESSION:AR200477
2073	15.2	0.5	21	1	AX463864	ACCESSION:AX463864	c2146	15	0.5	15	1	AR200477	ACCESSION:AR200477
2074	15.2	0.5	21	1	BD089734	ACCESSION:BD089734	2147	15	0.5	15	1	AR222461	ACCESSION:AR222461
c2075	15.2	0.5	21	1	BD196252	ACCESSION:BD196252	c2148	15	0.5	15	1	AR222461	ACCESSION:AR222461
c2076	15.2	0.5	22	1	AR135198	ACCESSION:AR135198	2149	15	0.5	15	1	AR266630	ACCESSION:AR266630
c2077	15.2	0.5	22	1	AR146694	ACCESSION:AR146694	c2150	15	0.5	15	1	AR266630	ACCESSION:AR266630

c1859	15.8	0.6	20	1	BD168596
c1860	15.8	0.6	21	1	AR084563
c1861	15.8	0.6	21	1	AR084566
c1862	15.8	0.6	21	1	AR084567
c1863	15.8	0.6	21	1	AR084578
c1864	15.8	0.6	21	1	AR084579
c1865	15.8	0.6	21	1	AR084582
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c1867	15.8	0.6	21	1	AR103576
c1868	15.8	0.6	21	1	AX154293
c1869	15.8	0.6	21	1	AX539548
1870	15.8	0.6	21	1	AX539549
c1871	15.8	0.6	21	1	BD129806
c1872	15.8	0.6	22	1	AX103869
c1873	15.8	0.6	22	1	AX546922
1874	15.8	0.6	22	1	BD230925
c1875	15.8	0.6	22	1	AX011524
1876	15.8	0.6	22	1	AX352320
c1877	15.8	0.6	22	1	BD226411
1878	15.8	0.6	23	1	AR053253
c1879	15.8	0.6	23	1	AR053257
1880	15.8	0.6	23	1	AX084400
c1881	15.8	0.6	24	1	AX103868
c1882	15.8	0.6	24	1	AX546921
c1883	15.8	0.6	24	1	A33476
c1884	15.8	0.6	24	1	AR078306
1885	15.8	0.6	24	1	AR078307
c1886	15.8	0.6	24	1	AR116903
c1887	15.8	0.6	24	1	BD229208
c1888	15.8	0.6	24	1	AR349460
1889	15.8	0.6	24	1	AX043137
c1890	15.8	0.6	24	1	BD085850
1891	15.8	0.6	24	1	S81366
1892	15.8	0.6	25	1	BD090045
c1893	15.8	0.6	25	1	AX043131
c1894	15.8	0.6	25	1	AX115872
c1895	15.8	0.6	25	1	AX042590
c1896	15.8	0.6	25	1	AX042992
c1897	15.8	0.6	25	1	I45922
c1898	15.8	0.6	25	1	AX042527
1899	15.8	0.6	25	1	AX042569
c1900	15.8	0.6	25	1	AX043112
1901	15.8	0.6	25	1	AX043284
1902	15.8	0.6	25	1	AX043413
c1903	15.8	0.6	34	1	AR098680
c1904	15.8	0.6	34	1	AR204754
1905	15.6	0.6	17	1	BD233654
c1906	15.6	0.6	17	1	BD233654
c1907	15.6	0.6	17	1	BD217905
c1908	15.6	0.6	22	1	A17252
c1909	15.6	0.6	22	1	AR027635
1910	15.6	0.6	22	1	AR106296
1911	15.6	0.6	22	1	AR178618
1912	15.6	0.6	22	1	AX088188
c1913	15.6	0.6	22	1	AX283017
1914	15.6	0.6	22	1	AX922725
1915	15.6	0.6	22	1	BD073283
1916	15.6	0.6	23	1	AR085444
1917	15.6	0.6	23	1	AR088850
1918	15.6	0.6	23	1	AR167324
1919	15.6	0.6	23	1	I36707
c1920	15.6	0.6	23	1	AX003445
c1921	15.6	0.6	23	1	BD087061
1922	15.6	0.6	24	1	AR162082
1923	15.6	0.6	24	1	AR166607
1924	15.6	0.6	24	1	BD238389
1925	15.6	0.6	24	1	AR279815
1926	15.6	0.6	24	1	A57515
c1927	15.6	0.6	24	1	I30522
c1928	15.6	0.6	24	1	AX207497
1929	15.6	0.6	24	1	AX291683
1930	15.6	0.6	24	1	AX451724
1931	15.6	0.6	24	1	AX493123

1932	15.6	0.6	24	1	AX493955
1933	15.6	0.6	24	1	AX554007
1934	15.6	0.6	24	1	BD082997
1935	15.6	0.6	24	1	BD091788
1936	15.6	0.6	25	1	AX042589
1937	15.6	0.6	25	1	AX043290
c1938	15.6	0.6	25	1	AX042902
1939	15.6	0.6	25	1	AX043108
1940	15.6	0.6	26	1	E31574
1941	15.6	0.6	26	1	AX118414
c1942	15.4	0.5	17	1	AX692524
1943	15.4	0.5	17	1	AR187058
1944	15.4	0.5	17	1	AR187059
1945	15.4	0.5	17	1	AR187060
c1946	15.4	0.5	17	1	AR187065
c1947	15.4	0.5	17	1	AR187066
1948	15.4	0.5	17	1	AR323668
1949	15.4	0.5	17	1	AR323669
1950	15.4	0.5	17	1	AR323670
c1951	15.4	0.5	17	1	AR323675
c1952	15.4	0.5	17	1	AR323676
1953	15.4	0.5	17	1	AX692523
c1954	15.4	0.5	17	1	AX692523
1955	15.4	0.5	17	1	AX692527
c1956	15.4	0.5	17	1	AX692527
1957	15.4	0.5	17	1	AX728891
1958	15.4	0.5	17	1	AX732819
1959	15.4	0.5	17	1	AX760024
c1960	15.4	0.5	18	1	E32456
1961	15.4	0.5	18	1	E32458
c1962	15.4	0.5	18	1	E32453
1963	15.4	0.5	18	1	E32455
c1964	15.4	0.5	18	1	E32459
1965	15.4	0.5	18	1	A67594
1966	15.4	0.5	18	1	AR089732
1967	15.4	0.5	18	1	E32454
c1968	15.4	0.5	18	1	E32457
1969	15.4	0.5	18	1	E32457
c1970	15.4	0.5	18	1	E32457
c1971	15.4	0.5	18	1	E32460
c1972	15.4	0.5	18	1	AX078832
c1973	15.4	0.5	18	1	AX804555
c1974	15.4	0.5	20	1	AR231312
c1975	15.4	0.5	20	1	AR086109
c1976	15.4	0.5	20	1	AR086110
c1977	15.4	0.5	20	1	E13187
c1978	15.4	0.5	20	1	E13188
1979	15.4	0.5	20	1	AX104239
c1980	15.4	0.5	20	1	AX294137
1981	15.4	0.5	20	1	AX355709
1982	15.4	0.5	20	1	AX547292
1983	15.4	0.5	20	1	AX613576
1984	15.4	0.5	20	1	BD171234
1985	15.4	0.5	20	1	BD185850
c1986	15.4	0.5	21	1	AR030787
c1987	15.4	0.5	21	1	AR045091
c1988	15.4	0.5	21	1	AR052947
c1989	15.4	0.5	21	1	AR122900
c1990	15.4	0.5	21	1	AR127822
c1991	15.4	0.5	21	1	AX038542
1992	15.4	0.5	21	1	AX094961
1993	15.4	0.5	21	1	AX095913
1994	15.4	0.5	21	1	AX810934
1995	15.4	0.5	21	1	BD185851
1996	15.4	0.5	22	1	AR003285
1997	15.4	0.5	22	1	AR003286
1998	15.4	0.5	22	1	AR003287
c1999	15.4	0.5	22	1	E36538
c2000	15.4	0.5	22	1	E40160
2001	15.4	0.5	22	1	I30196
2002	15.4	0.5	22	1	I30197
2003	15.4	0.5	22	1	I30198
c2004	15.4	0.5	22	1	AX038543

ACCESSION:BD168596	AX493955
ACCESSION:AR084563	AX554007
ACCESSION:AR084566	BD082997
ACCESSION:AR084567	BD091788
ACCESSION:AR084578	AX042589
ACCESSION:AR084579	AX043290
ACCESSION:AR084582	AX042902
ACCESSION:AR093142	AX043108
ACCESSION:AR103576	AX043108
ACCESSION:AX154293	E31574
ACCESSION:AX539548	AX118414
ACCESSION:AX539549	AX692524
ACCESSION:BD129806	AR187058
ACCESSION:AX103869	AR187059
ACCESSION:AX546922	AR187060
ACCESSION:BD230925	AR187065
ACCESSION:AX011524	AR187066
ACCESSION:AX352320	AR323668
ACCESSION:BD226411	AR323669
ACCESSION:AR053253	AR323670
ACCESSION:AR053257	AR323675
ACCESSION:AX084400	AR323676
ACCESSION:AX103868	AX692523
ACCESSION:AX546921	AX692523
ACCESSION:A33476	AX692527
ACCESSION:AR078306	AX692527
ACCESSION:AR078307	AX728891
ACCESSION:AR116903	AX732819
ACCESSION:BD229208	AX760024
ACCESSION:AR349460	E32456
ACCESSION:AX043137	E32458
ACCESSION:BD085850	E32453
ACCESSION:S81366	E32455
ACCESSION:BD090045	E32459
ACCESSION:AX043131	AX67594
ACCESSION:AX115872	AX089732
ACCESSION:AX042590	E32454
ACCESSION:AX042992	E32454
ACCESSION:I45922	E32457
ACCESSION:AX042527	E32457
ACCESSION:AX042569	E32457
ACCESSION:AX043112	E32460
ACCESSION:AX043284	AX078832
ACCESSION:AX043413	AX804555
ACCESSION:AR098680	AR231312
ACCESSION:AR204754	AR086109
ACCESSION:BD233654	AR086110
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ACCESSION:BD217905	AX038542
ACCESSION:A17252	E13187
ACCESSION:AR027635	E13188
ACCESSION:AR106296	AX104239
ACCESSION:AR178618	AX294137
ACCESSION:AX088188	AX355709
ACCESSION:AX283017	AX547292
ACCESSION:AX922725	AX613576
ACCESSION:BD073283	BD171234
ACCESSION:AR085444	BD185850
ACCESSION:AR088850	AR030787
ACCESSION:AR167324	AR045091
ACCESSION:I36707	AR052947
ACCESSION:AX003445	AR122900
ACCESSION:BD087061	AR127822
ACCESSION:AR162082	AX038542
ACCESSION:AR166607	AX094961
ACCESSION:BD238389	AX095913
ACCESSION:AR279815	AX810934
ACCESSION:A57515	BD185851
ACCESSION:I30522	AR003285
ACCESSION:AX207497	AR003286
ACCESSION:AX291683	AR003287
ACCESSION:AX451724	E36538
ACCESSION:AX493123	E40160

1713	16	0.6	16	1	BD167413	1786	16	0.6	20	1	BD143136	ACCESSION:BD143136
c1714	16	0.6	16	1	BD167413	c1787	16	0.6	20	1	BD143136	ACCESSION:BD143136
1715	16	0.6	16	1	BD167414	c1788	16	0.6	21	1	AR142678	ACCESSION:AR142678
c1716	16	0.6	16	1	BD167414	c1789	16	0.6	21	1	E28097	ACCESSION:E28097
c1717	16	0.6	16	1	AR187062	1790	16	0.6	21	1	AX394604	ACCESSION:AX394604
1718	16	0.6	17	1	AR187063	c1791	16	0.6	21	1	AX394604	ACCESSION:AX394604
c1719	16	0.6	17	1	AR323672	1792	16	0.6	21	1	AX498247	ACCESSION:AX498247
1720	16	0.6	17	1	AR323673	1793	16	0.6	22	1	AX394605	ACCESSION:AX394605
1721	16	0.6	17	1	AX361606	c1794	16	0.6	22	1	AX394605	ACCESSION:AX394605
c1722	16	0.6	17	1	AX692525	c1795	16	0.6	23	1	I79497	ACCESSION:I79497
1723	16	0.6	17	1	AX814938	c1796	16	0.6	23	1	BD133515	ACCESSION:BD133515
1724	16	0.6	17	1	AR172076	c1797	16	0.6	23	1	E12393	ACCESSION:E12393
c1725	16	0.6	17	1	AR172076	c1798	16	0.6	23	1	E12391	ACCESSION:E12391
1726	16	0.6	17	1	AR173367	c1799	16	0.6	23	1	I79499	ACCESSION:I79499
c1727	16	0.6	17	1	AR173367	c1800	16	0.6	23	1	BD187389	ACCESSION:BD187389
1728	16	0.6	17	1	E34258	c1801	16	0.6	23	1	BD245241	ACCESSION:BD245241
c1729	16	0.6	17	1	E34259	c1802	16	0.6	23	1	BD245233	ACCESSION:BD245233
1730	16	0.6	17	1	AR187061	1804	16	0.6	23	1	AX394606	ACCESSION:AX394606
c1731	16	0.6	17	1	AR187064	c1805	16	0.6	23	1	AX394606	ACCESSION:AX394606
c1732	16	0.6	17	1	AR241830	c1806	16	0.6	24	1	I33155	ACCESSION:I33155
1733	16	0.6	17	1	AR266625	1807	16	0.6	24	1	AR081684	ACCESSION:AR081684
1734	16	0.6	17	1	AR323671	c1808	16	0.6	24	1	AR140017	ACCESSION:AR140017
c1735	16	0.6	17	1	AR323674	1809	16	0.6	24	1	BD235199	ACCESSION:BD235199
1736	16	0.6	17	1	AX146683	1810	16	0.6	24	1	AR364668	ACCESSION:AR364668
1737	16	0.6	17	1	AX692524	1811	16	0.6	24	1	AX300680	ACCESSION:AX300680
1738	16	0.6	17	1	AX692526	1812	16	0.6	24	1	AX394608	ACCESSION:AX394608
c1739	16	0.6	17	1	AX692526	c1813	16	0.6	24	1	AX394608	ACCESSION:AX394608
1740	16	0.6	17	1	AX724426	c1814	16	0.6	24	1	BD187293	ACCESSION:BD187293
1741	16	0.6	17	1	BD011730	c1815	16	0.6	25	1	AX042549	ACCESSION:AX042549
c1742	16	0.6	17	1	BD011731	c1816	16	0.6	25	1	AX043230	ACCESSION:AX043230
1743	16	0.6	17	1	BD091742	1817	16	0.6	25	1	AX042901	ACCESSION:AX042901
c1744	16	0.6	17	1	BD091743	c1818	16	0.6	25	1	AX043067	ACCESSION:AX043067
1745	16	0.6	17	1	BD091750	1819	16	0.6	25	1	AX042691	ACCESSION:AX042691
c1746	16	0.6	17	1	BD091751	1820	16	0.6	25	1	AX117632	ACCESSION:AX117632
c1747	16	0.6	17	1	BD091773	c1821	16	0.6	25	1	AX043286	ACCESSION:AX043286
1748	16	0.6	17	1	BD091774	c1822	16	0.6	25	1	AX043616	ACCESSION:AX043616
c1749	16	0.6	17	1	BD097334	1823	16	0.6	25	1	AX042714	ACCESSION:AX042714
1750	16	0.6	17	1	BD097335	c1824	16	0.6	25	1	AX042891	ACCESSION:AX042891
c1751	16	0.6	17	1	BD142808	1825	16	0.6	25	1	AX043076	ACCESSION:AX043076
1752	16	0.6	17	1	BD142809	c1826	16	0.6	25	1	AX043747	ACCESSION:AX043747
c1753	16	0.6	17	1	BD143834	c1827	16	0.6	26	1	E64577	ACCESSION:E64577
1754	16	0.6	17	1	BD143835	c1828	16	0.6	26	1	AR164510	ACCESSION:AR164510
c1755	16	0.6	17	1	BD167835	1829	16	0.6	26	1	AR078461	ACCESSION:AR078461
c1756	16	0.6	17	1	BD167836	1830	16	0.6	27	1	AX589115	ACCESSION:AX589115
1757	16	0.6	17	1	BD167907	1831	16	0.6	28	1	AX394618	ACCESSION:AX394618
c1758	16	0.6	17	1	BD167908	1832	16	0.6	29	1	AX394620	ACCESSION:AX394620
1759	16	0.6	17	1	BD168111	c1833	15.8	0.6	20	1	AX067205	ACCESSION:AX067205
c1760	16	0.6	17	1	BD168112	c1834	15.8	0.6	20	1	A40129	ACCESSION:A40129
1761	16	0.6	17	1	BD171177	c1835	15.8	0.6	20	1	AR065945	ACCESSION:AR065945
c1762	16	0.6	17	1	BD171178	c1836	15.8	0.6	20	1	AR080767	ACCESSION:AR080767
1763	16	0.6	18	1	AX361600	1837	15.8	0.6	20	1	AR107646	ACCESSION:AR107646
c1764	16	0.6	18	1	AX814932	c1838	15.8	0.6	20	1	AR157688	ACCESSION:AR157688
1765	16	0.6	18	1	A14689	c1839	15.8	0.6	20	1	BD243970	ACCESSION:BD243970
c1766	16	0.6	18	1	AR208425	c1840	15.8	0.6	20	1	I25826	ACCESSION:I25826
1767	16	0.6	18	1	AX085251	c1841	15.8	0.6	20	1	I50039	ACCESSION:I50039
c1768	16	0.6	18	1	E32450	c1842	15.8	0.6	20	1	I59872	ACCESSION:I59872
1769	16	0.6	18	1	E32452	1843	15.8	0.6	20	1	AR182885	ACCESSION:AR182885
c1770	16	0.6	18	1	E32453	c1844	15.8	0.6	20	1	AR204058	ACCESSION:AR204058
1771	16	0.6	18	1	E32455	c1845	15.8	0.6	20	1	AR264951	ACCESSION:AR264951
c1772	16	0.6	18	1	E32459	c1846	15.8	0.6	20	1	AR300019	ACCESSION:AR300019
1773	16	0.6	18	1	E32461	c1847	15.8	0.6	20	1	AR309119	ACCESSION:AR309119
c1774	16	0.6	20	1	AR086111	c1848	15.8	0.6	20	1	AR373534	ACCESSION:AR373534
1775	16	0.6	20	1	E13189	1849	15.8	0.6	20	1	AX078047	ACCESSION:AX078047
c1776	16	0.6	20	1	AR309844	1850	15.8	0.6	20	1	AX104051	ACCESSION:AX104051
1777	16	0.6	20	1	AR309844	c1851	15.8	0.6	20	1	AX184029	ACCESSION:AX184029
c1778	16	0.6	20	1	AR312356	1852	15.8	0.6	20	1	AX355382	ACCESSION:AX355382
1779	16	0.6	20	1	AX048445	c1853	15.8	0.6	20	1	AX495922	ACCESSION:AX495922
c1780	16	0.6	20	1	AX048447	1854	15.8	0.6	20	1	AX547104	ACCESSION:AX547104
1781	16	0.6	20	1	AX224877	c1855	15.8	0.6	20	1	AX645713	ACCESSION:AX645713
c1782	16	0.6	20	1	AX394603	1856	15.8	0.6	20	1	BD069976	ACCESSION:BD069976
1783	16	0.6	20	1	AX394603	1857	15.8	0.6	20	1	BD128070	ACCESSION:BD128070
c1784	16	0.6	20	1	AX404077	1858	15.8	0.6	20	1	BD128107	ACCESSION:BD128107
1785	16	0.6	20	1	AX404077							

c1567	16.6	0.6	25	1	AX043108	ACCESSION:AX043108	c1640	16.4	0.6	35	1	A63566	ACCESSION:A63566
c1568	16.6	0.6	25	1	AX043216	ACCESSION:AX043216	1641	16.2	0.6	21	1	AR142678	ACCESSION:AR142678
1569	16.6	0.6	25	1	AX043257	ACCESSION:AX043257	1642	16.2	0.6	21	1	BD246728	ACCESSION:BD246728
c1570	16.6	0.6	25	1	AX043259	ACCESSION:AX043259	1643	16.2	0.6	21	1	E28097	ACCESSION:E28097
1571	16.6	0.6	25	1	AX043286	ACCESSION:AX043286	c1644	16.2	0.6	21	1	AR241776	ACCESSION:AR241776
1572	16.6	0.6	25	1	AX043312	ACCESSION:AX043312	1645	16.2	0.6	21	1	AR296425	ACCESSION:AR296425
1573	16.6	0.6	25	1	AX043616	ACCESSION:AX043616	1646	16.2	0.6	21	1	AX026215	ACCESSION:AX026215
c1574	16.6	0.6	25	1	AX043642	ACCESSION:AX043642	c1647	16.2	0.6	22	1	AX457060	ACCESSION:AX457060
1575	16.6	0.6	25	1	AX104992	ACCESSION:AX104992	1648	16.2	0.6	24	1	A93098	ACCESSION:A93098
1576	16.6	0.6	25	1	BD074369	ACCESSION:BD074369	1649	16.2	0.6	24	1	AR091179	ACCESSION:AR091179
1577	16.6	0.6	25	1	BD074392	ACCESSION:BD074392	1650	16.2	0.6	24	1	AR174054	ACCESSION:AR174054
c1578	16.6	0.6	25	1	BD08021	ACCESSION:BD08021	1651	16.2	0.6	24	1	AR198214	ACCESSION:AR198214
1579	16.6	0.6	25	1	AJ588309	ACCESSION:AJ588309	1652	16.2	0.6	24	1	AR260368	ACCESSION:AR260368
c1580	16.6	0.6	25	1	AB068802	ACCESSION:AB068802	1653	16.2	0.6	24	1	AX377075	ACCESSION:AX377075
c1581	16.6	0.6	25	1	E04206	ACCESSION:E04206	1654	16.2	0.6	24	1	BD064144	ACCESSION:BD064144
1582	16.4	0.6	18	1	AR208427	ACCESSION:AR208427	c1655	16.2	0.6	25	1	A85331	ACCESSION:A85331
1583	16.4	0.6	18	1	AX085253	ACCESSION:AX085253	c1656	16.2	0.6	25	1	AR370671	ACCESSION:AR370671
1584	16.4	0.6	18	1	A14689	ACCESSION:A14689	c1657	16.2	0.6	25	1	AR431257	ACCESSION:AR431257
c1585	16.4	0.6	18	1	AR208425	ACCESSION:AR208425	c1658	16.2	0.6	25	1	BD057791	ACCESSION:BD057791
1586	16.4	0.6	18	1	AR208426	ACCESSION:AR208426	c1659	16.2	0.6	25	1	AX042981	ACCESSION:AX042981
c1587	16.4	0.6	18	1	AR208426	ACCESSION:AR208426	1660	16.2	0.6	25	1	AX115700	ACCESSION:AX115700
c1588	16.4	0.6	18	1	AX085251	ACCESSION:AX085251	1661	16.2	0.6	25	1	AX042591	ACCESSION:AX042591
1589	16.4	0.6	18	1	AX085252	ACCESSION:AX085252	1662	16.2	0.6	25	1	AX043292	ACCESSION:AX043292
c1590	16.4	0.6	18	1	AX085252	ACCESSION:AX085252	1663	16.2	0.6	25	1	AX043119	ACCESSION:AX043119
1591	16.4	0.6	20	1	E59328	ACCESSION:E59328	c1664	16.2	0.6	25	1	AR104584	ACCESSION:AR104584
1592	16.4	0.6	20	1	AR231312	ACCESSION:AR231312	1665	16.2	0.6	16	1	AR104584	ACCESSION:AR104584
1593	16.4	0.6	20	1	AX048436	ACCESSION:AX048436	1666	16	0.6	16	1	AR175845	ACCESSION:AR175845
1594	16.4	0.6	20	1	AX326966	ACCESSION:AX326966	c1667	16	0.6	16	1	AR175845	ACCESSION:AR175845
1595	16.4	0.6	21	1	AX356851	ACCESSION:AX356851	1668	16	0.6	16	1	BD259919	ACCESSION:BD259919
1596	16.4	0.6	21	1	AX838805	ACCESSION:AX838805	c1669	16	0.6	16	1	BD268989	ACCESSION:BD268989
1597	16.4	0.6	22	1	AR003288	ACCESSION:AR003288	1670	16	0.6	16	1	I38676	ACCESSION:I38676
1598	16.4	0.6	22	1	I30199	ACCESSION:I30199	c1671	16	0.6	16	1	I38676	ACCESSION:I38676
1599	16.4	0.6	22	1	BD206201	ACCESSION:BD206201	1672	16	0.6	16	1	I38682	ACCESSION:I38682
1600	16.4	0.6	23	1	AR123791	ACCESSION:AR123791	c1673	16	0.6	16	1	I38700	ACCESSION:I38700
1601	16.4	0.6	23	1	BD245238	ACCESSION:BD245238	1674	16	0.6	16	1	I38700	ACCESSION:I38700
1602	16.4	0.6	23	1	BD245242	ACCESSION:BD245242	1675	16	0.6	16	1	AR221692	ACCESSION:AR221692
1603	16.4	0.6	23	1	AX052992	ACCESSION:AX052992	c1676	16	0.6	16	1	AR222462	ACCESSION:AR222462
1604	16.4	0.6	23	1	AX052993	ACCESSION:AX052993	1677	16	0.6	16	1	AR222462	ACCESSION:AR222462
1605	16.4	0.6	23	1	AX053002	ACCESSION:AX053002	c1678	16	0.6	16	1	AR227681	ACCESSION:AR227681
c1606	16.4	0.6	24	1	AR162082	ACCESSION:AR162082	1679	16	0.6	16	1	AR232208	ACCESSION:AR232208
c1607	16.4	0.6	24	1	AR166607	ACCESSION:AR166607	c1680	16	0.6	16	1	AR257437	ACCESSION:AR257437
c1608	16.4	0.6	24	1	BD238389	ACCESSION:BD238389	1681	16	0.6	16	1	AR257437	ACCESSION:AR257437
1609	16.4	0.6	24	1	AR257304	ACCESSION:AR257304	c1682	16	0.6	16	1	AR266618	ACCESSION:AR266618
c1610	16.4	0.6	24	1	AR279815	ACCESSION:AR279815	1683	16	0.6	16	1	AR266645	ACCESSION:AR266645
1611	16.4	0.6	24	1	AX043291	ACCESSION:AX043291	c1684	16	0.6	16	1	AR282683	ACCESSION:AR282683
c1612	16.4	0.6	24	1	AX498250	ACCESSION:AX498250	1685	16	0.6	16	1	AR369775	ACCESSION:AR369775
1613	16.4	0.6	25	1	AX043077	ACCESSION:AX043077	c1686	16	0.6	16	1	AR429377	ACCESSION:AR429377
c1614	16.4	0.6	25	1	AX043412	ACCESSION:AX043412	1687	16	0.6	16	1	AX039049	ACCESSION:AX039049
c1615	16.4	0.6	25	1	AX043581	ACCESSION:AX043581	1688	16	0.6	16	1	AX127437	ACCESSION:AX127437
c1616	16.4	0.6	25	1	AX042984	ACCESSION:AX042984	c1689	16	0.6	16	1	AX146679	ACCESSION:AX146679
c1617	16.4	0.6	25	1	AX043693	ACCESSION:AX043693	1690	16	0.6	16	1	AX235176	ACCESSION:AX235176
c1618	16.4	0.6	25	1	AX692829	ACCESSION:AX692829	1691	16	0.6	16	1	AX235176	ACCESSION:AX235176
1619	16.4	0.6	25	1	AX043114	ACCESSION:AX043114	1692	16	0.6	16	1	AX253409	ACCESSION:AX253409
1620	16.4	0.6	25	1	AX042547	ACCESSION:AX042547	1693	16	0.6	16	1	AX306362	ACCESSION:AX306362
c1621	16.4	0.6	25	1	AX042585	ACCESSION:AX042585	1694	16	0.6	16	1	AX320075	ACCESSION:AX320075
c1622	16.4	0.6	25	1	AX042614	ACCESSION:AX042614	1695	16	0.6	16	1	AX352386	ACCESSION:AX352386
1623	16.4	0.6	25	1	AX042616	ACCESSION:AX042616	c1696	16	0.6	16	1	AX391467	ACCESSION:AX391467
c1624	16.4	0.6	25	1	AX042714	ACCESSION:AX042714	1697	16	0.6	16	1	AX394754	ACCESSION:AX394754
1625	16.4	0.6	25	1	AX042891	ACCESSION:AX042891	1698	16	0.6	16	1	AX394785	ACCESSION:AX394785
c1626	16.4	0.6	25	1	AX043076	ACCESSION:AX043076	1699	16	0.6	16	1	AX419606	ACCESSION:AX419606
1627	16.4	0.6	25	1	AX043184	ACCESSION:AX043184	c1700	16	0.6	16	1	AX522006	ACCESSION:AX522006
c1628	16.4	0.6	25	1	AX043287	ACCESSION:AX043287	1701	16	0.6	16	1	BD073502	ACCESSION:BD073502
1629	16.4	0.6	25	1	AX043367	ACCESSION:AX043367	1702	16	0.6	16	1	BD073877	ACCESSION:BD073877
1630	16.4	0.6	25	1	AX043374	ACCESSION:AX043374	1703	16	0.6	16	1	BD138638	ACCESSION:BD138638
1631	16.4	0.6	25	1	AX043481	ACCESSION:AX043481	1704	16	0.6	16	1		
1632	16.4	0.6	25	1	AX043747	ACCESSION:AX043747	1705	16	0.6	16	1		
c1633	16.4	0.6	25	1	AX498245	ACCESSION:AX498245	1706	16	0.6	16	1		
1634	16.4	0.6	25	1	AX692820	ACCESSION:AX692820	1707	16	0.6	16	1		
c1635	16.4	0.6	25	1	AX692820	ACCESSION:AX692820	1708	16	0.6	16	1		
1636	16.4	0.6	25	1	AX692830	ACCESSION:AX692830	1709	16	0.6	16	1		
c1637	16.4	0.6	25	1	AX692830	ACCESSION:AX692830	1710	16	0.6	16	1		
1638	16.4	0.6	26	1	A63569	ACCESSION:A63569	1711	16	0.6	16	1		
1639	16.4	0.6	30	1	AX351711	ACCESSION:AX351711	1712	16	0.6	16	1		

c1421	17	0.6	23	1	BD245245	ACCESSION:BD245245	17	0.6	26	1	AX118414	ACCESSION:AX118414
c1422	17	0.6	23	1	AR084981	ACCESSION:AR084981	17	0.6	26	1	BD169479	ACCESSION:BD169479
c1423	17	0.6	23	1	I32906	ACCESSION:I32906	17	0.6	28	1	AR055108	ACCESSION:AR055108
c1424	17	0.6	23	1	AR306617	ACCESSION:AR306617	17	0.6	28	1	AR055109	ACCESSION:AR055109
c1425	17	0.6	23	1	BD105197	ACCESSION:BD105197	17	0.6	28	1	AR068449	ACCESSION:AR068449
c1426	17	0.6	23	1	BD245234	ACCESSION:BD245234	17	0.6	28	1	AR068450	ACCESSION:AR068450
c1427	17	0.6	23	1	BD245241	ACCESSION:BD245241	17	0.6	28	1	AR162868	ACCESSION:AR162868
c1428	17	0.6	23	1	AX496104	ACCESSION:AX496104	17	0.6	29	1	AR194018	ACCESSION:AR194018
c1429	17	0.6	23	1	AX496104	ACCESSION:AX496104	17	0.6	29	1	AR093063	ACCESSION:AR093063
c1430	17	0.6	23	1	I33155	ACCESSION:I33155	17	0.6	20	1	AR107647	ACCESSION:AR107647
c1431	17	0.6	25	1	AX043282	ACCESSION:AX043282	17	0.6	20	1	AR163839	ACCESSION:AR163839
c1432	17	0.6	25	1	AX043152	ACCESSION:AX043152	17	0.6	20	1	E12411	ACCESSION:E12411
c1433	17	0.6	25	1	I56670	ACCESSION:I56670	17	0.6	20	1	AR359565	ACCESSION:AR359565
c1434	17	0.6	25	1	AR211579	ACCESSION:AR211579	17	0.6	20	1	AR360401	ACCESSION:AR360401
c1435	17	0.6	25	1	AR434873	ACCESSION:AR434873	17	0.6	20	1	AR360428	ACCESSION:AR360428
c1436	17	0.6	25	1	AR435380	ACCESSION:AR435380	17	0.6	20	1	AR371269	ACCESSION:AR371269
c1437	17	0.6	25	1	AR435381	ACCESSION:AR435381	17	0.6	20	1	AX067205	ACCESSION:AX067205
c1438	17	0.6	25	1	AX042591	ACCESSION:AX042591	17	0.6	20	1	AX441512	ACCESSION:AX441512
c1439	17	0.6	25	1	AX042684	ACCESSION:AX042684	17	0.6	20	1	BD196314	ACCESSION:BD196314
c1440	17	0.6	25	1	AX042691	ACCESSION:AX042691	17	0.6	20	1	AR066407	ACCESSION:AR066407
c1441	17	0.6	25	1	AX042718	ACCESSION:AX042718	17	0.6	22	1	ACCESSION:D50257	ACCESSION:D50257
c1442	17	0.6	25	1	AX042718	ACCESSION:AX042718	17	0.6	22	1	ACCESSION:BD245233	ACCESSION:BD245233
c1443	17	0.6	25	1	AX042718	ACCESSION:AX042718	17	0.6	23	1	ACCESSION:BD245237	ACCESSION:BD245237
c1444	17	0.6	25	1	AX042825	ACCESSION:AX042825	17	0.6	23	1	AX053001	ACCESSION:AX053001
c1445	17	0.6	25	1	AX042938	ACCESSION:AX042938	17	0.6	23	1	AX053001	ACCESSION:AX053001
c1446	17	0.6	25	1	AX042984	ACCESSION:AX042984	17	0.6	23	1	AX115478	ACCESSION:AX115478
c1447	17	0.6	25	1	AX043019	ACCESSION:AX043019	17	0.6	23	1	AX115478	ACCESSION:AX115478
c1448	17	0.6	25	1	AX043034	ACCESSION:AX043034	17	0.6	24	1	AX803836	ACCESSION:AX803836
c1449	17	0.6	25	1	AX043034	ACCESSION:AX043034	17	0.6	25	1	AX692828	ACCESSION:AX692828
c1450	17	0.6	25	1	AX043035	ACCESSION:AX043035	17	0.6	25	1	I45922	ACCESSION:I45922
c1451	17	0.6	25	1	AX043035	ACCESSION:AX043035	17	0.6	25	1	AR435374	ACCESSION:AR435374
c1452	17	0.6	25	1	AX043035	ACCESSION:AX043035	17	0.6	25	1	AX042527	ACCESSION:AX042527
c1453	17	0.6	25	1	AX043045	ACCESSION:AX043045	17	0.6	25	1	AX042543	ACCESSION:AX042543
c1454	17	0.6	25	1	AX043060	ACCESSION:AX043060	17	0.6	25	1	AX042569	ACCESSION:AX042569
c1455	17	0.6	25	1	AX043082	ACCESSION:AX043082	17	0.6	25	1	AX042831	ACCESSION:AX042831
c1456	17	0.6	25	1	AX043206	ACCESSION:AX043206	17	0.6	25	1	AX042902	ACCESSION:AX042902
c1457	17	0.6	25	1	AX043237	ACCESSION:AX043237	17	0.6	25	1	AX042933	ACCESSION:AX042933
c1458	17	0.6	25	1	AX043292	ACCESSION:AX043292	17	0.6	25	1	AX043112	ACCESSION:AX043112
c1459	17	0.6	25	1	AX043296	ACCESSION:AX043296	17	0.6	25	1	AX043114	ACCESSION:AX043114
c1460	17	0.6	25	1	AX043461	ACCESSION:AX043461	17	0.6	25	1	AX043119	ACCESSION:AX043119
c1461	17	0.6	25	1	AX043487	ACCESSION:AX043487	17	0.6	25	1	AX043218	ACCESSION:AX043218
c1462	17	0.6	25	1	AX043647	ACCESSION:AX043647	17	0.6	25	1	AX043284	ACCESSION:AX043284
c1463	17	0.6	25	1	AX043651	ACCESSION:AX043651	17	0.6	25	1	AX043295	ACCESSION:AX043295
c1464	17	0.6	25	1	AX043651	ACCESSION:AX043651	17	0.6	25	1	AX043297	ACCESSION:AX043297
c1465	17	0.6	25	1	AX043680	ACCESSION:AX043680	17	0.6	25	1	AX043310	ACCESSION:AX043310
c1466	17	0.6	25	1	AX043693	ACCESSION:AX043693	17	0.6	25	1	AX043311	ACCESSION:AX043311
c1467	17	0.6	25	1	AX104751	ACCESSION:AX104751	17	0.6	25	1	AX043318	ACCESSION:AX043318
c1468	17	0.6	25	1	AX104751	ACCESSION:AX104751	17	0.6	25	1	AX043413	ACCESSION:AX043413
c1469	17	0.6	25	1	AX117632	ACCESSION:AX117632	17	0.6	25	1	AX744661	ACCESSION:AX744661
c1470	17	0.6	25	1	AX166683	ACCESSION:AX166683	17	0.6	25	1	ACCESSION:AX744667	ACCESSION:AX744667
c1471	17	0.6	25	1	AX320851	ACCESSION:AX320851	17	0.6	25	1	ACCESSION:I16929	ACCESSION:I16929
c1472	17	0.6	25	1	AX494260	ACCESSION:AX494260	17	0.6	24	1	ACCESSION:AX093547	ACCESSION:AX093547
c1473	17	0.6	25	1	AX494261	ACCESSION:AX494261	17	0.6	24	1	ACCESSION:BD143588	ACCESSION:BD143588
c1474	17	0.6	25	1	AX494264	ACCESSION:AX494264	17	0.6	25	1	ACCESSION:AX043064	ACCESSION:AX043064
c1475	17	0.6	25	1	AX547804	ACCESSION:AX547804	17	0.6	25	1	ACCESSION:AX043082	ACCESSION:AX043082
c1476	17	0.6	25	1	AX547804	ACCESSION:AX547804	17	0.6	25	1	ACCESSION:AX320851	ACCESSION:AX320851
c1477	17	0.6	25	1	AX692828	ACCESSION:AX692828	17	0.6	25	1	ACCESSION:AX042831	ACCESSION:AX042831
c1478	17	0.6	25	1	BD075857	ACCESSION:BD075857	17	0.6	25	1	ACCESSION:AR028113	ACCESSION:AR028113
c1479	17	0.6	25	1	AJ595474	ACCESSION:AJ595474	17	0.6	25	1	ACCESSION:AR030289	ACCESSION:AR030289
c1480	17	0.6	26	1	AR010003	ACCESSION:AR010003	17	0.6	25	1	ACCESSION:AR065818	ACCESSION:AR065818
c1481	17	0.6	26	1	AR034738	ACCESSION:AR034738	17	0.6	25	1	ACCESSION:AR146859	ACCESSION:AR146859
c1482	17	0.6	26	1	I24758	ACCESSION:I24758	17	0.6	25	1	ACCESSION:E55072	ACCESSION:E55072
c1483	17	0.6	26	1	AR050239	ACCESSION:AR050239	17	0.6	25	1	ACCESSION:I42108	ACCESSION:I42108
c1484	17	0.6	26	1	AX055876	ACCESSION:AX055876	17	0.6	25	1	ACCESSION:AR435047	ACCESSION:AR435047
c1485	17	0.6	26	1	AR034927	ACCESSION:AR034927	17	0.6	25	1	ACCESSION:AR435048	ACCESSION:AR435048
c1486	17	0.6	26	1	AR078461	ACCESSION:AR078461	17	0.6	25	1	ACCESSION:AR435049	ACCESSION:AR435049
c1487	17	0.6	26	1	AR145386	ACCESSION:AR145386	17	0.6	25	1	ACCESSION:AX000308	ACCESSION:AX000308
c1488	17	0.6	26	1	E31574	ACCESSION:E31574	17	0.6	25	1	ACCESSION:AX000331	ACCESSION:AX000331
c1489	17	0.6	26	1	I18346	ACCESSION:I18346	17	0.6	25	1	ACCESSION:AX042593	ACCESSION:AX042593
c1490	17	0.6	26	1	I21333	ACCESSION:I21333	17	0.6	25	1	ACCESSION:AX042904	ACCESSION:AX042904
c1491	17	0.6	26	1	I35739	ACCESSION:I35739	17	0.6	25	1	ACCESSION:AX042952	ACCESSION:AX042952
c1492	17	0.6	26	1	I36757	ACCESSION:I36757	17	0.6	25	1	ACCESSION:AX042955	ACCESSION:AX042955
c1493	17	0.6	26	1	I40322	ACCESSION:I40322	17	0.6	25	1	ACCESSION:AX042962	ACCESSION:AX042962

c1275	17.4	0.6	20	1	AX136903	ACCESSION:AX136903
c1276	17.4	0.6	20	1	E59328	ACCESSION:E59328
c1277	17.4	0.6	21	1	AR241831	ACCESSION:AR241831
1278	17.4	0.6	21	1	AX838821	ACCESSION:AX838821
1279	17.4	0.6	23	1	E12392	ACCESSION:E12392
c1280	17.4	0.6	23	1	E12392	ACCESSION:E12392
1281	17.4	0.6	23	1	I79498	ACCESSION:I79498
c1282	17.4	0.6	23	1	I79498	ACCESSION:I79498
c1283	17.4	0.6	24	1	AR431312	ACCESSION:AR431312
c1284	17.4	0.6	24	1	AR431308	ACCESSION:AR431308
c1285	17.4	0.6	25	1	AX043130	ACCESSION:AX043130
c1286	17.4	0.6	25	1	AX115988	ACCESSION:AX115988
1287	17.4	0.6	25	1	AX042590	ACCESSION:AX042590
c1288	17.4	0.6	25	1	AX043064	ACCESSION:AX043064
1289	17.4	0.6	25	1	AX043581	ACCESSION:AX043581
1290	17.4	0.6	25	1	AX117576	ACCESSION:AX117576
c1291	17.4	0.6	25	1	AX117576	ACCESSION:AX117576
1292	17.4	0.6	25	1	AX692821	ACCESSION:AX692821
c1293	17.4	0.6	25	1	AX692821	ACCESSION:AX692821
1294	17.4	0.6	25	1	AX692822	ACCESSION:AX692822
c1295	17.4	0.6	25	1	AX692822	ACCESSION:AX692822
c1296	17.4	0.6	25	1	AR006733	ACCESSION:AR006733
1297	17.4	0.6	28	1	AR055117	ACCESSION:AR055117
1298	17.4	0.6	28	1	AR068458	ACCESSION:AR068458
c1299	17.4	0.6	30	1	AR264925	ACCESSION:AR264925
c1300	17.4	0.6	30	1	BD072870	ACCESSION:BD072870
c1301	17.4	0.6	30	1	BD107497	ACCESSION:BD107497
c1302	17.4	0.6	30	1	BD145029	ACCESSION:BD145029
c1303	17.4	0.6	30	1	BD166029	ACCESSION:BD166029
c1304	17.4	0.6	30	1	AR264926	ACCESSION:AR264926
c1305	17.4	0.6	30	1	AR264927	ACCESSION:AR264927
c1306	17.4	0.6	30	1	BD072871	ACCESSION:BD072871
c1307	17.4	0.6	30	1	BD072872	ACCESSION:BD072872
c1308	17.4	0.6	30	1	BD107498	ACCESSION:BD107498
c1309	17.4	0.6	30	1	BD107499	ACCESSION:BD107499
c1310	17.4	0.6	30	1	BD145030	ACCESSION:BD145030
c1311	17.4	0.6	30	1	BD145031	ACCESSION:BD145031
c1312	17.4	0.6	30	1	BD166030	ACCESSION:BD166030
c1313	17.4	0.6	30	1	BD166031	ACCESSION:BD166031
c1314	17.4	0.6	30	1	AR264920	ACCESSION:AR264920
c1315	17.4	0.6	30	1	BD072865	ACCESSION:BD072865
c1316	17.4	0.6	30	1	BD107492	ACCESSION:BD107492
c1317	17.4	0.6	30	1	BD145024	ACCESSION:BD145024
c1318	17.4	0.6	30	1	BD166025	ACCESSION:BD166025
c1319	17.4	0.6	30	1	AR264921	ACCESSION:AR264921
c1320	17.4	0.6	30	1	AR264922	ACCESSION:AR264922
c1321	17.4	0.6	30	1	AR264923	ACCESSION:AR264923
c1322	17.4	0.6	30	1	AR264924	ACCESSION:AR264924
c1323	17.4	0.6	30	1	AR264928	ACCESSION:AR264928
c1324	17.4	0.6	30	1	AR264929	ACCESSION:AR264929
c1325	17.4	0.6	30	1	BD072866	ACCESSION:BD072866
c1326	17.4	0.6	30	1	BD072867	ACCESSION:BD072867
c1327	17.4	0.6	30	1	BD072868	ACCESSION:BD072868
c1328	17.4	0.6	30	1	BD072869	ACCESSION:BD072869
c1329	17.4	0.6	30	1	BD072873	ACCESSION:BD072873
c1330	17.4	0.6	30	1	BD072874	ACCESSION:BD072874
c1331	17.4	0.6	30	1	BD107493	ACCESSION:BD107493
c1332	17.4	0.6	30	1	BD107494	ACCESSION:BD107494
c1333	17.4	0.6	30	1	BD107495	ACCESSION:BD107495
c1334	17.4	0.6	30	1	BD107496	ACCESSION:BD107496
c1335	17.4	0.6	30	1	BD107500	ACCESSION:BD107500
c1336	17.4	0.6	30	1	BD107501	ACCESSION:BD107501
c1337	17.4	0.6	30	1	BD145025	ACCESSION:BD145025
c1338	17.4	0.6	30	1	BD145026	ACCESSION:BD145026
c1339	17.4	0.6	30	1	BD145027	ACCESSION:BD145027
c1340	17.4	0.6	30	1	BD145028	ACCESSION:BD145028
c1341	17.4	0.6	30	1	BD145032	ACCESSION:BD145032
c1342	17.4	0.6	30	1	BD145033	ACCESSION:BD145033
c1343	17.4	0.6	30	1	BD166026	ACCESSION:BD166026
c1344	17.4	0.6	30	1	BD166027	ACCESSION:BD166027
c1345	17.4	0.6	30	1	BD166028	ACCESSION:BD166028
c1346	17.4	0.6	30	1	BD166032	ACCESSION:BD166032
c1347	17.4	0.6	30	1	BD166033	ACCESSION:BD166033

c1348	17.4	0.6	30	1	BD166129	ACCESSION:BD166129
1349	17.2	0.6	19	1	AR163080	ACCESSION:AR163080
c1350	17.2	0.6	19	1	AR163080	ACCESSION:AR163080
1351	17.2	0.6	19	1	E08331	ACCESSION:E08331
c1352	17.2	0.6	19	1	E08331	ACCESSION:E08331
1353	17.2	0.6	20	1	E08332	ACCESSION:E08332
c1354	17.2	0.6	20	1	E08332	ACCESSION:E08332
1355	17.2	0.6	21	1	E08333	ACCESSION:E08333
c1356	17.2	0.6	21	1	E08333	ACCESSION:E08333
c1357	17.2	0.6	23	1	AX457061	ACCESSION:AX457061
c1358	17.2	0.6	23	1	BD245234	ACCESSION:BD245234
c1359	17.2	0.6	23	1	BD245238	ACCESSION:BD245238
c1360	17.2	0.6	23	1	BD245242	ACCESSION:BD245242
1361	17.2	0.6	23	1	I79499	ACCESSION:I79499
c1362	17.2	0.6	23	1	AX053000	ACCESSION:AX053000
c1363	17.2	0.6	23	1	AX119432	ACCESSION:AX119432
c1364	17.2	0.6	23	1	AX921569	ACCESSION:AX921569
1365	17.2	0.6	23	1	BD187389	ACCESSION:BD187389
1366	17.2	0.6	25	1	BD244864	ACCESSION:BD244864
c1367	17.2	0.6	25	1	AX042923	ACCESSION:AX042923
c1368	17.2	0.6	25	1	AX042823	ACCESSION:AX042823
c1369	17.2	0.6	25	1	AX042978	ACCESSION:AX042978
1370	17.2	0.6	25	1	AX042992	ACCESSION:AX042992
1371	17.2	0.6	25	1	AX043038	ACCESSION:AX043038
1372	17.2	0.6	25	1	AX043067	ACCESSION:AX043067
c1373	17.2	0.6	26	1	AX055876	ACCESSION:AX055876
1374	17.2	0.6	26	1	BD082357	ACCESSION:BD082357
c1375	17.2	0.6	28	1	AR022650	ACCESSION:AR022650
c1376	17.2	0.6	28	1	AR150988	ACCESSION:AR150988
c1377	17.2	0.6	28	1	AR156058	ACCESSION:AR156058
c1378	17.2	0.6	28	1	AR172065	ACCESSION:AR172065
c1379	17.2	0.6	28	1	AR173356	ACCESSION:AR173356
c1380	17.2	0.6	28	1	I87998	ACCESSION:I87998
c1381	17.2	0.6	28	1	AR340907	ACCESSION:AR340907
c1382	17.2	0.6	28	1	AX029525	ACCESSION:AX029525
c1383	17.2	0.6	35	1	I35032	ACCESSION:I35032
1384	17	0.6	17	1	A28997	ACCESSION:A28997
c1385	17	0.6	17	1	A28997	ACCESSION:A28997
1386	17	0.6	17	1	AR104585	ACCESSION:AR104585
c1387	17	0.6	17	1	AR104585	ACCESSION:AR104585
1388	17	0.6	17	1	AR141074	ACCESSION:AR141074
c1389	17	0.6	17	1	AR141074	ACCESSION:AR141074
1390	17	0.6	17	1	AR175846	ACCESSION:AR175846
c1391	17	0.6	17	1	AR175846	ACCESSION:AR175846
1392	17	0.6	17	1	AR187062	ACCESSION:AR187062
c1393	17	0.6	17	1	AR187063	ACCESSION:AR187063
1394	17	0.6	17	1	AR222463	ACCESSION:AR222463
c1395	17	0.6	17	1	AR222463	ACCESSION:AR222463
1396	17	0.6	17	1	AR236087	ACCESSION:AR236087
c1397	17	0.6	17	1	AR236087	ACCESSION:AR236087
1398	17	0.6	17	1	AR323672	ACCESSION:AR323672
c1399	17	0.6	17	1	AR323673	ACCESSION:AR323673
1400	17	0.6	17	1	AX146682	ACCESSION:AX146682
c1401	17	0.6	17	1	AX361606	ACCESSION:AX361606
1402	17	0.6	17	1	AX692525	ACCESSION:AX692525
1403	17	0.6	17	1	AX762112	ACCESSION:AX762112
c1404	17	0.6	17	1	AX814938	ACCESSION:AX814938
c1405	17	0.6	18	1	AX028843	ACCESSION:AX028843
1406	17	0.6	18	1	AX028844	ACCESSION:AX028844
c1407	17	0.6	18	1	BD190553	ACCESSION:BD190553
1408	17	0.6	18	1	E32456	ACCESSION:E32456
c1409	17	0.6	18	1	E32458	ACCESSION:E32458
1410	17	0.6	18	1	AX028845	ACCESSION:AX028845
c1411	17	0.6	18	1	AX028845	ACCESSION:AX028845
c1412	17	0.6	18	1	AX361600	ACCESSION:AX361600
c1413	17	0.6	18	1	AX814932	ACCESSION:AX814932
c1414	17	0.6	20	1	AR030917	ACCESSION:AR030917
c1415	17	0.6	20	1	I28309	ACCESSION:I28309
c1416	17	0.6	20	1	I47310	ACCESSION:I47310
1417	17	0.6	20	1	BD161924	ACCESSION:BD161924
c1418	17	0.6	20	1	BD161924	ACCESSION:BD161924
c1419	17	0.6	23	1	BD244863	ACCESSION:BD244863
c1420	17	0.6	23	1	BD244865	ACCESSION:BD244865

1129	18	0.6	21	1	AX825130	ACCESSION:AX825130	1202	18	0.6	32	1	AX394625	ACCESSION:AX394625
c1130	18	0.6	21	1	AX825132	ACCESSION:AX825132	c1203	18	0.6	32	1	AR014684	ACCESSION:AR014684
1131	18	0.6	21	1	AX825123	ACCESSION:AX825123	c1204	18	0.6	32	1	AR341692	ACCESSION:AR341692
c1132	18	0.6	21	1	AX825123	ACCESSION:AX825123	c1205	18	0.6	32	1	AR366811	ACCESSION:AR366811
1133	18	0.6	21	1	AX825124	ACCESSION:AX825124	c1206	18	0.6	32	1	AR432384	ACCESSION:AR432384
c1134	18	0.6	21	1	AX825124	ACCESSION:AX825124	c1207	18	0.6	32	1	AR409897	ACCESSION:AR409897
1135	18	0.6	21	1	AX825125	ACCESSION:AX825125	1208	17.8	0.6	19	1	A79657	ACCESSION:A79657
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1137	18	0.6	21	1	AX825126	ACCESSION:AX825126	1210	17.8	0.6	19	1	AR147331	ACCESSION:AR147331
c1138	18	0.6	21	1	AX825126	ACCESSION:AX825126	c1211	17.8	0.6	19	1	AR147331	ACCESSION:AR147331
1139	18	0.6	22	1	AR164318	ACCESSION:AR164318	1212	17.8	0.6	22	1	AX103869	ACCESSION:AX103869
c1140	18	0.6	22	1	AR164318	ACCESSION:AR164318	1213	17.8	0.6	22	1	AX457060	ACCESSION:AX457060
1141	18	0.6	22	1	AR164319	ACCESSION:AR164319	1214	17.8	0.6	22	1	AX546922	ACCESSION:AX546922
c1142	18	0.6	22	1	AR164319	ACCESSION:AR164319	1215	17.8	0.6	23	1	AX457061	ACCESSION:AX457061
1143	18	0.6	22	1	I31810	ACCESSION:I31810	1216	17.8	0.6	24	1	AR431313	ACCESSION:AR431313
c1144	18	0.6	22	1	I31810	ACCESSION:I31810	1217	17.8	0.6	24	1	AX103868	ACCESSION:AX103868
1145	18	0.6	22	1	I31811	ACCESSION:I31811	1218	17.8	0.6	24	1	AX546921	ACCESSION:AX546921
c1146	18	0.6	22	1	I31811	ACCESSION:I31811	c1219	17.8	0.6	25	1	E36888	ACCESSION:E36888
1147	18	0.6	22	1	I69407	ACCESSION:I69407	1220	17.8	0.6	25	1	AR207710	ACCESSION:AR207710
c1148	18	0.6	22	1	I69407	ACCESSION:I69407	c1221	17.8	0.6	25	1	AR243409	ACCESSION:AR243409
1149	18	0.6	22	1	I69408	ACCESSION:I69408	1222	17.8	0.6	25	1	AR265036	ACCESSION:AR265036
c1150	18	0.6	22	1	I69408	ACCESSION:I69408	1223	17.8	0.6	25	1	AR390565	ACCESSION:AR390565
1151	18	0.6	23	1	BD245230	ACCESSION:BD245230	c1224	17.8	0.6	25	1	AR393179	ACCESSION:AR393179
1152	18	0.6	23	1	E12391	ACCESSION:E12391	1225	17.8	0.6	25	1	AR435375	ACCESSION:AR435375
1153	18	0.6	23	1	AX394607	ACCESSION:AX394607	1226	17.8	0.6	25	1	AR435376	ACCESSION:AR435376
c1154	18	0.6	23	1	AX394607	ACCESSION:AX394607	1227	17.8	0.6	25	1	AR435377	ACCESSION:AR435377
c1155	18	0.6	24	1	AR168453	ACCESSION:AR168453	1228	17.8	0.6	25	1	AR435378	ACCESSION:AR435378
1156	18	0.6	24	1	AX394609	ACCESSION:AX394609	1229	17.8	0.6	25	1	AR435379	ACCESSION:AR435379
c1157	18	0.6	24	1	AX394609	ACCESSION:AX394609	c1230	17.8	0.6	25	1	AX042571	ACCESSION:AX042571
1158	18	0.6	24	1	BD097127	ACCESSION:BD097127	1231	17.8	0.6	25	1	AX042981	ACCESSION:AX042981
c1159	18	0.6	24	1	BD097127	ACCESSION:BD097127	1232	17.8	0.6	25	1	AX115872	ACCESSION:AX115872
1160	18	0.6	24	1	BD161931	ACCESSION:BD161931	1233	17.8	0.6	25	1	AX692823	ACCESSION:AX692823
c1161	18	0.6	24	1	BD161931	ACCESSION:BD161931	c1234	17.8	0.6	25	1	AX692823	ACCESSION:AX692823
1162	18	0.6	25	1	AX394611	ACCESSION:AX394611	1235	17.8	0.6	25	1	AX692824	ACCESSION:AX692824
c1163	18	0.6	25	1	AX394611	ACCESSION:AX394611	c1236	17.8	0.6	25	1	AX692824	ACCESSION:AX692824
c1164	18	0.6	26	1	AR144828	ACCESSION:AR144828	1237	17.8	0.6	25	1	AX692825	ACCESSION:AX692825
c1165	18	0.6	26	1	AR410280	ACCESSION:AR410280	c1238	17.8	0.6	25	1	AX692825	ACCESSION:AX692825
c1166	18	0.6	26	1	AX191907	ACCESSION:AX191907	1239	17.8	0.6	25	1	AX692826	ACCESSION:AX692826
c1167	18	0.6	26	1	BD064385	ACCESSION:BD064385	c1240	17.8	0.6	25	1	AX692826	ACCESSION:AX692826
c1168	18	0.6	26	1	AR013918	ACCESSION:AR013918	1241	17.8	0.6	25	1	AX692827	ACCESSION:AX692827
c1169	18	0.6	26	1	AR136778	ACCESSION:AR136778	c1242	17.8	0.6	25	1	AX692827	ACCESSION:AX692827
1170	18	0.6	26	1	AR050239	ACCESSION:AR050239	1243	17.8	0.6	25	1	AX744662	ACCESSION:AX744662
1171	18	0.6	26	1	AR090583	ACCESSION:AR090583	1244	17.8	0.6	25	1	AX744663	ACCESSION:AX744663
c1172	18	0.6	26	1	AR106358	ACCESSION:AR106358	1245	17.8	0.6	25	1	AX744664	ACCESSION:AX744664
1173	18	0.6	26	1	AR164510	ACCESSION:AR164510	1246	17.8	0.6	25	1	AX744665	ACCESSION:AX744665
1174	18	0.6	26	1	AR197618	ACCESSION:AR197618	1247	17.8	0.6	25	1	AX744666	ACCESSION:AX744666
1175	18	0.6	26	1	AR259772	ACCESSION:AR259772	c1248	17.8	0.6	25	1	AX810470	ACCESSION:AX810470
1176	18	0.6	26	1	AX394613	ACCESSION:AX394613	c1249	17.8	0.6	25	1	BD011139	ACCESSION:BD011139
c1177	18	0.6	26	1	AX394613	ACCESSION:AX394613	c1250	17.8	0.6	26	1	E33560	ACCESSION:E33560
1178	18	0.6	26	1	AX827015	ACCESSION:AX827015	c1251	17.6	0.6	24	1	AR159556	ACCESSION:AR159556
c1179	18	0.6	26	1	AX827015	ACCESSION:AX827015	1252	17.6	0.6	24	1	AX443659	ACCESSION:AX443659
1180	18	0.6	26	1	AX839907	ACCESSION:AX839907	1253	17.6	0.6	25	1	A71580	ACCESSION:A71580
c1181	18	0.6	26	1	AX839907	ACCESSION:AX839907	1254	17.6	0.6	25	1	BD245989	ACCESSION:BD245989
c1182	18	0.6	27	1	AR142409	ACCESSION:AR142409	1255	17.6	0.6	25	1	AR237790	ACCESSION:AR237790
c1183	18	0.6	27	1	AR182555	ACCESSION:AR182555	1256	17.6	0.6	25	1	AX015674	ACCESSION:AX015674
c1184	18	0.6	27	1	AR027002	ACCESSION:AR027002	c1257	17.6	0.6	25	1	AX042589	ACCESSION:AX042589
1185	18	0.6	27	1	AX394614	ACCESSION:AX394614	c1258	17.6	0.6	25	1	AX042901	ACCESSION:AX042901
c1186	18	0.6	27	1	AX394614	ACCESSION:AX394614	c1259	17.6	0.6	25	1	AX043100	ACCESSION:AX043100
c1187	18	0.6	28	1	AR055110	ACCESSION:AR055110	c1260	17.6	0.6	25	1	AX043152	ACCESSION:AX043152
c1188	18	0.6	28	1	AR068451	ACCESSION:AR068451	c1261	17.6	0.6	25	1	AX043290	ACCESSION:AX043290
c1189	18	0.6	28	1	AR371171	ACCESSION:AR371171	c1262	17.6	0.6	25	1	AX043309	ACCESSION:AX043309
c1190	18	0.6	28	1	BD015304	ACCESSION:BD015304	1263	17.6	0.6	25	1	AX043412	ACCESSION:AX043412
1191	18	0.6	28	1	AX394616	ACCESSION:AX394616	c1264	17.6	0.6	25	1	AX115700	ACCESSION:AX115700
1192	18	0.6	28	1	AX394617	ACCESSION:AX394617	1265	17.6	0.6	25	1	BD008572	ACCESSION:BD008572
1193	18	0.6	29	1	AX394619	ACCESSION:AX394619	1266	17.6	0.6	25	1	BD222040	ACCESSION:BD222040
1194	18	0.6	30	1	AX394621	ACCESSION:AX394621	1267	17.6	0.6	26	1	AR098647	ACCESSION:AR098647
c1195	18	0.6	30	1	AR242448	ACCESSION:AR242448	1268	17.6	0.6	26	1	AR204721	ACCESSION:AR204721
c1196	18	0.6	30	1	AR280216	ACCESSION:AR280216	c1269	17.6	0.6	27	1	AX589115	ACCESSION:AX589115
c1197	18	0.6	30	1	AR322431	ACCESSION:AR322431	c1270	17.6	0.6	29	1	AR098648	ACCESSION:AR098648
1198	18	0.6	31	1	AR394623	ACCESSION:AR394623	c1271	17.6	0.6	29	1	AR204722	ACCESSION:AR204722
c1199	18	0.6	32	1	AR051291	ACCESSION:AR051291	1272	17.4	0.6	20	1	AX078001	ACCESSION:AX078001
c1200	18	0.6	32	1	I16939	ACCESSION:I16939	c1273	17.4	0.6	20	1	AR211367	ACCESSION:AR211367
c1201	18	0.6	32	1	I45733	ACCESSION:I45733	1274	17.4	0.6	20	1	AR371268	ACCESSION:AR371268

983	18.4	0.7	21	1	AX825132	AX028844	18	0.6	18	1	AX028844	ACCESSION:AX028844
984	18.4	0.7	21	1	AX825133	AX047271	18	0.6	18	1	AX047271	ACCESSION:AX047271
C 985	18.4	0.7	21	1	AX825133	AX047271	18	0.6	18	1	AX047271	ACCESSION:AX047271
986	18.4	0.7	22	1	BD085544	AX047273	18	0.6	18	1	AX047273	ACCESSION:AX047273
987	18.4	0.7	23	1	BD245245	AX047273	18	0.6	18	1	AX047273	ACCESSION:AX047273
988	18.4	0.7	26	1	AR136778	AX085253	18	0.6	18	1	AX085253	ACCESSION:AX085253
989	18.4	0.7	26	1	E64577	AX104721	18	0.6	18	1	AX104721	ACCESSION:AX104721
C 990	18.4	0.7	28	1	AX394616	AX104721	18	0.6	18	1	AX104721	ACCESSION:AX104721
C 991	18.4	0.7	28	1	AX394617	AX104747	18	0.6	18	1	AX104747	ACCESSION:AX104747
C 992	18.4	0.7	28	1	AX394618	AX104747	18	0.6	18	1	AX104747	ACCESSION:AX104747
993	18.2	0.6	19	1	AR102020	AX105651	18	0.6	18	1	AX105651	ACCESSION:AX105651
C 994	18.2	0.6	19	1	AR102020	AX105651	18	0.6	18	1	AX105651	ACCESSION:AX105651
995	18.2	0.6	19	1	AR134802	AX108642	18	0.6	18	1	AX108642	ACCESSION:AX108642
C 996	18.2	0.6	19	1	AR134802	AX108642	18	0.6	18	1	AX108642	ACCESSION:AX108642
997	18.2	0.6	19	1	AR134802	AX108642	18	0.6	18	1	AX108642	ACCESSION:AX108642
C 998	18.2	0.6	20	1	E28098	AX268883	18	0.6	18	1	AX268883	ACCESSION:AX268883
999	18.2	0.6	20	1	E28098	AX268883	18	0.6	18	1	AX268883	ACCESSION:AX268883
1000	18.2	0.6	23	1	AR084981	AX355809	18	0.6	18	1	AX355809	ACCESSION:AX355809
C 1001	18.2	0.6	23	1	AR100207	AX547774	18	0.6	18	1	AX547774	ACCESSION:AX547774
1002	18.2	0.6	23	1	AR123791	AX547774	18	0.6	18	1	AX547774	ACCESSION:AX547774
1003	18.2	0.6	23	1	BD263052	AX547774	18	0.6	18	1	AX547774	ACCESSION:AX547774
1004	18.2	0.6	23	1	I32906	AX547800	18	0.6	18	1	AX547800	ACCESSION:AX547800
1005	18.2	0.6	23	1	AR306617	AX814716	18	0.6	18	1	AX814716	ACCESSION:AX814716
C 1006	18.2	0.6	23	1	BD105197	AX814716	18	0.6	18	1	AX814716	ACCESSION:AX814716
1007	18.2	0.6	25	1	AX454028	AX814723	18	0.6	18	1	AX814723	ACCESSION:AX814723
C 1007	18.2	0.6	25	1	AX042942	AX814723	18	0.6	18	1	AX814723	ACCESSION:AX814723
1008	18.2	0.6	25	1	I20186	AX814725	18	0.6	18	1	AX814725	ACCESSION:AX814725
1009	18.2	0.6	25	1	AX042923	AX814736	18	0.6	18	1	AX814736	ACCESSION:AX814736
1010	18.2	0.6	25	1	AX043281	AX814736	18	0.6	18	1	AX814736	ACCESSION:AX814736
1011	18.2	0.6	25	1	AX115988	BD085545	18	0.6	18	1	BD085545	ACCESSION:BD085545
1012	18.2	0.6	26	1	AR172578	BD085545	18	0.6	18	1	BD085545	ACCESSION:BD085545
1013	18.2	0.6	26	1	AR430169	BD190553	18	0.6	18	1	BD190553	ACCESSION:BD190553
C 1014	18.2	0.6	28	1	AX391845	BD222596	18	0.6	18	1	BD222596	ACCESSION:BD222596
C 1015	18.2	0.6	28	1	AR055117	BD222596	18	0.6	18	1	BD222596	ACCESSION:BD222596
C 1016	18.2	0.6	28	1	AR068458	AR432617	19	0.6	19	1	AR432617	ACCESSION:AR432617
C 1017	18.2	0.6	28	1	AR034896	AR432617	19	0.6	19	1	AR432617	ACCESSION:AR432617
C 1018	18.2	0.6	28	1	AR034899	AR139961	20	0.6	20	1	AR139961	ACCESSION:AR139961
C 1019	18.2	0.6	28	1	AR034899	AR139962	20	0.6	20	1	AR139962	ACCESSION:AR139962
1020	18	0.6	18	1	AR058305	AR140280	20	0.6	20	1	AR140280	ACCESSION:AR140280
C 1021	18	0.6	18	1	AR058305	AR140558	20	0.6	20	1	AR140558	ACCESSION:AR140558
1022	18	0.6	18	1	AR097579	AR140559	20	0.6	20	1	AR140559	ACCESSION:AR140559
C 1023	18	0.6	18	1	AR097579	AR139960	20	0.6	20	1	AR139960	ACCESSION:AR139960
C 1025	18	0.6	18	1	AR097579	AR140279	20	0.6	20	1	AR140279	ACCESSION:AR140279
C 1026	18	0.6	18	1	AR097579	AR140557	20	0.6	20	1	AR140557	ACCESSION:AR140557
C 1027	18	0.6	18	1	AR106506	AR140557	20	0.6	20	1	AR140557	ACCESSION:AR140557
C 1028	18	0.6	18	1	AR106506	BD234126	20	0.6	20	1	BD234126	ACCESSION:BD234126
C 1029	18	0.6	18	1	AR106506	BD234126	20	0.6	20	1	BD234126	ACCESSION:BD234126
1030	18	0.6	18	1	E28535	AX825109	21	0.6	21	1	AX825109	ACCESSION:AX825109
C 1031	18	0.6	18	1	E28535	AX825115	21	0.6	21	1	AX825115	ACCESSION:AX825115
1032	18	0.6	18	1	E28536	AX825118	21	0.6	21	1	AX825118	ACCESSION:AX825118
C 1033	18	0.6	18	1	E28536	AX825127	21	0.6	21	1	AX825127	ACCESSION:AX825127
1034	18	0.6	18	1	E28536	AX825131	21	0.6	21	1	AX825131	ACCESSION:AX825131
C 1035	18	0.6	18	1	I79509	AX825134	21	0.6	21	1	AX825134	ACCESSION:AX825134
C 1036	18	0.6	18	1	I79509	AX825139	21	0.6	21	1	AX825139	ACCESSION:AX825139
1037	18	0.6	18	1	AR208427	AX825143	21	0.6	21	1	AX825143	ACCESSION:AX825143
C 1038	18	0.6	18	1	AR215435	AX825147	21	0.6	21	1	AX825147	ACCESSION:AX825147
1039	18	0.6	18	1	AR215435	AX825107	21	0.6	21	1	AX825107	ACCESSION:AX825107
C 1040	18	0.6	18	1	AR222464	AX825110	21	0.6	21	1	AX825110	ACCESSION:AX825110
1041	18	0.6	18	1	AR222464	AX825116	21	0.6	21	1	AX825116	ACCESSION:AX825116
C 1042	18	0.6	18	1	AR412363	AX825140	21	0.6	21	1	AX825140	ACCESSION:AX825140
1043	18	0.6	18	1	AR412363	AX825141	21	0.6	21	1	AX825141	ACCESSION:AX825141
C 1044	18	0.6	18	1	AX004875	AX825142	21	0.6	21	1	AX825142	ACCESSION:AX825142
1045	18	0.6	18	1	AX004875	AX825144	21	0.6	21	1	AX825144	ACCESSION:AX825144
C 1046	18	0.6	18	1	AX004879	AX825145	21	0.6	21	1	AX825145	ACCESSION:AX825145
1047	18	0.6	18	1	AX004879	AX825146	21	0.6	21	1	AX825146	ACCESSION:AX825146
C 1048	18	0.6	18	1	AX008117	AX825128	21	0.6	21	1	AX825128	ACCESSION:AX825128
1049	18	0.6	18	1	AX008117	AX825129	21	0.6	21	1	AX825129	ACCESSION:AX825129
C 1050	18	0.6	18	1	AX008118							
1051	18	0.6	18	1	AX008118							
C 1052	18	0.6	18	1	AX008122							
1053	18	0.6	18	1	AX008122							
C 1054	18	0.6	18	1	AX008123							
1055	18	0.6	18	1	AX028843							

c1056	18	0.6	18	1	AX028844	ACCESSION:AX028844
1057	18	0.6	18	1	AX047271	ACCESSION:AX047271
c1058	18	0.6	18	1	AX047271	ACCESSION:AX047271
1059	18	0.6	18	1	AX047273	ACCESSION:AX047273
c1060	18	0.6	18	1	AX047273	ACCESSION:AX047273
c1061	18	0.6	18	1	AX085253	ACCESSION:AX085253
1062	18	0.6	18	1	AX104721	ACCESSION:AX104721
c1063	18	0.6	18	1	AX104721	ACCESSION:AX104721
1064	18	0.6	18	1	AX104747	ACCESSION:AX104747
c1065	18	0.6	18	1	AX104747	ACCESSION:AX104747
1066	18	0.6	18	1	AX105651	ACCESSION:AX105651
c1067	18	0.6	18	1	AX105651	ACCESSION:AX105651
1068	18	0.6	18	1	AX108642	ACCESSION:AX108642
c1069	18	0.6	18	1	AX108642	ACCESSION:AX108642
1070	18	0.6	18	1	AX268883	ACCESSION:AX268883
c1071	18	0.6	18	1	AX268883	ACCESSION:AX268883
1072	18	0.6	18	1	AX355809	ACCESSION:AX355809
c1073	18	0.6	18	1	AX355809	ACCESSION:AX355809
1074	18	0.6	18	1	AX547774	ACCESSION:AX547774
c1075	18	0.6	18	1	AX547774	ACCESSION:AX547774
1076	18	0.6	18	1	AX547800	ACCESSION:AX547800
c1077	18	0.6	18	1	AX547800	ACCESSION:AX547800
1078	18	0.6	18	1	AX814716	ACCESSION:AX814716
c1079	18	0.6	18	1	AX814716	ACCESSION:AX814716
1080	18	0.6	18	1	AX814723	ACCESSION:AX814723
c1081	18	0.6	18	1	AX814723	ACCESSION:AX814723
1082	18	0.6	18	1	AX814724	ACCESSION:AX814724
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1084	18	0.6	18	1	AX814725	ACCESSION:AX814725
c1085	18	0.6	18	1	AX814725	ACCESSION:AX814725
1086	18	0.6	18	1	AX814736	ACCESSION:AX814736
c1087	18	0.6	18	1	AX814736	ACCESSION:AX814736
1088	18	0.6	18	1	BD085545	ACCESSION:BD085545
c1089	18	0.6	18	1	BD085545	ACCESSION:BD085545
1090	18	0.6	18	1	BD190553	ACCESSION:BD190553
1091	18	0.6	18	1	BD222596	ACCESSION:BD222596
c1092	18	0.6	18	1	BD222596	ACCESSION:BD222596
1093	18	0.6	19	1	AR432617	ACCESSION:AR432617
c1094	18	0.6	19	1	AR432617	ACCESSION:AR432617
c1095	18	0.6	20	1	AR139961	ACCESSION:AR139961
1096	18	0.6	20	1	AR139962	ACCESSION:AR139962
c1097	18	0.6	20	1	AR140280	ACCESSION:AR140280
1098	18	0.6	20	1	AR140281	ACCESSION:AR140281
c1099	18	0.6	20	1	AR140558	ACCESSION:AR140558
1100	18	0.6	20	1	AR140559	ACCESSION:AR140559
c1101	18	0.6	20	1	AR139960	ACCESSION:AR139960
1102	18	0.6	20	1	AR139960	ACCESSION:AR139960
1103	18	0.6	20	1	AR140279	ACCESSION:AR140279
c1104	18	0.6	20	1	AR140279	ACCESSION:AR140279
1105	18	0.6	20	1	AR140557	ACCESSION:AR140557
c1106	18	0.6	20	1	AR140557	ACCESSION:AR140557
1107	18	0.6	20	1	BD234126	ACCESSION:BD234126
c1108	18	0.6	20	1	BD234126	ACCESSION:BD234126
c1109	18	0.6	21	1	AX825109	ACCESSION:AX825109
c1110	18	0.6	21	1	AX825115	ACCESSION:AX825115
c1111	18	0.6	21	1	AX825118	ACCESSION:AX825118
1112	18	0.6	21	1	AX825127	ACCESSION:AX825127
c1113	18	0.6	21	1	AX825131	ACCESSION:AX825131
1114	18	0.6	21	1	AX825134	ACCESSION:AX825134
1115	18	0.6	21	1	AX825139	ACCESSION:AX825139
1116	18	0.6	21	1	AX825143	ACCESSION:AX825143
c1117	18	0.6	21	1	AX825107	ACCESSION:AX825107
c1118	18	0.6	21	1	AX825108	ACCESSION:AX825108
c1119	18	0.6	21	1	AX825110	ACCESSION:AX825110
c1120	18	0.6	21	1	AX825116	ACCESSION:AX825116
1121	18	0.6	21	1	AX825140	ACCESSION:AX825140
1122	18	0.6	21	1	AX825141	ACCESSION:AX825141
1123	18	0.6	21	1	AX825142	ACCESSION:AX825142
1124	18	0.6	21	1	AX825144	ACCESSION:AX825144
1125	18	0.6	21	1	AX825145	ACCESSION:AX825145
1126	18	0.6	21	1	AX825146	ACCESSION:AX825146
1127	18	0.6	21	1	AX825128	ACCESSION:AX825128
1128	18	0.6	21	1	AX825129	ACCESSION:AX825129

837	19	0.7	20	1	AX556139	ACCESSION:AX556139	910	19	0.7	24	1	E13209	ACCESSION:E13209
838	19	0.7	20	1	AX664307	ACCESSION:AX664307	911	19	0.7	25	1	AX394507	ACCESSION:AX394507
C 839	19	0.7	20	1	AX664308	ACCESSION:AX664308	C 912	19	0.7	25	1	AX394514	ACCESSION:AX394514
C 840	19	0.7	20	1	AX741040	ACCESSION:AX741040	C 913	19	0.7	25	1	AX116188	ACCESSION:AX116188
841	19	0.7	20	1	AX741052	ACCESSION:AX741052	914	19	0.7	25	1	A85331	ACCESSION:A85331
842	19	0.7	20	1	BD08523	ACCESSION:BD08523	915	19	0.7	25	1	AR370671	ACCESSION:AR370671
C 843	19	0.7	20	1	BD08522	ACCESSION:BD08522	916	19	0.7	25	1	AR431257	ACCESSION:AR431257
C 844	19	0.7	20	1	BD107450	ACCESSION:BD107450	917	19	0.7	25	1	BD057791	ACCESSION:BD057791
845	19	0.7	20	1	BD218101	ACCESSION:BD218101	918	19	0.7	28	1	AX427136	ACCESSION:AX427136
846	19	0.7	20	1	ARI39961	ACCESSION:ARI39961	C 919	19	0.7	28	1	I06459	ACCESSION:I06459
C 847	19	0.7	20	1	ARI39962	ACCESSION:ARI39962	920	19	0.7	28	1	AR371171	ACCESSION:AR371171
848	19	0.7	20	1	ARI40280	ACCESSION:ARI40280	921	19	0.7	28	1	BD015304	ACCESSION:BD015304
C 849	19	0.7	20	1	ARI40281	ACCESSION:ARI40281	C 922	19	0.7	29	1	I65795	ACCESSION:I65795
850	19	0.7	20	1	ARI40558	ACCESSION:ARI40558	923	19	0.7	29	1	AR268128	ACCESSION:AR268128
C 851	19	0.7	20	1	ARI40559	ACCESSION:ARI40559	C 924	19	0.7	30	1	AX079109	ACCESSION:AX079109
C 852	19	0.7	20	1	AX078001	ACCESSION:AX078001	925	19	0.7	30	1	AX196237	ACCESSION:AX196237
C 853	19	0.7	21	1	AR080294	ACCESSION:AR080294	926	19	0.7	30	1	AX440138	ACCESSION:AX440138
854	19	0.7	21	1	AR084521	ACCESSION:AR084521	927	19	0.7	30	1	AX465324	ACCESSION:AX465324
C 855	19	0.7	21	1	AR084524	ACCESSION:AR084524	928	19	0.7	30	1	AX556137	ACCESSION:AX556137
C 856	19	0.7	21	1	AR093143	ACCESSION:AR093143	929	19	0.7	30	1	AX079108	ACCESSION:AX079108
C 857	19	0.7	21	1	AR095412	ACCESSION:AR095412	C 930	19	0.7	32	1	AX080522	ACCESSION:AX080522
C 858	19	0.7	21	1	I65744	ACCESSION:I65744	C 931	19	0.7	32	1	I32124	ACCESSION:I32124
C 859	19	0.7	21	1	AR322245	ACCESSION:AR322245	932	19	0.7	32	1	AR274390	ACCESSION:AR274390
C 860	19	0.7	21	1	AX104720	ACCESSION:AX104720	933	19	0.7	32	1	AR344932	ACCESSION:AR344932
C 861	19	0.7	21	1	AX355812	ACCESSION:AX355812	934	19	0.7	32	1	AR382308	ACCESSION:AR382308
C 862	19	0.7	21	1	AX547773	ACCESSION:AX547773	935	19	0.7	32	1	AR429649	ACCESSION:AR429649
C 863	19	0.7	21	1	AX825166	ACCESSION:AX825166	936	19	0.7	32	1	AX196220	ACCESSION:AX196220
C 864	19	0.7	21	1	BD080832	ACCESSION:BD080832	937	19	0.7	32	1	AX440121	ACCESSION:AX440121
C 865	19	0.7	21	1	BD224108	ACCESSION:BD224108	938	19	0.7	32	1	AX465307	ACCESSION:AX465307
366	19	0.7	21	1	AR153849	ACCESSION:AR153849	C 939	19	0.7	32	1	AX556120	ACCESSION:AX556120
867	19	0.7	21	1	I36166	ACCESSION:I36166	C 940	19	0.7	34	1	AR174572	ACCESSION:AR174572
C 868	19	0.7	21	1	AX825152	ACCESSION:AX825152	C 941	19	0.7	34	1	BD248965	ACCESSION:BD248965
C 869	19	0.7	21	1	AX825153	ACCESSION:AX825153	C 942	19	0.7	34	1	AR374064	ACCESSION:AR374064
C 870	19	0.7	21	1	AX825154	ACCESSION:AX825154	C 943	19	0.7	34	1	AX179588	ACCESSION:AX179588
871	19	0.7	21	1	AX825160	ACCESSION:AX825160	C 944	19	0.7	35	1	AR029830	ACCESSION:AR029830
872	19	0.7	21	1	AX825161	ACCESSION:AX825161	C 945	19	0.7	41	1	AX516913	ACCESSION:AX516913
C 873	19	0.7	21	1	AX825164	ACCESSION:AX825164	C 946	19	0.7	41	1	AX519424	ACCESSION:AX519424
874	19	0.7	21	1	BD087491	ACCESSION:BD087491	C 947	19	0.7	22	1	BD085544	ACCESSION:BD085544
875	19	0.7	21	1	AX825111	ACCESSION:AX825111	C 948	19	0.7	23	1	BD245230	ACCESSION:BD245230
C 876	19	0.7	21	1	AX825150	ACCESSION:AX825150	C 949	19	0.7	23	1	E12393	ACCESSION:E12393
C 877	19	0.7	21	1	AX825158	ACCESSION:AX825158	950	19	0.7	25	1	AX043130	ACCESSION:AX043130
C 878	19	0.7	21	1	AR118155	ACCESSION:AR118155	951	19	0.7	25	1	AX043131	ACCESSION:AX043131
C 879	19	0.7	21	1	AR118155	ACCESSION:AR118155	C 952	19	0.7	26	1	E30823	ACCESSION:E30823
880	19	0.7	21	1	I84433	ACCESSION:I84433	C 953	19	0.7	25	1	AX042549	ACCESSION:AX042549
C 881	19	0.7	21	1	I84433	ACCESSION:I84433	954	19	0.7	25	1	AX042942	ACCESSION:AX042942
882	19	0.7	21	1	AX825107	ACCESSION:AX825107	C 955	19	0.7	25	1	AX043077	ACCESSION:AX043077
883	19	0.7	21	1	AX825108	ACCESSION:AX825108	956	19	0.7	25	1	AX043230	ACCESSION:AX043230
884	19	0.7	21	1	AX825110	ACCESSION:AX825110	957	19	0.7	27	1	AR409915	ACCESSION:AR409915
885	19	0.7	21	1	AX825112	ACCESSION:AX825112	958	19	0.7	29	1	AX052989	ACCESSION:AX052989
886	19	0.7	21	1	AX825116	ACCESSION:AX825116	959	19	0.7	20	1	AR030917	ACCESSION:AR030917
C 887	19	0.7	21	1	AX825140	ACCESSION:AX825140	960	19	0.7	20	1	I28309	ACCESSION:I28309
C 888	19	0.7	21	1	AX825141	ACCESSION:AX825141	961	19	0.7	20	1	I47310	ACCESSION:I47310
C 889	19	0.7	21	1	AX825142	ACCESSION:AX825142	962	19	0.7	20	1	AR211367	ACCESSION:AR211367
C 890	19	0.7	21	1	AX825144	ACCESSION:AX825144	C 963	19	0.7	20	1	AR371268	ACCESSION:AR371268
C 891	19	0.7	21	1	AX825145	ACCESSION:AX825145	964	19	0.7	20	1	AX136903	ACCESSION:AX136903
C 892	19	0.7	21	1	AX825146	ACCESSION:AX825146	C 965	19	0.7	21	1	AX825105	ACCESSION:AX825105
C 893	19	0.7	21	1	AX825148	ACCESSION:AX825148	C 966	19	0.7	21	1	AX825136	ACCESSION:AX825136
C 894	19	0.7	21	1	AX825149	ACCESSION:AX825149	967	19	0.7	21	1	AX825138	ACCESSION:AX825138
895	19	0.7	21	1	AX825156	ACCESSION:AX825156	968	19	0.7	21	1	AX825113	ACCESSION:AX825113
C 896	19	0.7	21	1	AX825156	ACCESSION:AX825156	C 969	19	0.7	21	1	AX825114	ACCESSION:AX825114
897	19	0.7	21	1	AX825157	ACCESSION:AX825157	C 970	19	0.7	21	1	AX825117	ACCESSION:AX825117
C 898	19	0.7	21	1	AR164336	ACCESSION:AR164336	C 971	19	0.7	21	1	AX825121	ACCESSION:AX825121
899	19	0.7	22	1	I31828	ACCESSION:I31828	C 972	19	0.7	21	1	AX825112	ACCESSION:AX825112
900	19	0.7	22	1	I69425	ACCESSION:I69425	C 973	19	0.7	21	1	AX825148	ACCESSION:AX825148
901	19	0.7	22	1	BD244857	ACCESSION:BD244857	974	19	0.7	21	1	AX825149	ACCESSION:AX825149
C 902	19	0.7	23	1	BD244863	ACCESSION:BD244863	975	19	0.7	21	1	AX825120	ACCESSION:AX825120
903	19	0.7	23	1	BD244865	ACCESSION:BD244865	976	19	0.7	21	1	AX825120	ACCESSION:AX825120
904	19	0.7	23	1	I79497	ACCESSION:I79497	C 977	19	0.7	21	1	AX825122	ACCESSION:AX825122
905	19	0.7	23	1	BD133515	ACCESSION:BD133515	978	19	0.7	21	1	AX825122	ACCESSION:AX825122
906	19	0.7	23	1	AR431310	ACCESSION:AR431310	C 979	19	0.7	21	1	AX825128	ACCESSION:AX825128
C 907	19	0.7	24	1	AX817782	ACCESSION:AX817782	C 980	19	0.7	21	1	AX825129	ACCESSION:AX825129
908	19	0.7	24	1	AX838369	ACCESSION:AX838369	C 981	19	0.7	21	1	AX825130	ACCESSION:AX825130
909	19	0.7	24	1			C 982	19	0.7	21	1		

545	19.4	0.7	28	1	AR173356	ACCESSION:AR173356	C 618	19	0.7	19	1	AR048767	ACCESSION:AR048767
546	19.4	0.7	28	1	I87998	ACCESSION:I87998	619	19	0.7	19	1	AR111371	ACCESSION:AR111371
547	19.4	0.7	28	1	AR340907	ACCESSION:AR340907	C 620	19	0.7	19	1	AR111371	ACCESSION:AR111371
548	19.4	0.7	28	1	AX029525	ACCESSION:AX029525	621	19	0.7	19	1	AR111946	ACCESSION:AR111946
549	19.4	0.7	28	1	AX391845	ACCESSION:AX391845	C 622	19	0.7	19	1	AR111946	ACCESSION:AR111946
550	19.4	0.7	29	1	AR162868	ACCESSION:AR162868	623	19	0.7	19	1	AR111947	ACCESSION:AR111947
551	19.4	0.7	29	1	AR194018	ACCESSION:AR194018	C 624	19	0.7	19	1	AR111947	ACCESSION:AR111947
552	19.4	0.7	29	1	AR409905	ACCESSION:AR409905	625	19	0.7	19	1	AR111948	ACCESSION:AR111948
C 553	19.4	0.7	29	1	AX181697	ACCESSION:AX181697	C 626	19	0.7	19	1	AR111948	ACCESSION:AR111948
C 554	19.4	0.7	29	1	AX394619	ACCESSION:AX394619	627	19	0.7	19	1	AR111949	ACCESSION:AR111949
C 555	19.4	0.7	29	1	AX394620	ACCESSION:AX394620	C 628	19	0.7	19	1	AR111949	ACCESSION:AR111949
556	19.4	0.7	32	1	AX838502	ACCESSION:AX838502	629	19	0.7	19	1	AR111950	ACCESSION:AR111950
C 557	19.2	0.7	22	1	AX583623	ACCESSION:AX583623	C 630	19	0.7	19	1	AR111950	ACCESSION:AR111950
C 558	19.2	0.7	24	1	AX391871	ACCESSION:AX391871	631	19	0.7	19	1	AR111951	ACCESSION:AR111951
C 559	19.2	0.7	24	1	AR010037	ACCESSION:AR010037	C 632	19	0.7	19	1	AR111951	ACCESSION:AR111951
560	19.2	0.7	24	1	AR034772	ACCESSION:AR034772	633	19	0.7	19	1	AR111952	ACCESSION:AR111952
561	19.2	0.7	24	1	AR068465	ACCESSION:AR068465	C 634	19	0.7	19	1	AR111952	ACCESSION:AR111952
562	19.2	0.7	24	1	AR05984	ACCESSION:AR105984	635	19	0.7	19	1	AR111953	ACCESSION:AR111953
563	19.2	0.7	24	1	AR107972	ACCESSION:AR107972	C 636	19	0.7	19	1	AR111953	ACCESSION:AR111953
C 564	19.2	0.7	24	1	BD234330	ACCESSION:BD234330	637	19	0.7	19	1	AR111957	ACCESSION:AR111957
565	19.2	0.7	24	1	I24762	ACCESSION:I24762	C 638	19	0.7	19	1	AR111957	ACCESSION:AR111957
566	19.2	0.7	24	1	AR184443	ACCESSION:AR184443	639	19	0.7	19	1	AR111959	ACCESSION:AR111959
567	19.2	0.7	24	1	AR202876	ACCESSION:AR202876	C 640	19	0.7	19	1	AR111959	ACCESSION:AR111959
568	19.2	0.7	24	1	AR213697	ACCESSION:AR213697	641	19	0.7	19	1	AR111960	ACCESSION:AR111960
569	19.2	0.7	24	1	AR232949	ACCESSION:AR232949	C 642	19	0.7	19	1	AR111960	ACCESSION:AR111960
570	19.2	0.7	24	1	AR340571	ACCESSION:AR340571	643	19	0.7	19	1	AR111970	ACCESSION:AR111970
571	19.2	0.7	24	1	AR345020	ACCESSION:AR345020	C 644	19	0.7	19	1	AR111970	ACCESSION:AR111970
C 572	19.2	0.7	24	1	AX104241	ACCESSION:AX104241	645	19	0.7	19	1	AR124843	ACCESSION:AR124843
C 573	19.2	0.7	24	1	AX104769	ACCESSION:AX104769	C 646	19	0.7	19	1	AR124843	ACCESSION:AR124843
574	19.2	0.7	24	1	AX104770	ACCESSION:AX104770	647	19	0.7	19	1	AR124844	ACCESSION:AR124844
575	19.2	0.7	24	1	AX354553	ACCESSION:AX354553	C 648	19	0.7	19	1	AR124844	ACCESSION:AR124844
C 576	19.2	0.7	24	1	AX355813	ACCESSION:AX355813	649	19	0.7	19	1	AR124845	ACCESSION:AR124845
C 577	19.2	0.7	24	1	AX427163	ACCESSION:AX427163	C 650	19	0.7	19	1	AR124845	ACCESSION:AR124845
578	19.2	0.7	24	1	AX428574	ACCESSION:AX428574	651	19	0.7	19	1	AR124846	ACCESSION:AR124846
C 579	19.2	0.7	24	1	AX547294	ACCESSION:AX547294	C 652	19	0.7	19	1	AR124846	ACCESSION:AR124846
C 580	19.2	0.7	24	1	AX547822	ACCESSION:AX547822	653	19	0.7	19	1	AR124847	ACCESSION:AR124847
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C 582	19.2	0.7	24	1	AX684290	ACCESSION:AX684290	655	19	0.7	19	1	AR124848	ACCESSION:AR124848
C 583	19.2	0.7	24	1	AX750585	ACCESSION:AX750585	C 656	19	0.7	19	1	AR124848	ACCESSION:AR124848
C 584	19.2	0.7	24	1	AX829247	ACCESSION:AX829247	C 657	19	0.7	19	1	AR124849	ACCESSION:AR124849
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586	19.2	0.7	24	1	AR168453	ACCESSION:AR168453	659	19	0.7	19	1	AR124850	ACCESSION:AR124850
C 587	19.2	0.7	25	1	AR105982	ACCESSION:AR105982	C 660	19	0.7	19	1	AR124850	ACCESSION:AR124850
C 588	19.2	0.7	25	1	BD234336	ACCESSION:BD234336	661	19	0.7	19	1	AR124854	ACCESSION:AR124854
C 589	19.2	0.7	25	1	I58009	ACCESSION:I58009	C 662	19	0.7	19	1	AR124854	ACCESSION:AR124854
C 590	19.2	0.7	25	1	I96072	ACCESSION:I96072	663	19	0.7	19	1	AR124856	ACCESSION:AR124856
C 591	19.2	0.7	25	1	AR288252	ACCESSION:AR288252	C 664	19	0.7	19	1	AR124856	ACCESSION:AR124856
592	19.2	0.7	25	1	BD187513	ACCESSION:BD187513	665	19	0.7	19	1	AR124857	ACCESSION:AR124857
C 593	19.2	0.7	25	1	BD187514	ACCESSION:BD187514	C 666	19	0.7	19	1	AR124857	ACCESSION:AR124857
C 594	19.2	0.7	25	1	BD204988	ACCESSION:BD204988	667	19	0.7	19	1	AR124867	ACCESSION:AR124867
595	19.2	0.7	25	1	I29929	ACCESSION:I29929	C 668	19	0.7	19	1	AR124867	ACCESSION:AR124867
596	19.2	0.7	25	1	AX043563	ACCESSION:AX043563	669	19	0.7	19	1	AR135291	ACCESSION:AR135291
C 597	19.2	0.7	25	1	BD090045	ACCESSION:BD090045	C 670	19	0.7	19	1	AR135291	ACCESSION:AR135291
C 598	19.2	0.7	26	1	I79496	ACCESSION:I79496	671	19	0.7	19	1	AR135292	ACCESSION:AR135292
C 599	19.2	0.7	26	1	BD192375	ACCESSION:BD192375	C 672	19	0.7	19	1	AR135292	ACCESSION:AR135292
600	19.2	0.7	26	1	E30823	ACCESSION:E30823	673	19	0.7	19	1	AR135293	ACCESSION:AR135293
C 601	19.2	0.7	27	1	AX327980	ACCESSION:AX327980	C 674	19	0.7	19	1	AR135293	ACCESSION:AR135293
602	19.2	0.7	27	1	S64862S3	ACCESSION:AX492939	675	19	0.7	19	1	AR135294	ACCESSION:AR135294
C 603	19.2	0.7	27	1	AX492939	ACCESSION:BD175131	C 676	19	0.7	19	1	AR135294	ACCESSION:AR135294
C 604	19.2	0.7	27	1	BD175131	ACCESSION:BD234339	677	19	0.7	19	1	AR135295	ACCESSION:AR135295
C 605	19.2	0.7	28	1	BD234339	ACCESSION:BD234335	C 678	19	0.7	19	1	AR135295	ACCESSION:AR135295
C 606	19.2	0.7	28	1	BD234335	ACCESSION:BD234335	679	19	0.7	19	1	AR135296	ACCESSION:AR135296
607	19.2	0.7	29	1	AX430216	ACCESSION:AX430216	C 680	19	0.7	19	1	AR135296	ACCESSION:AR135296
608	19.2	0.7	29	1	BD165919	ACCESSION:BD165919	681	19	0.7	19	1	AR135297	ACCESSION:AR135297
609	19.2	0.7	29	1	BD274324	ACCESSION:BD274324	C 682	19	0.7	19	1	AR135297	ACCESSION:AR135297
610	19.2	0.7	29	1	BD274342	ACCESSION:BD274342	683	19	0.7	19	1	AR135298	ACCESSION:AR135298
611	19.2	0.7	29	1	E04206	ACCESSION:E04206	C 684	19	0.7	19	1	AR135298	ACCESSION:AR135298
C 612	19.2	0.7	32	1	BD234356	ACCESSION:BD234356	685	19	0.7	19	1	AR135302	ACCESSION:AR135302
C 613	19.2	0.7	33	1	BD171339	ACCESSION:BD171339	C 686	19	0.7	19	1	AR135302	ACCESSION:AR135302
C 614	19.2	0.7	33	1	BD173750	ACCESSION:BD173750	687	19	0.7	19	1	AR135304	ACCESSION:AR135304
C 615	19	0.7	19	1	A68209	ACCESSION:A68209	C 688	19	0.7	19	1	AR135304	ACCESSION:AR135304
C 616	19	0.7	19	1	A68209	ACCESSION:A68209	689	19	0.7	19	1	AR135305	ACCESSION:AR135305
617	19	0.7	19	1	AR048767	ACCESSION:AR048767	C 690	19	0.7	19	1	AR135305	ACCESSION:AR135305

399	20	0.7	30	1	BD145026	ACCESSION:BD145026	C 472	19.6	0.7	30	1	AR067555	ACCESSION:AR067555
400	20	0.7	30	1	BD145027	ACCESSION:BD145027	C 473	19.6	0.7	30	1	I38507	ACCESSION:I38507
401	20	0.7	30	1	BD145028	ACCESSION:BD145028	C 474	19.6	0.7	30	1	I56982	ACCESSION:I56982
402	20	0.7	30	1	BD145029	ACCESSION:BD145029	C 475	19.6	0.7	30	1	I59848	ACCESSION:I59848
403	20	0.7	30	1	BD145030	ACCESSION:BD145030	C 476	19.6	0.7	30	1	I75175	ACCESSION:I75175
404	20	0.7	30	1	BD166026	ACCESSION:BD166026	C 477	19.6	0.7	30	1	AR409723	ACCESSION:AR409723
405	20	0.7	30	1	BD166027	ACCESSION:BD166027	478	19.6	0.7	30	1	AR028195	ACCESSION:AR028195
406	20	0.7	30	1	BD166028	ACCESSION:BD166028	479	19.6	0.7	30	1	AR138598	ACCESSION:AR138598
407	20	0.7	30	1	BD166032	ACCESSION:BD166032	480	19.6	0.7	30	1	AX267026	ACCESSION:AX267026
408	20	0.7	30	1	BD166033	ACCESSION:BD166033	C 481	19.6	0.7	32	1	I29892	ACCESSION:I29892
409	20	0.7	30	1	BD166129	ACCESSION:BD166129	C 482	19.6	0.7	33	1	BD011883	ACCESSION:BD011883
C 410	19.8	0.7	24	1	AR431313	ACCESSION:AR431313	C 483	19.6	0.7	33	1	AR099615	ACCESSION:AR099615
C 411	19.8	0.7	25	1	AX338548	ACCESSION:AX338548	C 484	19.6	0.7	33	1	AR120128	ACCESSION:AR120128
C 412	19.8	0.7	25	1	BD244864	ACCESSION:BD244864	C 485	19.6	0.7	34	1	A63578	ACCESSION:A63578
C 413	19.8	0.7	25	1	AX043282	ACCESSION:AX043282	486	19.6	0.7	37	1	I29931	ACCESSION:I29931
C 414	19.8	0.7	26	1	AX338547	ACCESSION:AX338547	C 487	19.6	0.7	37	1	AX106972	ACCESSION:AX106972
C 415	19.8	0.7	27	1	AX7111956	ACCESSION:AX7111956	C 488	19.6	0.7	38	1	E50766	ACCESSION:E50766
C 416	19.8	0.7	27	1	BD097128	ACCESSION:BD097128	489	19.6	0.7	40	1	A48799	ACCESSION:A48799
C 417	19.8	0.7	27	1	BD161932	ACCESSION:BD161932	490	19.6	0.7	40	1	AR232955	ACCESSION:AR232955
C 418	19.6	0.7	26	1	AR174581	ACCESSION:AR174581	C 491	19.6	0.7	41	1	AR309630	ACCESSION:AR309630
C 419	19.6	0.7	26	1	BD248974	ACCESSION:BD248974	C 492	19.6	0.7	43	1	AX225198	ACCESSION:AX225198
C 420	19.6	0.7	26	1	I79494	ACCESSION:I79494	C 493	19.4	0.7	21	1	AX825135	ACCESSION:AX825135
C 421	19.6	0.7	26	1	AR263648	ACCESSION:AR263648	C 494	19.4	0.7	21	1	AX825151	ACCESSION:AX825151
C 422	19.6	0.7	26	1	AR374073	ACCESSION:AR374073	495	19.4	0.7	21	1	AX825159	ACCESSION:AX825159
C 423	19.6	0.7	26	1	AX106717	ACCESSION:AX106717	C 496	19.4	0.7	21	1	AX825163	ACCESSION:AX825163
C 424	19.6	0.7	26	1	AR137712	ACCESSION:AR137712	C 497	19.4	0.7	21	1	AX825103	ACCESSION:AX825103
C 425	19.6	0.7	26	1	AX427154	ACCESSION:AX427154	C 498	19.4	0.7	21	1	AX825106	ACCESSION:AX825106
C 426	19.6	0.7	26	1	AX528804	ACCESSION:AX528804	499	19.4	0.7	21	1	AX825137	ACCESSION:AX825137
C 427	19.6	0.7	26	1	A63569	ACCESSION:A63569	500	19.4	0.7	21	1	AX825162	ACCESSION:AX825162
C 428	19.6	0.7	26	1	AR010003	ACCESSION:AR010003	501	19.4	0.7	21	1	AR241831	ACCESSION:AR241831
C 429	19.6	0.7	26	1	AR034738	ACCESSION:AR034738	502	19.4	0.7	21	1	AX825109	ACCESSION:AX825109
C 430	19.6	0.7	26	1	AR098647	ACCESSION:AR098647	C 503	19.4	0.7	21	1	AX825111	ACCESSION:AX825111
C 431	19.6	0.7	26	1	I24758	ACCESSION:I24758	504	19.4	0.7	21	1	AX825113	ACCESSION:AX825113
C 432	19.6	0.7	26	1	AR204721	ACCESSION:AR204721	505	19.4	0.7	21	1	AX825114	ACCESSION:AX825114
C 433	19.6	0.7	27	1	E04985	ACCESSION:E04985	506	19.4	0.7	21	1	AX825115	ACCESSION:AX825115
C 434	19.6	0.7	27	1	AX104719	ACCESSION:AX104719	507	19.4	0.7	21	1	AX825117	ACCESSION:AX825117
C 435	19.6	0.7	27	1	AX355814	ACCESSION:AX355814	508	19.4	0.7	21	1	AX825118	ACCESSION:AX825118
C 436	19.6	0.7	27	1	AX547772	ACCESSION:AX547772	509	19.4	0.7	21	1	AX825119	ACCESSION:AX825119
C 437	19.6	0.7	29	1	AR162080	ACCESSION:AR162080	C 510	19.4	0.7	21	1	AX825121	ACCESSION:AX825121
C 438	19.6	0.7	29	1	AR166605	ACCESSION:AR166605	C 511	19.4	0.7	21	1	AX825127	ACCESSION:AX825127
C 439	19.6	0.7	29	1	BD238387	ACCESSION:BD238387	C 512	19.4	0.7	21	1	AX825131	ACCESSION:AX825131
C 440	19.6	0.7	29	1	AR279813	ACCESSION:AR279813	513	19.4	0.7	21	1	AX825133	ACCESSION:AX825133
C 441	19.6	0.7	29	1	AR282322	ACCESSION:AR282322	514	19.4	0.7	21	1	AX825134	ACCESSION:AX825134
C 442	19.6	0.7	29	1	AX048408	ACCESSION:AX048408	C 515	19.4	0.7	21	1	AX825139	ACCESSION:AX825139
C 443	19.6	0.7	29	1	AX048409	ACCESSION:AX048409	C 516	19.4	0.7	21	1	AX825143	ACCESSION:AX825143
C 444	19.6	0.7	29	1	AX052994	ACCESSION:AX052994	517	19.4	0.7	21	1	AX825147	ACCESSION:AX825147
C 445	19.6	0.7	29	1	AX353685	ACCESSION:AX353685	C 518	19.4	0.7	21	1	AX825147	ACCESSION:AX825147
C 446	19.6	0.7	29	1	AX662302	ACCESSION:AX662302	519	19.4	0.7	21	1	AX825150	ACCESSION:AX825150
C 447	19.6	0.7	29	1	BD204968	ACCESSION:BD204968	520	19.4	0.7	21	1	AX825155	ACCESSION:AX825155
C 448	19.6	0.7	30	1	A43784	ACCESSION:A43784	C 521	19.4	0.7	21	1	AX825158	ACCESSION:AX825158
C 449	19.6	0.7	30	1	A62991	ACCESSION:A62991	522	19.4	0.7	21	1	AX431308	ACCESSION:AX431308
C 450	19.6	0.7	30	1	A62995	ACCESSION:A62995	523	19.4	0.7	24	1	AX708815	ACCESSION:AX708815
C 451	19.6	0.7	30	1	AR179066	ACCESSION:AR179066	524	19.4	0.7	24	1	AX708815	ACCESSION:AX708815
C 452	19.6	0.7	30	1	AR179070	ACCESSION:AR179070	C 525	19.4	0.7	24	1	AX708815	ACCESSION:AX708815
C 453	19.6	0.7	30	1	E04638	ACCESSION:E04638	C 526	19.4	0.7	25	1	BD056964	ACCESSION:BD056964
C 454	19.6	0.7	30	1	I84450	ACCESSION:I84450	527	19.4	0.7	25	1	AX708814	ACCESSION:AX708814
C 455	19.6	0.7	30	1	AX104902	ACCESSION:AX104902	C 528	19.4	0.7	26	1	BD237566	ACCESSION:BD237566
C 456	19.6	0.7	30	1	AX104903	ACCESSION:AX104903	C 529	19.4	0.7	26	1	AR257336	ACCESSION:AR257336
C 457	19.6	0.7	30	1	AX474673	ACCESSION:AX474673	C 530	19.4	0.7	26	1	AR263647	ACCESSION:AR263647
C 458	19.6	0.7	30	1	AX474674	ACCESSION:AX474674	C 531	19.4	0.7	26	1	AX814950	ACCESSION:AX814950
C 459	19.6	0.7	30	1	AX521609	ACCESSION:AX521609	C 532	19.4	0.7	26	1	BD062456	ACCESSION:BD062456
C 460	19.6	0.7	30	1	BD105776	ACCESSION:BD105776	C 533	19.4	0.7	26	1	AR013918	ACCESSION:AR013918
C 461	19.6	0.7	30	1	BD132851	ACCESSION:BD132851	C 534	19.4	0.7	27	1	AX513052	ACCESSION:AX513052
C 462	19.6	0.7	30	1	BD181358	ACCESSION:BD181358	535	19.4	0.7	28	1	AR022650	ACCESSION:AR022650
C 463	19.6	0.7	30	1	BD181359	ACCESSION:BD181359	536	19.4	0.7	28	1	AR055108	ACCESSION:AR055108
C 464	19.6	0.7	30	1	AR051244	ACCESSION:AR051244	537	19.4	0.7	28	1	AR055109	ACCESSION:AR055109
C 465	19.6	0.7	30	1	AR127791	ACCESSION:AR127791	538	19.4	0.7	28	1	AR055110	ACCESSION:AR055110
C 466	19.6	0.7	30	1	I28373	ACCESSION:I28373	539	19.4	0.7	28	1	AR068449	ACCESSION:AR068449
C 467	19.6	0.7	30	1	AR016852	ACCESSION:AR016852	540	19.4	0.7	28	1	AR068450	ACCESSION:AR068450
C 468	19.6	0.7	30	1	AR020878	ACCESSION:AR020878	541	19.4	0.7	28	1	AR068451	ACCESSION:AR068451
C 469	19.6	0.7	30	1	AR027201	ACCESSION:AR027201	542	19.4	0.7	28	1	AR150988	ACCESSION:AR150988
C 470	19.6	0.7	30	1	AR038488	ACCESSION:AR038488	543	19.4	0.7	28	1	AR156058	ACCESSION:AR156058
C 471	19.6	0.7	30	1	AR064630	ACCESSION:AR064630	544	19.4	0.7	28	1	AR172065	ACCESSION:AR172065

C 107	22	0.8	30	1	AX079108	ACCESSION:AX079108	C 180	21	0.7	24	1	AR010037	ACCESSION:AR010037
108	22	0.8	30	1	BD072870	ACCESSION:BD072870	C 181	21	0.7	24	1	AR034772	ACCESSION:AR034772
109	22	0.8	30	1	BD107497	ACCESSION:BD107497	C 182	21	0.7	24	1	AR068465	ACCESSION:AR068465
110	22	0.8	30	1	BD145029	ACCESSION:BD145029	C 183	21	0.7	24	1	AR105984	ACCESSION:AR105984
111	22	0.8	30	1	BD166029	ACCESSION:BD166029	C 184	21	0.7	24	1	AR107972	ACCESSION:AR107972
C 112	22	0.8	32	1	AX838502	ACCESSION:AX838502	C 185	21	0.7	24	1	BD234330	ACCESSION:BD234330
113	21.8	0.8	27	1	AR214918	ACCESSION:AR214918	C 186	21	0.7	24	1	I24762	ACCESSION:I24762
114	21.8	0.8	27	1	AX009609	ACCESSION:AX009609	C 187	21	0.7	24	1	AR184443	ACCESSION:AR184443
115	21.8	0.8	28	1	BD234335	ACCESSION:BD234335	C 188	21	0.7	24	1	AR202876	ACCESSION:AR202876
116	21.8	0.8	32	1	BD234356	ACCESSION:BD234356	C 189	21	0.7	24	1	AR213697	ACCESSION:AR213697
C 117	21.8	0.8	35	1	AX556148	ACCESSION:AX556148	C 190	21	0.7	24	1	AR232949	ACCESSION:AR232949
118	21.6	0.8	29	1	AR098648	ACCESSION:AR098648	C 191	21	0.7	24	1	AR241846	ACCESSION:AR241846
119	21.6	0.8	29	1	AR204722	ACCESSION:AR204722	C 192	21	0.7	24	1	AR340571	ACCESSION:AR340571
C 120	21.6	0.8	30	1	AR051244	ACCESSION:AR051244	C 193	21	0.7	24	1	AR345020	ACCESSION:AR345020
C 121	21.6	0.8	30	1	AR127791	ACCESSION:AR127791	C 194	21	0.7	24	1	AX104241	ACCESSION:AX104241
C 122	21.6	0.8	30	1	I28373	ACCESSION:I28373	C 195	21	0.7	24	1	AX104769	ACCESSION:AX104769
123	21.6	0.8	30	1	AR264926	ACCESSION:AR264926	C 196	21	0.7	24	1	AX104770	ACCESSION:AX104770
124	21.6	0.8	30	1	AR264927	ACCESSION:AR264927	C 197	21	0.7	24	1	AX354553	ACCESSION:AX354553
125	21.6	0.8	30	1	BD072871	ACCESSION:BD072871	C 198	21	0.7	24	1	AX355813	ACCESSION:AX355813
126	21.6	0.8	30	1	BD072872	ACCESSION:BD072872	C 199	21	0.7	24	1	AX427163	ACCESSION:AX427163
127	21.6	0.8	30	1	BD107498	ACCESSION:BD107498	C 200	21	0.7	24	1	AX428574	ACCESSION:AX428574
128	21.6	0.8	30	1	BD107499	ACCESSION:BD107499	C 201	21	0.7	24	1	AX547294	ACCESSION:AX547294
129	21.6	0.8	30	1	BD145030	ACCESSION:BD145030	C 202	21	0.7	24	1	AX547822	ACCESSION:AX547822
130	21.6	0.8	30	1	BD145031	ACCESSION:BD145031	C 203	21	0.7	24	1	AX547823	ACCESSION:AX547823
131	21.6	0.8	30	1	BD166030	ACCESSION:BD166030	C 204	21	0.7	24	1	AX684290	ACCESSION:AX684290
132	21.6	0.8	30	1	BD166031	ACCESSION:BD166031	C 205	21	0.7	24	1	AX750585	ACCESSION:AX750585
133	21.4	0.8	25	1	AX116188	ACCESSION:AX116188	C 206	21	0.7	24	1	AX817782	ACCESSION:AX817782
134	21.4	0.8	27	1	AX711956	ACCESSION:AX711956	C 207	21	0.7	24	1	AX829247	ACCESSION:AX829247
135	21.4	0.8	27	1	BD097128	ACCESSION:BD097128	C 208	21	0.7	24	1	AX838369	ACCESSION:AX838369
136	21.4	0.8	27	1	BD161932	ACCESSION:BD161932	C 209	21	0.7	24	1	BD136714	ACCESSION:BD136714
C 137	21.4	0.8	28	1	AX427136	ACCESSION:AX427136	C 210	21	0.7	25	1	AR105982	ACCESSION:AR105982
C 138	21.4	0.8	29	1	AR268128	ACCESSION:AR268128	C 211	21	0.7	25	1	BD234336	ACCESSION:BD234336
C 139	21.4	0.8	31	1	AX394623	ACCESSION:AX394623	C 212	21	0.7	25	1	I58009	ACCESSION:I58009
C 140	21.4	0.8	32	1	AX394625	ACCESSION:AX394625	C 213	21	0.7	25	1	I96072	ACCESSION:I96072
141	21.2	0.8	24	1	AX391871	ACCESSION:AX391871	C 214	21	0.7	25	1	AR288252	ACCESSION:AR288252
142	21.2	0.8	26	1	AR137712	ACCESSION:AR137712	C 215	21	0.7	25	1	BD187513	ACCESSION:BD187513
143	21.2	0.8	26	1	BD237566	ACCESSION:BD237566	C 216	21	0.7	25	1	BD187514	ACCESSION:BD187514
144	21.2	0.8	26	1	I79496	ACCESSION:I79496	C 217	21	0.7	25	1	BD204988	ACCESSION:BD204988
145	21.2	0.8	26	1	AR257336	ACCESSION:AR257336	C 218	21	0.7	25	1	AR174582	ACCESSION:AR174582
146	21.2	0.8	26	1	AR263647	ACCESSION:AR263647	C 219	21	0.7	26	1	BD248975	ACCESSION:BD248975
C 147	21.2	0.8	26	1	AX338547	ACCESSION:AX338547	C 220	21	0.7	26	1	I79495	ACCESSION:I79495
148	21.2	0.8	26	1	AX427154	ACCESSION:AX427154	C 221	21	0.7	26	1	AR279358	ACCESSION:AR279358
149	21.2	0.8	26	1	AX528804	ACCESSION:AX528804	C 222	21	0.7	26	1	AR374074	ACCESSION:AR374074
150	21.2	0.8	26	1	AX814950	ACCESSION:AX814950	C 223	21	0.7	26	1	AR404597	ACCESSION:AR404597
151	21.2	0.8	26	1	BD062456	ACCESSION:BD062456	C 224	21	0.7	26	1	BD007174	ACCESSION:BD007174
152	21.2	0.8	26	1	BD192375	ACCESSION:BD192375	C 225	21	0.7	27	1	AX492939	ACCESSION:AX492939
153	21.2	0.8	27	1	AX327980	ACCESSION:AX327980	C 226	21	0.7	27	1	BD175131	ACCESSION:BD175131
154	21.2	0.8	27	1	AX513052	ACCESSION:AX513052	C 227	21	0.7	30	1	A79651	ACCESSION:A79651
C 155	21.2	0.8	27	1	S6486253	ACCESSION:S64864	C 228	21	0.7	30	1	AX351705	ACCESSION:AX351705
156	21.2	0.8	32	1	I29892	ACCESSION:I29892	C 229	21	0.7	30	1	AX351706	ACCESSION:AX351706
C 157	21.2	0.8	32	1	AR222454	ACCESSION:AR222454	C 230	21	0.7	30	1	AX351707	ACCESSION:AX351707
158	21	0.7	31	1	AR080294	ACCESSION:AR080294	C 231	21	0.7	30	1	AX351708	ACCESSION:AX351708
C 159	21	0.7	21	1	AR084521	ACCESSION:AR084521	C 232	21	0.7	30	1	AX351715	ACCESSION:AX351715
160	21	0.7	21	1	AR084524	ACCESSION:AR084524	C 233	21	0.7	32	1	AX430213	ACCESSION:AX430213
161	21	0.7	21	1	AR093143	ACCESSION:AR093143	C 234	21	0.7	32	1	BD165916	ACCESSION:BD165916
162	21	0.7	21	1	AR095412	ACCESSION:AR095412	C 235	21	0.7	32	1	AR014684	ACCESSION:AR014684
163	21	0.7	21	1	I65744	ACCESSION:I65744	C 236	21	0.7	32	1	AR341692	ACCESSION:AR341692
164	21	0.7	21	1	AR322245	ACCESSION:AR322245	C 237	21	0.7	32	1	AR366811	ACCESSION:AR366811
165	21	0.7	21	1	AX104720	ACCESSION:AX104720	C 238	21	0.7	32	1	AR432384	ACCESSION:AR432384
166	21	0.7	21	1	AX355812	ACCESSION:AX355812	C 239	21	0.7	45	1	AX287571	ACCESSION:AX287571
167	21	0.7	21	1	AX547773	ACCESSION:AX547773	C 240	21	0.7	45	1	AX287575	ACCESSION:AX287575
168	21	0.7	21	1	AX825105	ACCESSION:AX825105	C 241	21	0.7	24	1	AR431307	ACCESSION:AR431307
C 169	21	0.7	21	1	AX825135	ACCESSION:AX825135	C 242	21	0.7	24	1	BD196419	ACCESSION:BD196419
C 170	21	0.7	21	1	AX825151	ACCESSION:AX825151	C 243	21	0.7	24	1	BD196419	ACCESSION:BD196419
C 171	21	0.7	21	1	AX825159	ACCESSION:AX825159	C 244	21	0.7	27	1	AR241865	ACCESSION:AR241865
172	21	0.7	21	1	AX825163	ACCESSION:AX825163	C 245	21	0.7	27	1	AR214918	ACCESSION:AR214918
173	21	0.7	21	1	AX825166	ACCESSION:AX825166	C 246	21	0.7	27	1	AX009609	ACCESSION:AX009609
174	21	0.7	21	1	BD080832	ACCESSION:BD080832	C 247	21	0.7	32	1	AR274390	ACCESSION:AR274390
175	21	0.7	21	1	BD224108	ACCESSION:BD224108	C 248	21	0.7	32	1	AR344932	ACCESSION:AR344932
C 176	21	0.7	22	1	AR164336	ACCESSION:AR164336	C 249	21	0.7	32	1	AR382308	ACCESSION:AR382308
C 177	21	0.7	22	1	I31828	ACCESSION:I31828	C 250	21	0.7	32	1	AR409897	ACCESSION:AR409897
C 178	21	0.7	22	1	I69425	ACCESSION:I69425	C 251	21	0.7	32	1	AR429649	ACCESSION:AR429649
179	21	0.7	23	1	BD244857	ACCESSION:BD244857	C 252	21	0.7	32	1	AX196220	ACCESSION:AX196220

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2004, 12:17:18 ; Search time 116 Seconds
(without alignments)
3.649 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgcatgctgct.....gaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 3579 seqs, 75484 residues

Total number of hits satisfying chosen parameters: 7158

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5590 summaries

Database : rng3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	31.4	1.1	47	1	AAL07489
2	30.4	1.1	44	1	ADD33791
3	30	1.1	45	1	AAS95728
4	30	1.1	45	1	AAS95724
C 5	29.4	1.0	33	1	ABQ80395
6	29.2	1.0	43	1	AAD17216
C 7	29.2	1.0	44	1	AAV09273
C 8	29	1.0	38	1	AAL07488
C 9	28.8	1.0	43	1	AAQ25031
10	28.4	1.0	40	1	AAQ25031
11	28.4	1.0	40	1	AAA39649
C 12	28.2	1.0	36	1	ABK99273
C 13	28.2	1.0	36	1	AAD27117
C 14	28.2	1.0	37	1	AAD27125
15	28	1.0	28	1	AAL62267
C 16	27.8	1.0	33	1	ABQ80394
17	27.8	1.0	42	1	AAA37946
C 18	27.4	1.0	38	1	AAZ57404
19	27.4	1.0	40	1	AAZ98722
20	27.2	1.0	32	1	AAZ70278
21	27.2	1.0	32	1	AAN92244
22	27.2	1.0	32	1	ADC33445
23	27.2	1.0	33	1	AAF29153
C 24	27.2	1.0	36	1	ABK99272
C 25	27.2	1.0	36	1	AAD27116
C 26	27.2	1.0	38	1	AAL07487
C 27	27.2	1.0	40	1	ABN89412
28	27.2	1.0	41	1	ABZ46327
29	27.2	1.0	41	1	ABZ48839
30	27	1.0	27	1	AAL62265
C 31	27	1.0	37	1	AAD27124
32	26.8	1.0	39	1	AAV12483
33	26.8	1.0	39	1	AAX30019

34	26.8	1.0	40	1	AAQ55168	Sequence of primer
35	26.8	1.0	41	1	AAV03013	Aspergillus oryzae
36	26.6	0.9	40	1	AAQ25023	Anti-sense oligonu
37	26	0.9	34	1	AAT93827	Antitumoural phosp
38	25.6	0.9	33	1	AAX88521	Conus stercusmusca
39	25.4	0.9	31	1	AAS17761	Oligo d(T) PCR pri
40	25.4	0.9	32	1	AAS09500	SMART PCR primer #
41	25.4	0.9	32	1	ABA01204	Mamushi fibrinolyt
42	25.2	0.9	30	1	AAN70277	Sequence of scissi
43	25.2	0.9	30	1	AAN92243	SS probe MRCO64.
44	25.2	0.9	30	1	AAQ36302	GST3anti, for GSTp
45	25.2	0.9	30	1	AAQ36301	GST3par, for GSTpi
46	25.2	0.9	30	1	AAX57020	WO9923258 oligonuc
C 47	25.2	0.9	30	1	AAF99889	Immunostimulatory
48	25.2	0.9	30	1	AAF99888	Immunostimulatory
C 49	25.2	0.9	30	1	ABK10416	Synthetic primer s
50	25.2	0.9	30	1	ABK10412	Synthetic primer s
51	25.2	0.9	30	1	ABK70490	In-situ analysis s
52	25.2	0.9	30	1	ABS53961	Method of measurin
53	24.8	0.9	40	1	ABN89412	Polymorphism detec
54	24.6	0.9	35	1	AAK14632	Triple helix formi
C 55	24.6	0.9	36	1	ABQ95487	Tumour suppression
56	24.4	0.9	29	1	AAK71190	Molecular interact
57	24.4	0.9	29	1	AAK71173	Molecular interact
C 58	24.4	0.9	36	1	AAD27121	RNA template. (AU)
59	24.2	0.9	29	1	AAQ05003	Sequence binding t
60	24.2	0.9	30	1	ADA26181	Rice semi-dwarf (s
61	24.2	0.9	37	1	AAF85682	Pea blight resista
62	24	0.9	30	1	AAF26222	APC binding protei
63	24	0.9	33	1	AAL44170	Porphyra yezoensis
64	24	0.9	34	1	AAA75564	PCR primer for DNA
65	24	0.9	34	1	AAD09727	ZC18698 primer, to
66	24	0.9	34	1	AAS20662	Primer ZC18698, ued
67	24	0.9	34	1	ADD68172	PCR primer relat
68	23.8	0.8	34	1	ADC65905	DNA oligonucleotid
C 69	23.6	0.8	32	1	ABN83375	Mononucleotide rep
70	23.6	0.8	35	1	AAD46356	Vp3 oligonucleotid
C 71	23.4	0.8	30	1	AAS63441	Oligonucleotide-na
C 72	23.4	0.8	30	1	AAS10385	Oligonucleotide-cy
C 73	23.4	0.8	30	1	ABK65048	Nanoparticle-oligo
C 74	23.4	0.8	30	1	ABS64686	Nucleic acid detec
C 75	23.4	0.8	30	1	AAL61658	Oligonucleotide #1
76	23.4	0.8	36	1	AAA94321	RNA-protein fusion
C 77	23.4	0.8	36	1	ABK99274	Hepatitis C virus
C 78	23.4	0.8	36	1	AAD27118	Hepatitis C virus
79	23.2	0.8	29	1	AAV15487	RNA template, (AU)
C 80	23.2	0.8	29	1	ABN83378	PR-1 promoter prim
C 81	23.2	0.8	29	1	ADA26489	Mononucleotide rep
C 82	23.2	0.8	36	1	AAA94321	DNA nanolithograph
83	23	0.8	23	1	AAQ30431	RNA-protein fusion
84	23	0.8	25	1	AAI72268	Oligomer IL6804 fo
85	23	0.8	27	1	AAV71935	P4 primer used in
86	23	0.8	28	1	AAA40362	Anchored poly T RT
87	23	0.8	32	1	AAQ87894	pBluescriptSK+ pha
88	23	0.8	32	1	AAF60568	Normalised library
89	23	0.8	35	1	AAT93816	Neuraminidase PCR
90	22.8	0.8	35	1	ABX79828	Antitumoural phosp
91	22.8	0.8	27	1	AAQ52157	EST polymorphic DN
92	22.8	0.8	35	1	ABS64697	Breast cancer spec
93	22.8	0.8	35	1	AAL61669	Nucleic acid detec
C 94	22.8	0.8	35	1	ABQ80396	Oligonucleotide #2
95	22.6	0.8	29	1	AAQ79096	Probe APC 2. Homo
C 96	22.6	0.8	29	1	AAA94315	Tobacco PMT PCR pr
C 97	22.6	0.8	29	1	AAS00066	RNA-protein fusion
C 98	22.6	0.8	29	1	AAH20990	Synthetic branched
C 99	22.6	0.8	29	1	AAK98637	C-myc epitope puro
C 100	22.6	0.8	30	1	AAV48087	S cerevisiae alpha
C 101	22.6	0.8	30	1	ABL35101	Oligonucleotide 30
C 102	22.4	0.8	24	1	ABK86169	Phosphorothioate s
103	22.4	0.8	24	1	ABK86168	Oligo dT primer #2
104	22.4	0.8	25	1	AAV42215	Oligo dT primer #1
105	22.4	0.8	30	1	ADC16682	Sequencing primer
106	22.4	0.8	33	1	AAA94322	Aminoacylation RNA

107	1	AAV12929	Oligonucleotide SE	180	21.2	0.8	26	1	AAAN70276	Sequence of scissi
108	34	AAV59243	Small synthetic DN	181	21.2	0.8	26	1	AAAN70275	SS probe MRCO59.
109	34	AAV48094	Oligonucleotide 34	182	21.2	0.8	26	1	AAAN22241	SS probe MRCO60.
110	34	AAC90605	Tomato spotted wil	183	21.2	0.8	26	1	AAAN22242	Human BSL24 specif
111	35	AAD46356	Vp3 oligonucleotid	184	21.2	0.8	26	1	AAAX07466	Human pancreatic p
112	27	AAAN70281	Sequence of scissi	185	21.2	0.8	26	1	AAAX78723	CDNA library produ
113	27	AAAN70274	Sequence of scissi	186	21.2	0.8	26	1	AAAF77536	Primer #4. Uniden
114	27	AAAN92240	SS probe MRCO46.	187	21.2	0.8	26	1	AAAF23526	Human zsig63 cDNA
115	27	AAAN92247	SS probe MRCO71.	188	21.2	0.8	26	1	AAAS20595	Human secreted sal
116	27	AAAN92247	DNA sequence used	189	21.2	0.8	26	1	ABAS2637	ZC7231 primer used
117	27	AAAF9706	Immunostimulatory	190	21.2	0.8	26	1	AAAD45054	Bacterial PNP DNA
118	27	ABAS78427	Angiogenesis inhib	191	21.2	0.8	26	1	AAAD26899	PolyPNP out-of-fra
119	27	ABL39406	Immunostimulatory	192	21.2	0.8	26	1	AAAD39650	Primer #2 used to
120	27	ACH03245	Immunostimulatory	193	21.2	0.8	26	1	AAAD3853	Bovine viral diarr
121	33	ADBC60749	Immunostimulatory	194	21.2	0.8	26	1	AAAD55692	Oligodeoxynucleic
122	33	ADBC60749	Termitomyces album	195	21.2	0.8	26	1	ABX93598	Human zsig63 PCR/s
123	43	AAAL31948	Human SNP oligonuc	196	21.2	0.8	26	1	ABX93598	Oligo (dT) primer
124	23	AAQ30432	Oligomer IL6805 fo	197	21.2	0.8	26	1	ACA62282	Nucleotide sequenc
125	23	AAQ30430	Oligomer IL6803 fo	198	21.2	0.8	26	1	ACF36382	Anchored poly T RT
126	23	ABL01773	Human MSH2 (hMSH2)	199	21.2	0.8	27	1	AAV71936	Murine SCCE 5'-RAC
127	24	AAI66361	Human phosphatidyl	200	21.2	0.8	27	1	ABQ76254	PolyA adapter DNA.
128	25	AAAX84259	PCR primer for hum	201	21.2	0.8	30	1	ABX89953	Reverse transcript
129	25	AAAD3264	Human CYP2D6 gene	202	21	0.7	21	1	AAQ75733	Reverse transcript
130	25	AAAD3264	Human full length	203	21	0.7	21	1	AAQ75757	Primer used to rev
131	26	AAAS20596	Human zsig63 cDNA	204	21	0.7	21	1	AAZ26973	Protein kinase inh
132	26	ABAS2638	Human secreted sal	205	21	0.7	21	1	AAZ44350	Immunostimulatory
133	26	AAAD45055	ZC7764a primer use	206	21	0.7	21	1	AAAF99707	Oligonucleotide us
134	26	AAAS20671	Human zsig63 PCR/s	207	21	0.7	21	1	AAH42480	Angiogenesis inhib
135	26	ABX93599	Sindbis virus mRNA	208	21	0.7	21	1	ABL39404	Immunostimulatory
136	30	AAA90394	Sindbis virus 3' R	209	21	0.7	21	1	ABL39404	Angiogenesis inhib
137	30	ABL56893	Synthetic deoxyrib	210	21	0.7	21	1	ABL39404	Immunostimulatory
138	30	ABAF26221	APC binding protei	211	21	0.7	21	1	AAAD51323	Regular oligo dt p
139	30	ABA97617	Poly f nucleotide	212	21	0.7	21	1	AAAL62266	Human TFAP2C DNA s
140	30	ABA97617	Probe poly f for a	213	21	0.7	21	1	ACH03246	Immunostimulatory
141	30	ABL95890	Tumour-suppressor	214	21	0.7	21	1	ACH03246	Immunostimulatory
142	31	ABAS5182	Nuclear transition	215	21	0.7	21	1	AAQ64724	2',5'-linked tetra
143	33	ACF42844	Gastric acid produ	216	21	0.7	21	1	AAAF17413	L1 cleavage site r
144	26	AAAF16616	M. tuberculosis rp	217	21	0.7	23	1	AAAC62450	Cleavage of nuclei
145	27	AAA57856	Deoxy-T22-tagged s	218	21	0.7	23	1	AAAF16627	Cleavage of nuclei
146	28	AAA40358	pBluescriptSK+ pha	219	21	0.7	24	1	AAAT99286	Gastric acid produ
147	28	AAA40358	Structural product	220	21	0.7	24	1	AAV31743	POLYA, a competito
148	31	AAQ3410	Nucleic acid detec	221	21	0.7	24	1	AAAX04086	Nucleotide sequenc
149	35	ABAS64697	Oligonucleotide #2	222	21	0.7	24	1	AAAX04086	Oligonucleotide PO
150	29	AAAL61669	Linear multimer pr	223	21	0.7	24	1	AAA40359	pBluescriptSK+ pha
151	29	AAV59216	Triplex forming ol	224	21	0.7	24	1	AAA40353	pBluescriptSK+ pha
152	29	AAAL44903	DNA oligonucleotid	225	21	0.7	24	1	AAAF99756	Immunostimulatory
153	29	ADC65873	Oligonucleotide cl	226	21	0.7	24	1	AAAF99756	Immunostimulatory
154	30	ABL56894	Synthetic deoxyrib	227	21	0.7	24	1	AAAF99757	Immunostimulatory
155	30	ABL56895	Synthetic deoxyrib	228	21	0.7	24	1	ABV14842	Human prostate exp
156	30	AAF60462	Oligonucleotide #7	229	21	0.7	24	1	ABV14842	Angiogenesis inhib
157	30	AAAD25661	Poly h nucleotide	230	21	0.7	24	1	ABV14842	Angiogenesis inhib
158	30	ABA97618	Poly g nucleotide	231	21	0.7	24	1	ABV14842	Angiogenesis inhib
159	30	ABL95891	Probe poly g for a	232	21	0.7	24	1	ABV14842	Angiogenesis inhib
160	30	ABL95892	Probe poly h for a	233	21	0.7	24	1	ABV14842	Angiogenesis inhib
161	33	AAV06769	Oligonucleotide co	234	21	0.7	24	1	ABV14842	Angiogenesis inhib
162	33	ABK15694	Human activating G	235	21	0.7	24	1	ABV14842	Angiogenesis inhib
163	33	AAQ25023	Anti-sense oligonu	236	21	0.7	24	1	ABV14842	Angiogenesis inhib
164	40	AAAH38515	SNP specific SNPE	237	21	0.7	24	1	ABV14842	Angiogenesis inhib
165	25	AAAH38515	Nucleotide sequenc	238	21	0.7	24	1	ABV14842	Angiogenesis inhib
166	27	AAH43080	Nucleotide sequenc	239	21	0.7	24	1	ABV14842	Angiogenesis inhib
167	27	ABQ79879	Coxsackie B virus	240	21	0.7	24	1	ABV14842	Angiogenesis inhib
168	27	ABX12469	Biosensor related	241	21	0.7	24	1	ABV14842	Angiogenesis inhib
169	27	ADC75074	Deoxy-A22-tagged s	242	21	0.7	24	1	ABV14842	Angiogenesis inhib
170	27	AAAS7855	Regulatable, catal	243	21	0.7	24	1	ABV14842	Angiogenesis inhib
171	28	AAAL43065	Substrate RNA rela	244	21	0.7	24	1	ABV14842	Angiogenesis inhib
172	28	ADA39569	tRNAPolyU reverse	245	21	0.7	24	1	ABV14842	Angiogenesis inhib
173	29	AAQ68614	Reverse trna prime	246	21	0.7	24	1	ABV14842	Angiogenesis inhib
174	29	AAAT09334	T7T18Apad PS4-31-0	247	21	0.7	24	1	ABV14842	Angiogenesis inhib
175	31	AAAD33519	T7T18Apad PS3-32-0	248	21	0.7	24	1	ABV14842	Angiogenesis inhib
176	32	AAAD33521	First strand synth	249	21	0.7	24	1	ABV14842	Angiogenesis inhib
177	32	ABAS3433	Aspergillus niger	250	21	0.7	24	1	ABV14842	Angiogenesis inhib
178	24	ABK48140		251	21	0.7	24	1	ABV14842	Angiogenesis inhib
179				252	21	0.7	24	1	ABV14842	Angiogenesis inhib

253	21	0.7	25	1	ABK49986	Example oligonucleotide of
254	21	0.7	25	1	ADC54009	Oligonucleotide of
c 255	21	0.7	25	1	ADC54008	Oligonucleotide of
256	21	0.7	26	1	AAI73048	Scaffold oligonucleotide
257	21	0.7	26	1	AAS20672	Human zaphall Lig
258	21	0.7	26	1	ABX93461	LS147-specific pol
259	21	0.7	27	1	AAI15434	PCR primer used to
260	21	0.7	27	1	ABX93461	Human androgen rec
261	21	0.7	27	1	ABS53863	Human ARAAP associ
c 262	21	0.7	28	1	ABS54324	Human haemoglobin
263	21	0.7	28	1	AAS11744	Rat type I steroid
264	21	0.7	29	1	AAQ97396	Primer for rat ste
c 265	21	0.7	29	1	AAT99803	Downstream primer
c 266	21	0.7	30	1	AAT69677	RNA/DNA hybrid con
c 267	21	0.7	30	1	ABL35095	Phosphorothioate s
c 268	21	0.7	30	1	ABL35096	Phosphorothioate s
c 269	21	0.7	30	1	ABL35097	RNA/DNA hybrid ass
c 270	21	0.7	30	1	ABL35105	Phosphorothioate s
c 271	21	0.7	30	1	ABL35098	Mononucleotide rep
272	21	0.7	32	1	ABN83375	Primer B for Non-A
273	21	0.7	32	1	AAQ43973	Triple helix formi
274	21	0.7	32	1	AAT77235	Rat fibroblast gro
275	21	0.7	32	1	AAT94579	Antifungal polypep
276	21	0.7	32	1	ADC87763	F. culmorum FCWP1
c 277	21	0.7	45	1	AAS95728	Allele discriminat
c 278	21	0.7	45	1	AAS95724	Allele discriminat
c 279	20.8	0.7	24	1	AZ00877	PCR primer PGRT32
c 280	20.8	0.7	24	1	AZ00877	PCR primer PGRT32
c 281	20.8	0.7	27	1	ABX79828	EST polymorphic DN
c 282	20.8	0.7	27	1	AZ43904	M. tuberculosis rp
c 283	20.8	0.7	32	1	AAS63424	Oligonucleotide-na
c 284	20.8	0.7	32	1	AAS10367	Alkanethiol-modifi
285	20.8	0.7	32	1	AAH28290	3' untranslated re
c 286	20.8	0.7	32	1	ABK65031	Nanoparticle-oligo
c 287	20.8	0.7	32	1	ABS64669	Nucleic acid detec
c 288	20.8	0.7	32	1	ACD27316	Nanotechnology nuc
c 289	20.8	0.7	32	1	AAI61641	Thiol-modified oli
c 290	20.8	0.7	32	1	ABX79177	Fluorescein-label
c 291	20.8	0.7	32	1	ABX92173	Nanoparticle-assoc
c 292	20.8	0.7	32	1	ACD27251	Nanotechnology nuc
c 293	20.8	0.7	32	1	ACD27121	Nanotechnology nuc
c 294	20.8	0.7	32	1	ACD27381	Nanotechnology nuc
c 295	20.8	0.7	32	1	ACD27186	Nanotechnology nuc
c 296	20.8	0.7	32	1	ACD27056	Nanotechnology nuc
c 297	20.8	0.7	32	1	ACH00060	Nanotechnology nuc
c 298	20.8	0.7	32	1	ADA06155	Nanotechnology nuc
c 299	20.8	0.7	32	1	ACD26991	Nanoparticle label
c 300	20.8	0.7	32	1	ADE71592	Nanotechnology nuc
c 301	20.8	0.7	47	1	AAI07489	Magneto-gold nanop
c 302	20.6	0.7	27	1	AAV71935	Human reproductive
c 303	20.6	0.7	30	1	ABX89953	Polymorphic poly T RT
c 304	20.6	0.7	31	1	ABS55182	PolyA adapter DNA
c 305	20.6	0.7	36	1	ABQ95487	Tumour-suppressor
c 306	20.4	0.7	24	1	ABK86169	Tumour suppression
c 307	20.4	0.7	24	1	ABK86168	Oligo dt primer #2
c 308	20.4	0.7	24	1	AAI66361	Oligo dt primer #1
c 309	20.4	0.7	30	1	AAD25661	Human phosphatidyl
c 310	20.4	0.7	30	1	AAT69677	Oligonucleotide #7
311	20.4	0.7	30	1	ABL56888	Downstream primer
312	20.4	0.7	30	1	ABA97612	Synthetic deoxyrib
c 313	20.4	0.7	30	1	AAD33517	Poly a nucleotide
314	20.4	0.7	30	1	ABL95885	Probe poly a for a
315	20.4	0.7	31	1	AAQ99582	Human TPO anti-sen
316	20.4	0.7	31	1	ABA97621	Poly j nucleotide
317	20.2	0.7	22	1	AAI50570	Molecular array pr

399	20	0.7	20	1	ABN87103	Capture probe CP5'	C 472	20	0.7	20	1	AAL62309	Human transcriptio
C 400	20	0.7	20	1	ABZ88267	Human oligonucleot	C 473	20	0.7	20	1	AAL62315	Human transcriptio
C 401	20	0.7	20	1	ABZ88565	Human oligonucleot	C 474	20	0.7	20	1	AAL62333	Human transcriptio
C 402	20	0.7	20	1	ABZ88619	Human oligonucleot	C 475	20	0.7	20	1	AAL62278	Human transcriptio
C 403	20	0.7	20	1	ABZ89705	Human oligonucleot	C 476	20	0.7	20	1	AAL62310	Human transcriptio
C 404	20	0.7	20	1	ABZ85312	Human oligonucleot	C 477	20	0.7	20	1	AAL62319	Human transcriptio
C 405	20	0.7	20	1	ABZ88816	Human oligonucleot	C 478	20	0.7	20	1	AAL62336	Human transcriptio
C 406	20	0.7	20	1	ABZ88881	Human oligonucleot	C 479	20	0.7	20	1	AAL62276	Human transcriptio
C 407	20	0.7	20	1	ABZ89546	Human oligonucleot	C 480	20	0.7	20	1	AAL62282	Human transcriptio
C 408	20	0.7	20	1	ABZ89706	Human oligonucleot	C 481	20	0.7	20	1	AAL62285	Human transcriptio
C 409	20	0.7	20	1	ABZ88620	Human oligonucleot	C 482	20	0.7	20	1	AAL62302	Human transcriptio
C 410	20	0.7	20	1	ABZ88880	Human oligonucleot	C 483	20	0.7	20	1	AAL62347	Human transcriptio
C 411	20	0.7	20	1	ABZ89179	Human oligonucleot	C 484	20	0.7	20	1	AAL62283	Human transcriptio
C 412	20	0.7	20	1	ABZ88814	Human oligonucleot	C 485	20	0.7	20	1	AAL62323	Human transcriptio
C 413	20	0.7	20	1	ABZ89241	Human oligonucleot	C 486	20	0.7	20	1	AAL62330	Human transcriptio
C 414	20	0.7	20	1	ABZ90650	Human oligonucleot	C 487	20	0.7	20	1	AAL62342	Human transcriptio
C 415	20	0.7	20	1	ABZ99050	Human PDE4C oligon	C 488	20	0.7	20	1	AAL62346	Human transcriptio
C 416	20	0.7	20	1	ABZ88815	Human oligonucleot	C 489	20	0.7	20	1	AAL62277	Human transcriptio
C 417	20	0.7	20	1	ABZ85311	Human oligonucleot	C 490	20	0.7	20	1	AAL62287	Human transcriptio
C 418	20	0.7	20	1	ABZ85435	Human oligonucleot	C 491	20	0.7	20	1	AAL62300	Human transcriptio
C 419	20	0.7	20	1	ABZ88817	Human oligonucleot	C 492	20	0.7	20	1	AAL62304	Human transcriptio
C 420	20	0.7	20	1	ABZ88939	Human oligonucleot	C 493	20	0.7	20	1	AAL62317	Human transcriptio
C 421	20	0.7	20	1	ABZ89302	Human oligonucleot	C 494	20	0.7	20	1	AAL62334	Human transcriptio
C 422	20	0.7	20	1	ABZ87681	Human oligonucleot	C 495	20	0.7	20	1	AAL62337	Human transcriptio
C 423	20	0.7	20	1	ABZ88566	Human oligonucleot	C 496	20	0.7	20	1	AAL62289	Human transcriptio
C 424	20	0.7	20	1	ABZ89086	Human oligonucleot	C 497	20	0.7	20	1	AAL62291	Human transcriptio
C 425	20	0.7	20	1	ABZ85533	Human oligonucleot	C 498	20	0.7	20	1	AAL62296	Human transcriptio
C 426	20	0.7	20	1	ABZ89015	Human oligonucleot	C 499	20	0.7	20	1	AAL62321	Human transcriptio
C 427	20	0.7	20	1	ABZ89441	Human oligonucleot	C 500	20	0.7	20	1	AAL62324	Human transcriptio
C 428	20	0.7	20	1	ABZ89016	Human oligonucleot	C 501	20	0.7	20	1	AAL62326	Human transcriptio
C 429	20	0.7	20	1	ABZ89120	Human oligonucleot	C 502	20	0.7	20	1	AAL62329	Human transcriptio
C 430	20	0.7	20	1	ABZ89704	Human oligonucleot	C 503	20	0.7	20	1	AAL62344	Human transcriptio
C 431	20	0.7	20	1	ACD27320	Nanotechnology nuc	C 504	20	0.7	20	1	AAL62279	Human transcriptio
C 432	20	0.7	20	1	ACC58867	Doubly labelled DN	C 505	20	0.7	20	1	AAL62280	Human transcriptio
C 433	20	0.7	20	1	ABZ22916	Phosphorothioate 2	C 506	20	0.7	20	1	AAL62281	Human transcriptio
C 434	20	0.7	20	1	AAL61645	Thiol-modified oli	C 507	20	0.7	20	1	AAL62297	Human transcriptio
C 435	20	0.7	20	1	ABZ59815	Potato gene PCR pr	C 508	20	0.7	20	1	AAL62318	Human transcriptio
C 436	20	0.7	20	1	ABX92177	Thio-modified 20dA	C 509	20	0.7	20	1	AAL62322	Human transcriptio
C 437	20	0.7	20	1	ACD27255	Nanoparticle-assoc	C 510	20	0.7	20	1	AAL62274	Human transcriptio
C 438	20	0.7	20	1	ACD27125	Nanotechnology nuc	C 511	20	0.7	20	1	AAL62299	Human transcriptio
C 439	20	0.7	20	1	ACD27385	Nanotechnology nuc	C 512	20	0.7	20	1	AAL62332	Human transcriptio
C 440	20	0.7	20	1	ACD27190	Nanotechnology nuc	C 513	20	0.7	20	1	AAL62338	Human transcriptio
C 441	20	0.7	20	1	ACD27060	Nanotechnology nuc	C 514	20	0.7	20	1	AAL62271	Human transcriptio
C 442	20	0.7	20	1	AAL62273	Human transcriptio	C 515	20	0.7	20	1	AAL62275	Human transcriptio
C 443	20	0.7	20	1	AAL62303	Human transcriptio	C 516	20	0.7	20	1	AAL62295	Human transcriptio
C 444	20	0.7	20	1	AAL62320	Human transcriptio	C 517	20	0.7	20	1	AAL62311	Human transcriptio
C 445	20	0.7	20	1	AAL62343	Human transcriptio	C 518	20	0.7	20	1	AAL62328	Human transcriptio
C 446	20	0.7	20	1	AAL62284	Human transcriptio	C 519	20	0.7	20	1	AAL62335	Human transcriptio
C 447	20	0.7	20	1	AAL62290	Human transcriptio	C 520	20	0.7	20	1	AAL62345	Human transcriptio
C 448	20	0.7	20	1	AAL62301	Human transcriptio	C 521	20	0.7	20	1	ACH00064	Nanotechnology nuc
C 449	20	0.7	20	1	AAL62306	Human transcriptio	C 522	20	0.7	20	1	ACD99851	Immunostimulatory
C 450	20	0.7	20	1	AAL62312	Human transcriptio	C 523	20	0.7	20	1	ACD99847	Immunostimulatory
C 451	20	0.7	20	1	AAL62325	Human transcriptio	C 524	20	0.7	20	1	ACD99532	Immunostimulatory
C 452	20	0.7	20	1	AAL62327	Human transcriptio	C 525	20	0.7	20	1	ADA14838	Hairpin target seq
C 453	20	0.7	20	1	AAL62341	Human transcriptio	C 526	20	0.7	20	1	ADA06159	Nanoparticle label
C 454	20	0.7	20	1	AAL62272	Human transcriptio	C 527	20	0.7	20	1	ACD26995	Nanotechnology nuc
C 455	20	0.7	20	1	AAL62288	Human transcriptio	C 528	20	0.7	20	1	ADB36933	Immunostimulatory
C 456	20	0.7	20	1	AAL62292	Human transcriptio	C 529	20	0.7	20	1	ADB36601	Immunostimulatory
C 457	20	0.7	20	1	AAL62307	Human transcriptio	C 530	20	0.7	20	1	ADB36929	Immunostimulatory
C 458	20	0.7	20	1	AAL62314	Human transcriptio	C 531	20	0.7	20	1	AAQ75732	Reverse transcript
C 459	20	0.7	20	1	AAL62331	Human transcriptio	C 532	20	0.7	20	1	AAQ75758	Reverse transcript
C 460	20	0.7	20	1	AAL62313	Human transcriptio	C 533	20	0.7	20	1	AAQ75756	Reverse transcript
C 461	20	0.7	20	1	AAL62286	Human transcriptio	C 534	20	0.7	20	1	AAQ75731	Reverse transcript
C 462	20	0.7	20	1	AAL62339	Human transcriptio	C 535	20	0.7	20	1	AAQ75734	Reverse transcript
C 463	20	0.7	20	1	AAL62340	Human transcriptio	C 536	20	0.7	20	1	AAQ75755	Reverse transcript
C 464	20	0.7	20	1	AAL62348	Human transcriptio	C 537	20	0.7	20	1	AAQ75732	Reverse transcript
C 465	20	0.7	20	1	AAL62293	Human transcriptio	C 538	20	0.7	20	1	AAQ75755	Reverse transcript
C 466	20	0.7	20	1	AAL62308	Human transcriptio	C 539	20	0.7	20	1	AAQ75755	Reverse transcript
C 467	20	0.7	20	1	AAL62316	Human transcriptio	C 540	20	0.7	20	1	AAQ75755	Reverse transcript
C 468	20	0.7	20	1	AAL62294	Human transcriptio	C 541	20	0.7	20	1	AAQ75755	Reverse transcript
C 469	20	0.7	20	1	AAL62298	Human transcriptio	C 542	20	0.7	20	1	AAQ75755	Reverse transcript
C 470	20	0.7	20	1	AAL62305	Human transcriptio	C 543	20	0.7	20	1	AAQ75755	Reverse transcript
C 471	20	0.7	20	1		Human transcriptio	C 544	20	0.7	20	1	AAQ75755	Reverse transcript

C 545	20	0.7	25	1	ABZ233535	fragment of a plas	C 618	19.6	0.7	27	1	AAN70281	Sequence of scissi
546	20	0.7	25	1	ACF79235	Calix(a)arene-olig	C 619	19.6	0.7	27	1	AAN70274	Sequence of scissi
547	20	0.7	27	1	AAT94842	Human ESF I 3' PCR	C 620	19.6	0.7	27	1	AAN92240	SS probe MRCO46.
548	20	0.7	27	1	AAA59740	PCR primer for hES	C 621	19.6	0.7	27	1	AAN92247	SS probe MRCO71.
549	20	0.7	27	1	AAF25224	3' primer for an e	C 622	19.6	0.7	27	1	AAQ40854	DNA sequence used
550	20	0.7	27	1	ABL41793	Primer for human e	C 623	19.6	0.7	27	1	AAF99706	Immunostimulatory
551	20	0.7	27	1	ABX14927	hESF I amplifying	C 624	19.6	0.7	27	1	ABS78427	Angiogenesis inhib
552	20	0.7	28	1	ADD35234	Mouse mitochondria	C 625	19.6	0.7	27	1	ABL39406	Immunostimulatory
C 553	20	0.7	29	1	AAA71190	Molecular interact	C 626	19.6	0.7	27	1	ACH03245	Immunostimulatory
C 554	20	0.7	29	1	AAA71173	Molecular interact	C 627	19.6	0.7	27	1	ADB37208	Immunostimulatory
555	20	0.7	29	1	AAQ85070	Oligonucleotide cl	C 628	19.6	0.7	29	1	AAQ05003	Sequence binding t
556	20	0.7	29	1	AAQ83933	Oligonucleotide cl	C 629	19.6	0.7	29	1	AAA94315	RNA-protein fusion
C 557	20	0.7	29	1	ACD18468	Oligonucleotide cl	C 630	19.6	0.7	29	1	AAAS0066	Synthetic branched
558	20	0.7	29	1	ACD18467	Human zinc finger	C 631	19.6	0.7	29	1	AAH20990	C-myc epitope puro
559	20	0.7	30	1	ABL56892	Human zinc finger	C 632	19.6	0.7	29	1	AAK98637	s cerevisiae alpha
560	20	0.7	30	1	ABL56896	Synthetic deoxyrib	C 633	19.6	0.7	30	1	AAN70277	Sequence of scissi
561	20	0.7	30	1	ABL56890	Synthetic deoxyrib	C 634	19.6	0.7	30	1	AAN92243	SS probe MRCO64.
562	20	0.7	30	1	ABL56891	Synthetic deoxyrib	C 635	19.6	0.7	30	1	AAQ36302	GST3anti, for GSTp
563	20	0.7	30	1	ABL56897	Synthetic deoxyrib	C 636	19.6	0.7	30	1	AAQ36301	GST3par, for GSTpi
564	20	0.7	30	1	ABL56889	Synthetic deoxyrib	C 637	19.6	0.7	30	1	AAQ36301	WO92323258 oligonuc
565	20	0.7	30	1	ABL56887	Synthetic deoxyrib	C 638	19.6	0.7	30	1	AAQ36301	Immunostimulatory
566	20	0.7	30	1	ABA97613	Poly b nucleotide	C 639	19.6	0.7	30	1	AAF99889	Immunostimulatory
567	20	0.7	30	1	ABA97620	Poly i nucleotide	C 640	19.6	0.7	30	1	ABK10416	Synthetic primer s
568	20	0.7	30	1	ABA97614	Poly c nucleotide	C 641	19.6	0.7	30	1	ABK10412	Synthetic primer s
569	20	0.7	30	1	ABA97615	Poly d nucleotide	C 642	19.6	0.7	30	1	ABK70490	In-situ analysis s
570	20	0.7	30	1	ABA97616	Poly e nucleotide	C 643	19.6	0.7	30	1	ABK70490	Method of measurin
571	20	0.7	30	1	ABL95886	Probe poly b for a	C 644	19.6	0.7	30	1	ABK70490	Oligonucleotide 30
572	20	0.7	30	1	ABL95887	Probe poly c for a	C 645	19.6	0.7	30	1	AAQ83940	Oligonucleotide cl
573	20	0.7	30	1	ABL95894	Probe poly j for a	C 646	19.6	0.7	30	1	AAQ83940	Oligonucleotide cl
574	20	0.7	30	1	ABL95888	Probe poly d for a	C 647	19.6	0.7	30	1	AAV62858	Primer for PR-Q ge
575	20	0.7	30	1	ABL95889	Probe poly e for a	C 648	19.6	0.7	30	1	AAV81666	Oligonucleotide SE
576	20	0.7	30	1	ABL95893	Probe poly i for a	C 649	19.6	0.7	30	1	AAI65862	Nucleotide sequenc
C 577	20	0.7	30	1	ADA14837	Hairpin oligonucle	C 650	19.6	0.7	32	1	AAN70278	Sequence of scissi
578	20	0.7	44	1	AAV09273	Hairpin oligonucle	C 651	19.6	0.7	32	1	AAN92244	SS probe MRCO68.
579	19.8	0.7	24	1	ABV77669	Nucleotide sequenc	C 652	19.6	0.7	32	1	ADC33445	Template oligonucl
580	19.8	0.7	25	1	AAD26900	Human zinc finger	C 653	19.6	0.7	33	1	AAF29153	PCR primer SEQ ID
581	19.8	0.7	25	1	AAC96419	Bacterial PNP DNA	C 654	19.6	0.7	33	1	AAQ88521	PCR primer SEQ ID
582	19.8	0.7	26	1	AAD26899	HLA DQA1 gene PCR	C 655	19.6	0.7	34	1	AAT93827	Conus stercusmusca
583	19.8	0.7	26	1	AAD39650	Bacterial PNP DNA	C 656	19.6	0.7	34	1	AAQ7488	Antitumoural phosph
C 584	19.8	0.7	27	1	AAH43080	PolyPNP out-of-fra	C 657	19.6	0.7	38	1	AAZ57404	Human reproductive
C 585	19.8	0.7	27	1	ABQ79879	Nucleotide sequenc	C 658	19.6	0.7	38	1	AAQ7487	Hepatitis C virus
C 586	19.8	0.7	27	1	ABX12469	Nucleotide sequenc	C 659	19.6	0.7	38	1	AAQ25031	Human reproductive
C 587	19.8	0.7	27	1	ADC75074	Coxsackie B virus	C 660	19.6	0.7	40	1	AAQ39649	Oligonucleotide sp
C 588	19.8	0.7	27	1	ADC75075	Biosensor related	C 661	19.6	0.7	40	1	AAZ98722	Primer used in con
C 589	19.8	0.7	28	1	AAA57856	Biosensor related	C 662	19.6	0.7	40	1	AAQ55168	Sequence of primer
C 590	19.8	0.7	29	1	AAQ90025	Deoxy-T22-tagged s	C 663	19.6	0.7	41	1	AAV03013	Aspergillus oryzae
C 591	19.8	0.7	31	1	AAS17761	PCR primer for fat	C 664	19.6	0.7	42	1	AAA37946	DNA synthesis prim
C 592	19.8	0.7	32	1	AAS09500	Oligo d(T) PCR pri	C 665	19.6	0.7	43	1	AAD17216	Human mRNA hybridi
C 593	19.8	0.7	32	1	ABA01204	SMART PCR primer #	C 666	19.6	0.7	44	1	ADD33791	Mouse mitochondria
C 594	19.8	0.7	32	1	ADA26489	Mamushi fibrinolyt	C 667	19.4	0.7	44	1	AAQ75758	Reverse transcript
C 595	19.6	0.7	32	1	ADA263682	DNA nanolithograph	C 668	19.4	0.7	21	1	AAQ75630	Reverse transcript
C 596	19.6	0.7	26	1	AAD03682	Human full length	C 669	19.4	0.7	21	1	AAQ75648	Reverse transcript
C 597	19.6	0.7	26	1	AAS20596	Human zsig63 cDNA	C 670	19.4	0.7	21	1	AAQ75676	Reverse transcript
C 598	19.6	0.7	26	1	ABS52638	Human secreted sal	C 671	19.4	0.7	21	1	AAQ75681	Reverse transcript
C 599	19.6	0.7	26	1	AAD45055	ZC7764a primer use	C 672	19.4	0.7	21	1	AAQ75629	Reverse transcript
C 600	19.6	0.7	26	1	AAS20671	Human zalphall Lig	C 673	19.4	0.7	21	1	AAQ75725	Reverse transcript
C 601	19.6	0.7	26	1	ABX93599	Human zsig63 PCR/s	C 674	19.4	0.7	21	1	AAQ75729	Reverse transcript
C 602	19.6	0.7	26	1	AAN70276	Sequence of scissi	C 675	19.4	0.7	21	1	AAQ75729	Reverse transcript
C 603	19.6	0.7	26	1	AAN70275	Sequence of scissi	C 676	19.4	0.7	21	1	AAQ75729	Reverse transcript
C 604	19.6	0.7	26	1	AAN92241	SS probe MRCO59.	C 677	19.4	0.7	21	1	AAQ75729	Reverse transcript
C 605	19.6	0.7	26	1	AAF77536	SS probe MRCO60.	C 678	19.4	0.7	21	1	AAQ75773	Reverse transcript
C 606	19.6	0.7	26	1	AAF23526	CDNA library produ	C 679	19.4	0.7	21	1	AAQ75780	Reverse transcript
C 607	19.6	0.7	26	1	AAD33853	Primer #4. Uniden	C 680	19.4	0.7	21	1	AAQ75660	Reverse transcript
C 608	19.6	0.7	26	1	ABZ24784	Primer #2 used to	C 681	19.4	0.7	21	1	AAQ75684	Reverse transcript
C 609	19.6	0.7	26	1	ACA62282	Oligodeoxynucleic	C 682	19.4	0.7	21	1	AAQ75741	Reverse transcript
610	19.6	0.7	26	1	AAT92265	Oligo (dT) primer	C 683	19.4	0.7	21	1	AAQ75652	Reverse transcript
611	19.6	0.7	26	1	AAT93819	Human PUR-alpha ge	C 684	19.4	0.7	21	1	AAQ75753	Reverse transcript
C 612	19.6	0.7	26	1	AAV12482	Antitumoural phosph	C 685	19.4	0.7	21	1	AAQ75788	Reverse transcript
C 613	19.6	0.7	26	1	AAV59215	Oligonucleotide SE	C 686	19.4	0.7	21	1	AAQ75680	Reverse transcript
614	19.6	0.7	26	1	AAV31721	Circular template	C 687	19.4	0.7	21	1	AAQ75649	Reverse transcript
615	19.6	0.7	26	1	AAV31721	Nucleotide sequenc	C 688	19.4	0.7	21	1	AAQ75726	Reverse transcript
C 616	19.6	0.7	26	1	AAX04087	PUR-alpha RACE rea	C 689	19.4	0.7	21	1	AAQ75692	Reverse transcript
C 617	19.6	0.7	26	1	AAX30018	Precircle DNA olig	C 690	19.4	0.7	21	1	AAQ75776	Reverse transcript
						DNA oligonucleotid						AAQ75697	Reverse transcript

691	19.4	0.7	21	1	AAQ75637	Reverse transcript	C 764	19.2	0.7	24	1	ABK48140	Aspergillus niger
692	19.4	0.7	21	1	AAQ75685	Reverse transcript	765	19.2	0.7	24	1	AAT99286	POLYA, a competitor
693	19.4	0.7	21	1	AAQ75717	Reverse transcript	766	19.2	0.7	24	1	AAV31743	Nucleotide sequenc
694	19.4	0.7	21	1	AAQ75777	Reverse transcript	767	19.2	0.7	24	1	AXX04086	Oligonucleotide PO
695	19.4	0.7	21	1	AAQ75644	Reverse transcript	768	19.2	0.7	24	1	AAA40359	pBluescriptSK+ pha
696	19.4	0.7	21	1	AAQ75761	Reverse transcript	769	19.2	0.7	24	1	AAA40353	pBluescriptSK+ pha
697	19.4	0.7	21	1	AAQ75765	Reverse transcript	770	19.2	0.7	24	1	AAF99756	Immunostimulatory
698	19.4	0.7	21	1	AAQ75765	Reverse transcript	771	19.2	0.7	24	1	AAF99304	Immunostimulatory
699	19.4	0.7	21	1	AAQ75772	Reverse transcript	772	19.2	0.7	24	1	AAF99757	Immunostimulatory
700	19.4	0.7	21	1	AAQ75789	Reverse transcript	773	19.2	0.7	24	1	ABV14842	Human prostate exp
701	19.4	0.7	21	1	AAQ75701	Reverse transcript	774	19.2	0.7	24	1	ABS78477	Angiogenesis inhib
702	19.4	0.7	21	1	AAQ75721	Reverse transcript	775	19.2	0.7	24	1	ABS77949	Angiogenesis inhib
703	19.4	0.7	21	1	AAF24290	Reverse transcript	776	19.2	0.7	24	1	ABS78478	Angiogenesis inhib
704	19.4	0.7	21	1	ABX79794	Complementary nucl	777	19.2	0.7	24	1	ABL39405	Immunostimulatory
705	19.4	0.7	23	1	AAQ30431	EST polymorphic DN	778	19.2	0.7	24	1	ABA98840	A24 oligonucleotid
706	19.4	0.7	23	1	AAQ30430	Oligomer IL6804 fo	779	19.2	0.7	24	1	AAK17869	A24 oligonucleotid
707	19.4	0.7	23	1	ABL01773	Oligomer IL6803 fo	780	19.2	0.7	24	1	ABK15639	RNA-PCR procedure
708	19.4	0.7	24	1	AAH24266	Human MSH2 (hMSH2)	781	19.2	0.7	24	1	ACA58802	Gastric ulcer trea
709	19.4	0.7	24	1	ABN85073	Human phosphatase	782	19.2	0.7	24	1	ABZ80181	Immunostimulatory
710	19.4	0.7	24	1	ABX91269	Human S4 ribosomal	783	19.2	0.7	24	1	ACA62284	Immunostimulatory
711	19.4	0.7	24	1	ABZ23536	Leukaemia related	784	19.2	0.7	24	1	ACD99729	Immunostimulatory
712	19.4	0.7	24	1	ABZ23536	fragment of a plas	785	19.2	0.7	24	1	ACH03285	Immunostimulatory
713	19.4	0.7	24	1	ABZ23536	fragment of a plas	786	19.2	0.7	24	1	ACH03284	Immunostimulatory
714	19.4	0.7	25	1	AAV42215	Sequencing primer	787	19.2	0.7	24	1	ADA66379	Immunostimulatory
715	19.4	0.7	25	1	AAH84259	PCR primer for hum	788	19.2	0.7	24	1	ADB37258	Immunostimulatory
716	19.4	0.7	25	1	ABZ23535	fragment of a plas	789	19.2	0.7	24	1	ADB36806	Immunostimulatory
717	19.4	0.7	26	1	AAS20595	Human zsig63 cDNA	790	19.2	0.7	24	1	ADB37259	Immunostimulatory
718	19.4	0.7	26	1	ABS52637	Human secreted sal	791	19.2	0.7	24	1	ADD31867	Immunostimulatory
719	19.4	0.7	26	1	AAD45054	ZC7231 primer used	792	19.2	0.7	24	1	ADE25524	Immunostimulatory
720	19.4	0.7	26	1	ABX93598	Bovine viral diarr	793	19.2	0.7	24	1	ABA97997	Immunostimulatory
721	19.4	0.7	26	1	ACF36382	Human zsig63 PCR/s	794	19.2	0.7	24	1	ABL55130	Human gonadotropin
722	19.4	0.7	26	1	AAV35002	Nucleotide sequenc	795	19.2	0.7	24	1	ABA98547	Human gonadotropin
723	19.4	0.7	26	1	AAF74913	Human endothelin-b	796	19.2	0.7	24	1	ADD06134	Insulin-like growt
724	19.4	0.7	27	1	ABQ76254	CD40L poly-A tract	797	19.2	0.7	25	1	AAQ95960	N-acetyl-galactosam
725	19.4	0.7	27	1	AAF74926	Murine SCCE 5'-RAC	798	19.2	0.7	25	1	AAK84258	Oligonucleotide bi
726	19.4	0.7	27	1	AAF74932	CD40L poly-A tract	799	19.2	0.7	25	1	AAK39306	PCR primer for hum
727	19.4	0.7	27	1	AAF74931	CD40L poly-A tract	800	19.2	0.7	25	1	AAZ30267	Rapid capture prob
728	19.4	0.7	27	1	AAF74934	CD40L poly-A tract	801	19.2	0.7	25	1	ABK49986	Capture probe CP12
729	19.4	0.7	28	1	AAT13977	CD40L poly-A tract	802	19.2	0.7	25	1	ADC54009	Example oligonucle
730	19.4	0.7	28	1	AAT70108	E. spinifera fumon	803	19.2	0.7	25	1	ADC54008	Oligonucleotide of
731	19.4	0.7	28	1	AAT70106	PolyTV primer 3.	804	19.2	0.7	25	1	ABK86170	Oligonucleotide of
732	19.4	0.7	28	1	AAT70107	PolyTV primer 1.	805	19.2	0.7	25	1	ACL96700	Oligo dT primer #3
733	19.4	0.7	28	1	AAV65735	PolyTV primer 2.	806	19.2	0.7	25	1	ABL45245	HLA HLA-A gene PCR
734	19.4	0.7	28	1	AAH05727	A. phoenices APOXD	807	19.2	0.7	26	1	AAK07466	Human chromosome 1
735	19.4	0.7	28	1	AAH05727	E. spinifera fumon	808	19.2	0.7	26	1	AAK07466	Human BS124 specif
736	19.4	0.7	28	1	AAF74920	CD40L poly-A tract	809	19.2	0.7	26	1	AAV71936	Human pancreatic P
737	19.4	0.7	28	1	AAF74906	CD40L poly-A tract	810	19.2	0.7	27	1	ABS53863	Anchored poly T RT
738	19.4	0.7	28	1	AAF74916	CD40L poly-A tract	811	19.2	0.7	27	1	AAK47309	Human androgen rec
739	19.4	0.7	28	1	AAF74927	CD40L poly-A tract	812	19.2	0.7	27	1	AAA40362	Human ARCAP associ
740	19.4	0.7	28	1	AAF60450	RNA oligonucleotid	813	19.2	0.7	28	1	AAA40358	Intracellular targ
741	19.4	0.7	28	1	ABZ70568	Puromycin linker D	814	19.2	0.7	28	1	AAQ52308	pBluescriptSK+ pha
742	19.4	0.7	29	1	AAQ49467	5' RACE primer Bam	815	19.2	0.7	28	1	ABN83378	pBluescriptSK+ pha
743	19.4	0.7	29	1	AAF74918	Oligo-dT primer "n	816	19.2	0.7	29	1	AAQ52308	Mononucleotide rep
744	19.4	0.7	29	1	AAF74907	CD40L poly-A tract	817	19.2	0.7	29	1	AAK44903	Triplex forming ol
745	19.4	0.7	29	1	AAF74935	CD40L poly-A tract	818	19.2	0.7	29	1	AAK44903	Molecular interact
746	19.4	0.7	29	1	AAF74921	CD40L poly-A tract	819	19.2	0.7	29	1	AAK44903	Molecular interact
747	19.4	0.7	29	1	AAF74928	CD40L poly-A tract	820	19.2	0.7	29	1	AAK44903	CD40L poly-A tract
748	19.4	0.7	29	1	AAH28298	CD40L poly-A tract	821	19.2	0.7	29	1	AAK44903	CD40L poly-A tract
749	19.4	0.7	29	1	AAH28298	3' untranslated re	822	19.2	0.7	32	1	AAQ34333	First strand synth
750	19.4	0.7	29	1	AAH28298	T7T18Apad PS6-29-0	823	19.2	0.7	32	1	AAQ34333	Triple helix formi
751	19.4	0.7	29	1	AAH28298	T7T18Apad PS18-29-	824	19.2	0.7	33	1	AAK44170	Porphyrin Yezoensis
752	19.4	0.7	30	1	ADC16682	Aminoacylation RNA	825	19.2	0.7	33	1	AAK44170	Probe APC 2. Homo
753	19.4	0.7	33	1	ACC42844	Nuclear transition	826	19.2	0.7	37	1	AAQ75552	Pea blight resista
754	19.2	0.7	21	1	ACC48482	Locked nucleic aci	827	19.2	0.7	19	1	AAQ75552	Reverse transcript
755	19.2	0.7	21	1	ACC48482	Locked nucleic aci	828	19.2	0.7	19	1	AAQ75552	Reverse transcript
756	19.2	0.7	21	1	ACC99729	Oligonucleotide.	829	19.2	0.7	19	1	AAQ75552	Oligonucleotide pr
757	19.2	0.7	21	1	ACC99729	Oligonucleotide.	830	19.2	0.7	19	1	AAQ75552	Oligonucleotide pr
758	19.2	0.7	22	1	AAK50570	Molecular array pr	831	19.2	0.7	19	1	AAQ75552	Aminoxy-modified
759	19.2	0.7	22	1	ABX74887	Oligo-dT primer us	832	19.2	0.7	19	1	AAQ75552	Aminoxy-modified
760	19.2	0.7	22	1	ACC48484	Locked nucleic aci	833	19.2	0.7	19	1	AAQ75552	Oligonucleotide co
761	19.2	0.7	22	1	ACC48485	Locked nucleic aci	834	19.2	0.7	19	1	AAQ75552	Oligonucleotide co
762	19.2	0.7	22	1	ACC48483	Locked nucleic aci	835	19.2	0.7	19	1	AAQ75552	5' amino oligonuc
763	19.2	0.7	23	1	AAD51324	Anchored oligo dT	836	19.2	0.7	19	1	AAQ75552	5' amino oligonuc
					3'-PCR primer used								

C 837	19	0.7	19	1	AAx81927	Polynucleotide str	C 910	19	0.7	19	1	AA42003	Oligonucleotide #6
C 838	19	0.7	19	1	AAx81927	Polynucleotide str	911	19	0.7	19	1	AA41998	Oligonucleotide #1
C 839	19	0.7	19	1	AAZ01358	PCR primer for PG1	C 912	19	0.7	19	1	AA41998	Oligonucleotide #1
C 840	19	0.7	19	1	AAZ01358	PCR primer for PG1	913	19	0.7	19	1	AA41999	Oligonucleotide #2
C 841	19	0.7	19	1	AAZ61390	Uniform phosphodie	C 914	19	0.7	19	1	AA41999	Oligonucleotide #2
C 842	19	0.7	19	1	AAZ61390	Uniform phosphodie	915	19	0.7	19	1	AA42009	Oligonucleotide #1
C 843	19	0.7	19	1	AAZ61404	2'-O-modified ribo	C 916	19	0.7	19	1	AA42009	Oligonucleotide #1
C 844	19	0.7	19	1	AAZ61404	2'-O-modified ribo	917	19	0.7	19	1	AA42009	Oligonucleotide #1
C 845	19	0.7	19	1	AAZ61404	2'-O-modified ribo	C 918	19	0.7	19	1	ABZ58336	Oligonucleotide wi
C 846	19	0.7	19	1	AAZ62422	T19 diester for us	C 919	19	0.7	19	1	ABZ58336	Oligonucleotide wi
C 847	19	0.7	19	1	AAZ62422	T19 diester for us	C 920	19	0.7	20	1	AAQ25565	Dye-coupled 3'-ami
C 848	19	0.7	19	1	AAZ95241	Modified oligonuc	C 921	19	0.7	20	1	AAQ33554	Microsatellite seq
C 849	19	0.7	19	1	AAZ95241	Modified oligonuc	C 922	19	0.7	20	1	AAQ58578	Sequence of synthe
C 850	19	0.7	19	1	AAZ95240	Modified oligonuc	C 923	19	0.7	20	1	AAQ94205	Alpha-anomeric oli
C 851	19	0.7	19	1	AAZ95240	Modified oligonuc	C 924	19	0.7	20	1	AAQ94205	T2 (synthetic DNA
C 852	19	0.7	19	1	AAA06839	Modified T-contain	C 925	19	0.7	20	1	AAV07752	Phosphorothioate o
C 853	19	0.7	19	1	AAA06839	Modified T-contain	C 926	19	0.7	20	1	AAT63649	Anti-HTLV antisens
C 854	19	0.7	19	1	AAA88952	Oligonucleotide IS	C 927	19	0.7	20	1	AAV34591	M. vaccae antigeni
C 855	19	0.7	19	1	AAA88952	Oligonucleotide IS	C 928	19	0.7	20	1	AAT86606	Oligonucleotide se
C 856	19	0.7	19	1	AAA88965	2'-Modified chim	C 929	19	0.7	20	1	AAx27533	Synthetic RNA sequ
C 857	19	0.7	19	1	AAA88965	2'-Modified chim	C 930	19	0.7	20	1	AAZ11326	Mycobacterial l6S
C 858	19	0.7	19	1	AAA88949	Oligonucleotide IS	C 931	19	0.7	20	1	AAA40449	Electrochemical det
C 859	19	0.7	19	1	AAA88949	Oligonucleotide IS	C 932	19	0.7	20	1	AAA40449	Electrochemical det
C 860	19	0.7	19	1	AAA88950	Oligonucleotide IS	C 933	19	0.7	20	1	AAZ91117	Oligonucleotide #5
C 861	19	0.7	19	1	AAA88950	Oligonucleotide IS	C 934	19	0.7	20	1	AAZ91117	2'-Methoxyethoxy-m
C 862	19	0.7	19	1	AAA88951	Oligonucleotide IS	C 935	19	0.7	20	1	AAZ91117	Phosphorothioate p
C 863	19	0.7	19	1	AAA88951	Oligonucleotide IS	C 936	19	0.7	20	1	AAZ91117	Digoxigenin-label
C 864	19	0.7	19	1	AAA88947	Oligonucleotide IS	C 937	19	0.7	20	1	AAZ91117	Poly T oligonucleo
C 865	19	0.7	19	1	AAA88947	Oligonucleotide IS	C 938	19	0.7	20	1	AAZ91117	DNA template for 3
C 866	19	0.7	19	1	AAA88948	Oligonucleotide IS	C 939	19	0.7	20	1	AAZ91117	Capture probe CP5'
C 867	19	0.7	19	1	AAA88948	Oligonucleotide IS	C 940	19	0.7	20	1	AAZ91117	Conjugate forming
C 868	19	0.7	19	1	AAA88948	Oligonucleotide IS	C 941	19	0.7	20	1	AAZ91117	Oligonucleotide-na
C 869	19	0.7	19	1	AAA88948	Oligonucleotide IS	C 942	19	0.7	20	1	AAZ91117	Random oligonucleo
C 870	19	0.7	19	1	AAA88948	Oligonucleotide IS	C 943	19	0.7	20	1	AAZ91117	Oligonucleotide-cy
C 871	19	0.7	19	1	AAA88948	Oligonucleotide IS	C 944	19	0.7	20	1	AAZ91117	Immunostimulatory
C 872	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 945	19	0.7	20	1	AAZ91117	Immunostimulatory
C 873	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 946	19	0.7	20	1	AAZ91117	Immunostimulatory
C 874	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 947	19	0.7	20	1	AAZ91117	Oligonucleotide #1
C 875	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 948	19	0.7	20	1	AAZ91117	Nucleotide sequenc
C 876	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 949	19	0.7	20	1	AAZ91117	DNA oligomer #1.
C 877	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 950	19	0.7	20	1	AAZ91117	Angiogenesis inhib
C 878	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 951	19	0.7	20	1	AAZ91117	Angiogenesis inhib
C 879	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 952	19	0.7	20	1	AAZ91117	Angiogenesis inhib
C 880	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 953	19	0.7	20	1	AAZ91117	Immunostimulatory
C 881	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 954	19	0.7	20	1	AAZ91117	Immunostimulatory
C 882	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 955	19	0.7	20	1	AAZ91117	Immunostimulatory
C 883	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 956	19	0.7	20	1	AAZ91117	Immunostimulatory
C 884	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 957	19	0.7	20	1	AAZ91117	Immunostimulatory
C 885	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 958	19	0.7	20	1	AAZ91117	Immunostimulatory
C 886	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 959	19	0.7	20	1	AAZ91117	Immunostimulatory
C 887	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 960	19	0.7	20	1	AAZ91117	Immunostimulatory
C 888	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 961	19	0.7	20	1	AAZ91117	Immunostimulatory
C 889	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 962	19	0.7	20	1	AAZ91117	Immunostimulatory
C 890	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 963	19	0.7	20	1	AAZ91117	Immunostimulatory
C 891	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 964	19	0.7	20	1	AAZ91117	Immunostimulatory
C 892	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 965	19	0.7	20	1	AAZ91117	Immunostimulatory
C 893	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 966	19	0.7	20	1	AAZ91117	Immunostimulatory
C 894	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 967	19	0.7	20	1	AAZ91117	Immunostimulatory
C 895	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 968	19	0.7	20	1	AAZ91117	Immunostimulatory
C 896	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 969	19	0.7	20	1	AAZ91117	Immunostimulatory
C 897	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 970	19	0.7	20	1	AAZ91117	Immunostimulatory
C 898	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 971	19	0.7	20	1	AAZ91117	Immunostimulatory
C 899	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 972	19	0.7	20	1	AAZ91117	Immunostimulatory
C 900	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 973	19	0.7	20	1	AAZ91117	Immunostimulatory
C 901	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 974	19	0.7	20	1	AAZ91117	Immunostimulatory
C 902	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 975	19	0.7	20	1	AAZ91117	Immunostimulatory
C 903	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 976	19	0.7	20	1	AAZ91117	Immunostimulatory
C 904	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 977	19	0.7	20	1	AAZ91117	Immunostimulatory
C 905	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 978	19	0.7	20	1	AAZ91117	Immunostimulatory
C 906	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 979	19	0.7	20	1	AAZ91117	Immunostimulatory
C 907	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 980	19	0.7	20	1	AAZ91117	Immunostimulatory
C 908	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 981	19	0.7	20	1	AAZ91117	Immunostimulatory
C 909	19	0.7	19	1	AAZ91117	Oligonucleotide IS	C 982	19	0.7	20	1	AAZ91117	Immunostimulatory

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983	19	0.7	20	1	ABZ87681	Human oligonucleot	c1056	19	0.7	21	1	ABS78428	Angiogenesis inhib
984	19	0.7	20	1	ABZ88566	Human oligonucleot	c1057	19	0.7	21	1	ABL39404	Immunostimulatory
985	19	0.7	20	1	ABZ89086	Human oligonucleot	c1058	19	0.7	21	1	AD51323	Regular oligo dT p
986	19	0.7	20	1	ABZ85533	Human oligonucleot	c1059	19	0.7	21	1	ACH03246	Immunostimulatory
987	19	0.7	20	1	ABZ89015	Human oligonucleot	c1060	19	0.7	21	1	ADB37209	Immunostimulatory
988	19	0.7	20	1	ABZ89441	Human oligonucleot	1061	19	0.7	21	1	AD90391	CP-1 (synthetic DN
989	19	0.7	20	1	ABZ89016	Human oligonucleot	1062	19	0.7	21	1	AAT10743	Oligonucleotide pr
990	19	0.7	20	1	ABZ89120	Human oligonucleot	1063	19	0.7	21	1	AA81302	3' ribonucleoside
991	19	0.7	20	1	ABZ89704	Human oligonucleot	1064	19	0.7	21	1	AA75724	Reverse transcript
992	19	0.7	20	1	ACD27320	Human oligonucleot	1065	19	0.7	21	1	AA75752	Reverse transcript
993	19	0.7	20	1	ACC58867	Nanotechnology nuc	c1066	19	0.7	21	1	AA75762	Reverse transcript
994	19	0.7	20	1	ABZ22916	Doubly labelled DN	1067	19	0.7	21	1	AA75719	Reverse transcript
995	19	0.7	20	1	AA161645	Phosphorothioate 2	1068	19	0.7	21	1	AA75730	Reverse transcript
996	19	0.7	20	1	ABZ59815	Thiol-modified oli	c1069	19	0.7	21	1	AA75763	Reverse transcript
997	19	0.7	20	1	ABX79181	Potato gene PCR pr	1070	19	0.7	21	1	AA75728	Reverse transcript
998	19	0.7	20	1	ABX92177	Thio-modified 20da	1071	19	0.7	21	1	AA75727	Reverse transcript
999	19	0.7	20	1	ACD27255	Nanoparticle-assoc	c1072	19	0.7	21	1	AA75764	Reverse transcript
1000	19	0.7	20	1	ACD27125	Nanotechnology nuc	1073	19	0.7	21	1	AA75722	Reverse transcript
1001	19	0.7	20	1	ACD27385	Nanotechnology nuc	1074	19	0.7	21	1	AA75723	Reverse transcript
1002	19	0.7	20	1	ACD27190	Nanotechnology nuc	c1075	19	0.7	21	1	AA75760	Reverse transcript
1003	19	0.7	20	1	ACD27060	Nanotechnology nuc	c1076	19	0.7	21	1	AA75751	Reverse transcript
1004	19	0.7	20	1	ACH00064	Nanotechnology nuc	c1077	19	0.7	21	1	AA75754	Reverse transcript
1005	19	0.7	20	1	ACD99851	Immunostimulatory	c1078	19	0.7	21	1	AA75759	Reverse transcript
1006	19	0.7	20	1	ACD99847	Immunostimulatory	1079	19	0.7	21	1	AA75720	Reverse transcript
1007	19	0.7	20	1	ACD99532	Immunostimulatory	c1080	19	0.7	21	1	AA75766	Reverse transcript
1008	19	0.7	20	1	ADA14838	Hairpin target seq	1081	19	0.7	21	1	AAV35395	HIV-1 gag protein
1009	19	0.7	20	1	ADA06159	Nanoparticle label	c1082	19	0.7	21	1	AAV35395	HIV-1 gag protein
1010	19	0.7	20	1	ADB36933	Nanotechnology nuc	1083	19	0.7	22	1	AAQ64724	2',5'-linked tetra
1011	19	0.7	20	1	ADB36601	Immunostimulatory	1084	19	0.7	22	1	AA71413	L1 cleavage site r
1012	19	0.7	20	1	ADB36929	Immunostimulatory	1085	19	0.7	22	1	AA72356	Amino modified oli
1013	19	0.7	20	1	AAQ75598	Reverse transcript	c1086	19	0.7	23	1	AA62450	Cleavage of nuclei
1014	19	0.7	20	1	AAQ75579	Reverse transcript	c1087	19	0.7	23	1	AA62451	Cleavage of nuclei
1015	19	0.7	20	1	AAQ75597	Reverse transcript	c1088	19	0.7	23	1	AA716627	Gastric acid produ
1016	19	0.7	20	1	AAQ75581	Reverse transcript	1089	19	0.7	23	1	AA73701	Primer #1 for tiss
1017	19	0.7	20	1	AAQ75595	Reverse transcript	1090	19	0.7	23	1	AAV61554	Double-anchored ol
1018	19	0.7	20	1	AAQ75580	Reverse transcript	1091	19	0.7	23	1	AA29753	Synthetic oligonuc
1019	19	0.7	20	1	AA704916	Mammalian stem cel	1092	19	0.7	23	1	AA08407	Oligonucleotide pr
1020	19	0.7	20	1	AAA13753	Mammalian stem cel	1093	19	0.7	23	1	ABA9682	Murine osteoporosi
1021	19	0.7	20	1	AAA13754	Stem cell factor u	c1094	19	0.7	24	1	ABK86172	Oligo dT primer #4
1022	19	0.7	20	1	AAA13754	Stem cell factor u	1095	19	0.7	24	1	AA768615	DNA probe used in
1023	19	0.7	20	1	AA91207	Antisense IGFBP-5	1097	19	0.7	25	1	AAH38515	Human gonadotropin
1024	19	0.7	20	1	AAH41332	Universal stem cel	c1098	19	0.7	25	1	AAV57477	Human CYP2D6 gene
1025	19	0.7	20	1	AAH41333	Universal stem cel	1099	19	0.7	25	1	AA57855	SNP specific SNPE
1026	19	0.7	20	1	AAH41112	Human SCF (stem ce	1100	19	0.7	28	1	AA57855	Cytochrome P450ox
1027	19	0.7	20	1	AAH41113	Human SCF (stem ce	1101	19	0.7	28	1	AA43065	Deoxy-A22-tagged s
1028	19	0.7	20	1	AAH41113	Human SCF (stem ce	1102	19	0.7	28	1	AA43065	Regulatable, catal
1029	19	0.7	20	1	AAH41113	Human SCF (stem ce	1103	19	0.7	28	1	AA39569	Substrate RNA rela
1030	19	0.7	20	1	AAH41113	Human SCF (stem ce	1104	19	0.7	28	1	AA61015	Human haemoglobin
1031	19	0.7	20	1	AAH41113	Human SCF (stem ce	1105	19	0.7	28	1	AAZ61254	HS/HIP reverse tra
1032	19	0.7	20	1	AAH41113	Human SCF (stem ce	1106	19	0.7	28	1	AAZ61254	Oligo dT primer fo
1033	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1107	19	0.7	28	1	AAQ79096	Single stranded DN
1034	19	0.7	20	1	AAH41113	Human SCF (stem ce	1108	19	0.7	29	1	AAQ68614	Tobacco PMT PCR pr
1035	19	0.7	20	1	AAH41113	Human SCF (stem ce	1109	19	0.7	29	1	AAQ68614	tRNAPolyU reverse
1036	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1110	19	0.7	29	1	AAQ68614	Reverse tRNA prime
1037	19	0.7	20	1	AAH41113	Human SCF (stem ce	1111	19	0.7	29	1	AAQ68614	Rat type I steroid
1038	19	0.7	20	1	AAH41113	Human SCF (stem ce	1112	19	0.7	29	1	AAQ68614	Primer for rat ste
1039	19	0.7	20	1	AAH41113	Human SCF (stem ce	1113	19	0.7	29	1	AAQ68614	Hepatitis E virus
1040	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1114	19	0.7	29	1	AAQ68614	Rice semi-dwarf (s
1041	19	0.7	20	1	AAH41113	Human SCF (stem ce	1115	19	0.7	30	1	AAQ68614	APC binding protei
1042	19	0.7	20	1	AAH41113	Human SCF (stem ce	1116	19	0.7	30	1	AAQ68614	Oligonucleotide-na
1043	19	0.7	20	1	AAH41113	Human SCF (stem ce	1117	19	0.7	30	1	AAQ68614	Oligonucleotide-cy
1044	19	0.7	20	1	AAH41113	Human SCF (stem ce	1118	19	0.7	30	1	AAQ68614	Nanoparticle-oligo
1045	19	0.7	20	1	AAH41113	Human SCF (stem ce	1119	19	0.7	30	1	AAQ68614	Nucleic acid detec
1046	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1120	19	0.7	30	1	AAQ68614	Oligonucleotide #1
1047	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1121	19	0.7	30	1	AAQ68614	Sindbis virus mRNA
1048	19	0.7	20	1	AAH41113	Human SCF (stem ce	1122	19	0.7	30	1	AAQ68614	Sindbis virus 3' R
1049	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1123	19	0.7	30	1	AAQ68614	APC binding protei
1050	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1124	19	0.7	30	1	AAQ68614	Structural product
1051	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1125	19	0.7	30	1	AAQ68614	Neuraminidase PCR
1052	19	0.7	20	1	AAH41113	Human SCF (stem ce	c1126	19	0.7	30	1	AAQ68614	Primer B for Non-A
1053	19	0.7	20	1	AAH41113	Human SCF (stem ce	1127	19	0.7	30	1	AAQ68614	Rat fibroblast gro
1054	19	0.7	20	1	AAH41113	Human SCF (stem ce	1128	19	0.7	30	1	AAQ68614	Oligonucleotide-na
1055	19	0.7	20	1	AAH41113	Human SCF (stem ce		19	0.7	30	1	AAQ68614	Alkanethiol-modifi

1129	19	0.7	32	1	ABK65031	Nanoparticle-oligo	c1202	18.4	0.7	20	1	ABZ85534	Human oligonucleot
1130	19	0.7	32	1	ABS64669	Nucleic acid detec	c1203	18.4	0.7	20	1	ABZ92865	Human oligonucleot
1131	19	0.7	32	1	ACD27316	Nanotechnology nuc	c1204	18.4	0.7	20	1	ABZ88938	Human oligonucleot
1132	19	0.7	32	1	AAL61641	Thiol-modified oli	1205	18.4	0.7	20	1	ABZ88813	Human oligonucleot
1133	19	0.7	32	1	ABX79177	Fluorescein-label	1206	18.4	0.7	21	1	AAQ75757	Reverse transcript
1134	19	0.7	32	1	ABX92173	Nanoparticle-assoc	1207	18.4	0.7	21	1	AAQ75756	Reverse transcript
1135	19	0.7	32	1	ACD27251	Nanotechnology nuc	1208	18.4	0.7	21	1	AAQ75755	Reverse transcript
1136	19	0.7	32	1	ACD27121	Nanotechnology nuc	1209	18.4	0.7	21	1	AAQ75630	Reverse transcript
1137	19	0.7	32	1	ACD27381	Nanotechnology nuc	1210	18.4	0.7	21	1	AAQ75629	Reverse transcript
1138	19	0.7	32	1	ACD27186	Nanotechnology nuc	1211	18.4	0.7	21	1	AAQ75773	Reverse transcript
1139	19	0.7	32	1	ACD27056	Nanotechnology nuc	1212	18.4	0.7	21	1	AAQ75684	Reverse transcript
1140	19	0.7	32	1	ACH00060	Nanotechnology nuc	1213	18.4	0.7	21	1	AAQ75726	Reverse transcript
1141	19	0.7	32	1	ADA06155	Nanotechnology nuc	1214	18.4	0.7	21	1	AAQ75685	Reverse transcript
1142	19	0.7	32	1	ACD26991	Nanoparticle label	1215	18.4	0.7	21	1	AAQ75772	Reverse transcript
1143	19	0.7	32	1	ADE71592	Nanotechnology nuc	1216	18.4	0.7	21	1	AAQ75724	Reverse transcript
1144	19	0.7	33	1	ABQ80395	Magneto-gold nanop	1217	18.4	0.7	21	1	AAQ75730	Reverse transcript
1145	19	0.7	33	1	ABQ80394	Probe APC 1-MUT.	1218	18.4	0.7	21	1	AAQ75763	Reverse transcript
c1146	19	0.7	33	1	ADC60749	Probe APC 1-WT. H	1219	18.4	0.7	21	1	AAQ75728	Reverse transcript
c1147	19	0.7	33	1	ABK15694	Termitomyces album	1220	18.4	0.7	21	1	AAQ75727	Reverse transcript
c1148	19	0.7	33	1	AA775564	Human activating G	1221	18.4	0.7	21	1	AAQ75764	Reverse transcript
c1149	19	0.7	34	1	AA09727	PCR primer for DNA	1222	18.4	0.7	21	1	AAQ75723	Reverse transcript
c1150	19	0.7	34	1	AA520662	ZC18698 primer, to	1223	18.4	0.7	21	1	AAQ75766	Reverse transcript
c1151	19	0.7	34	1	ADD68172	Primer ZC18698 ued	1224	18.4	0.7	21	1	AAQ75651	Reverse transcript
c1152	19	0.7	35	1	AA74632	PCR primer relat	1225	18.4	0.7	21	1	AAQ75702	Reverse transcript
c1153	19	0.7	41	1	ABZ46327	Triple helix formi	1226	18.4	0.7	21	1	AAQ75661	Reverse transcript
c1154	19	0.7	41	1	ABZ48839	Human aldehyde deh	1227	18.4	0.7	21	1	AAQ75675	Reverse transcript
c1155	18.8	0.7	41	1	ABA93238	Human aldehyde deh	1228	18.4	0.7	21	1	AAQ75771	Reverse transcript
1156	18.8	0.7	22	1	ABV77669	PolyA adaptor olig	1229	18.4	0.7	21	1	AAQ75627	Reverse transcript
1157	18.8	0.7	24	1	AAH75510	Human zinc finger	1230	18.4	0.7	21	1	AAQ75627	Reverse transcript
1158	18.8	0.7	24	1	AAH44623	Human CCR4 related	c1231	18.4	0.7	21	1	AAQ75693	Reverse transcript
1159	18.8	0.7	24	1	ABK13715	Human FD 17 PCR pr	c1232	18.4	0.7	21	1	AAQ75739	Reverse transcript
1160	18.8	0.7	25	1	AAC96267	RT-PCR primer #2 f	c1233	18.4	0.7	21	1	AAQ75778	Reverse transcript
1161	18.8	0.7	25	1	AAC96268	HLA DPAl gene PCR	1234	18.4	0.7	21	1	AAQ75778	Reverse transcript
1162	18.8	0.7	25	1	ABA03917	HLA DPAl gene PCR	c1235	18.4	0.7	21	1	AAQ75787	Reverse transcript
c1163	18.8	0.7	27	1	AAF74933	Human connexin 9 P	c1236	18.4	0.7	21	1	AAQ75643	Reverse transcript
1164	18.6	0.7	25	1	AAC95686	CD40L poly-A tract	1237	18.4	0.7	21	1	AAQ75781	Reverse transcript
1165	18.6	0.7	25	1	AAC95686	16s rRNA gene PCR	c1238	18.4	0.7	21	1	AAQ75695	Reverse transcript
c1166	18.6	0.7	25	1	AAC96214	HLA DPB1 gene PCR	1239	18.4	0.7	21	1	AAQ75718	Reverse transcript
1167	18.6	0.7	25	1	AAC96367	16s rRNA gene PCR	1240	18.4	0.7	21	1	AAQ75646	Reverse transcript
c1168	18.6	0.7	25	1	ACI00608	HLA DPB1 gene PCR	1241	18.4	0.7	21	1	AAQ75650	Reverse transcript
c1169	18.6	0.7	25	1	ACI61005	Human microarray D	1242	18.4	0.7	21	1	AAQ75650	Reverse transcript
1170	18.6	0.7	26	1	AAA88688	Human microarray D	c1243	18.4	0.7	21	1	AAQ75682	Reverse transcript
1171	18.4	0.7	20	1	AAQ75596	Oligo-dT-XhoI prim	1244	18.4	0.7	21	1	AAQ75682	Reverse transcript
1172	18.4	0.7	20	1	ABZ85312	Reverse transcript	c1245	18.4	0.7	21	1	AAQ75678	Reverse transcript
1173	18.4	0.7	20	1	ABZ89546	Human oligonucleot	1246	18.4	0.7	21	1	AAQ75694	Reverse transcript
1174	18.4	0.7	20	1	AAQ75598	Reverse transcript	c1247	18.4	0.7	21	1	AAQ75700	Reverse transcript
c1175	18.4	0.7	20	1	AAQ75581	Reverse transcript	1248	18.4	0.7	21	1	AAQ75742	Reverse transcript
c1176	18.4	0.7	20	1	AAQ75580	Reverse transcript	c1249	18.4	0.7	21	1	AAQ75659	Reverse transcript
c1177	18.4	0.7	20	1	ABZ89085	Reverse transcript	c1250	18.4	0.7	21	1	AAQ75715	Reverse transcript
1178	18.4	0.7	20	1	ABZ88694	Human oligonucleot	1251	18.4	0.7	21	1	AAQ75716	Reverse transcript
1179	18.4	0.7	20	1	AAQ49436	Human oligonucleot	1252	18.4	0.7	21	1	AAQ75740	Reverse transcript
1180	18.4	0.7	20	1	AAQ75566	Cytochrome P450 se	c1253	18.4	0.7	21	1	AAQ75779	Reverse transcript
1181	18.4	0.7	20	1	AAQ75569	Reverse transcript	1254	18.4	0.7	21	1	AAQ75628	Reverse transcript
1182	18.4	0.7	20	1	AAQ75584	Reverse transcript	1255	18.4	0.7	21	1	AAQ75628	Reverse transcript
1183	18.4	0.7	20	1	AAQ75585	Reverse transcript	c1256	18.4	0.7	21	1	AAQ75636	Reverse transcript
c1184	18.4	0.7	20	1	AAQ75568	Reverse transcript	1257	18.4	0.7	21	1	AAQ75686	Reverse transcript
c1185	18.4	0.7	20	1	AAQ75570	Reverse transcript	1258	18.4	0.7	21	1	AAQ75686	Reverse transcript
c1186	18.4	0.7	20	1	AAQ75572	Reverse transcript	c1259	18.4	0.7	21	1	AAQ75775	Reverse transcript
1187	18.4	0.7	20	1	AAQ75586	Reverse transcript	1260	18.4	0.7	21	1	AAQ75790	Reverse transcript
c1188	18.4	0.7	20	1	AAQ75589	Reverse transcript	c1261	18.4	0.7	21	1	AAQ75698	Reverse transcript
c1190	18.4	0.7	20	1	AAQ75604	Reverse transcript	1262	18.4	0.7	21	1	AAQ75699	Reverse transcript
c1191	18.4	0.7	20	1	AAQ75588	Reverse transcript	1263	18.4	0.7	21	1	AAQ75699	Reverse transcript
1192	18.4	0.7	20	1	AAQ75601	Reverse transcript	1264	18.4	0.7	21	1	AAQ75635	Reverse transcript
1193	18.4	0.7	20	1	AAQ75564	Reverse transcript	1265	18.4	0.7	21	1	AAQ75645	Reverse transcript
c1194	18.4	0.7	20	1	AAQ75564	Reverse transcript	c1266	18.4	0.7	21	1	AAQ75691	Reverse transcript
1195	18.4	0.7	20	1	AAQ75564	Reverse transcript	c1267	18.4	0.7	21	1	AAQ75782	Reverse transcript
c1196	18.4	0.7	20	1	AAQ75600	Reverse transcript	c1268	18.4	0.7	21	1	AAQ75662	Reverse transcript
1197	18.4	0.7	20	1	AAQ75578	Reverse transcript	1269	18.4	0.7	21	1	AAQ75679	Reverse transcript
1198	18.4	0.7	20	1	AAQ75590	Reverse transcript	1270	18.4	0.7	21	1	AAQ75774	Reverse transcript
c1199	18.4	0.7	20	1	AAQ75602	Reverse transcript	c1271	18.4	0.7	21	1	AAQ75774	Reverse transcript
c1200	18.4	0.7	20	1	AAQ75592	Reverse transcript	1272	18.4	0.7	21	1	AAQ75638	Reverse transcript
c1201	18.4	0.7	20	1	ABZ88266	Human oligonucleot	c1273	18.4	0.7	21	1	AAQ75653	Reverse transcript
							1274	18.4	0.7	21	1	AAQ75677	Reverse transcript

1275	18.4	0.7	21	1	AAQ75683	Reverse transcript	c1348	18	0.6	18	1	AAQ34110	Sequence of a micr
c1276	18.4	0.7	21	1	AAQ75683	Reverse transcript	1349	18	0.6	18	1	AAQ75025	PCR primer. Synth
1277	18.4	0.7	21	1	AAQ75696	Reverse transcript	c1350	18	0.6	18	1	AAQ75025	PCR primer. Synth
1278	18.4	0.7	21	1	AAQ75647	Reverse transcript	1351	18	0.6	18	1	AAT94667	Anchored poly(T) o
c1279	18.4	0.7	21	1	AAQ75654	Reverse transcript	c1352	18	0.6	18	1	AAT94668	Anchored poly(T) o
1280	18.4	0.7	22	1	ABA93238	PolyA adaptor olig	1353	18	0.6	18	1	AAV37712	Human protein AQ2_
1281	18.4	0.7	24	1	ABK12409	RT-PCR primer #1 f	1354	18	0.6	18	1	AAV21970	Nuclease resistant
1282	18.4	0.7	24	1	AAL47515	Human cyclophilin-	c1355	18	0.6	18	1	AAV19943	Primer SEQ ID NO:3
c1283	18.4	0.7	25	1	AAF74925	CD40L poly-A tract	1356	18	0.6	18	1	AAV19943	Primer SEQ ID NO:3
c1284	18.4	0.7	25	1	AAF74930	CD40L poly-A tract	c1357	18	0.6	18	1	AAV19942	Primer SEQ ID NO:2
1285	18.4	0.7	26	1	AAA62140	A. auricaliformis	1358	18	0.6	18	1	AAV19942	Primer SEQ ID NO:2
c1286	18.4	0.7	26	1	AAC93128	Stephania tetrandr	c1359	18	0.6	18	1	AAV18372	RT-PCR primer of t
1287	18.4	0.7	28	1	AAQ33612	GL6anti, targetted	1360	18	0.6	18	1	AAV18372	Human adult ovary
c1288	18.4	0.7	28	1	AAQ33514	T7T18Apad PS19-28-	1361	18	0.6	18	1	AAA40563	Oligoarabinonucleo
c1289	18.4	0.7	28	1	AAQ33512	T7T18Apad PS8-28-0	1362	18	0.6	18	1	AAZ87161	Oligoarabinonucleo
1290	18.2	0.6	19	1	AAQ06572	(-)-limonene-6-hyd	c1363	18	0.6	18	1	AAZ87161	Oligoarabinonucleo
c1291	18.2	0.6	19	1	AAQ06572	(-)-limonene-6-hyd	1364	18	0.6	18	1	AAZ87162	Oligoarabinonucleo
1292	18.2	0.6	19	1	AAZ99489	Primer HOOK for CD	c1365	18	0.6	18	1	AAZ87162	Oligoarabinonucleo
c1293	18.2	0.6	19	1	AAZ99489	Primer HOOK for CD	1366	18	0.6	18	1	AAZ87166	Deoxyarabinonucleo
1294	18.2	0.6	19	1	AAZ15201	3' sequencing prim	c1367	18	0.6	18	1	AAZ87166	Deoxyarabinonucleo
c1295	18.2	0.6	19	1	AAH21968	3' sequencing prim	1368	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1296	18.2	0.6	19	1	AAH21968	Mouse total gene e	c1369	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1297	18.2	0.6	19	1	AAF76617	Mouse total gene e	1370	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1298	18.2	0.6	19	1	AAF76617	Spearmint (-)-limo	c1371	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1299	18.2	0.6	19	1	AAF76617	Spearmint (-)-limo	1372	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1300	18.2	0.6	19	1	AAS06525	Mouse microglia an	c1373	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1301	18.2	0.6	19	1	AAS06525	Mouse microglia an	c1374	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1302	18.2	0.6	19	1	ABK71509	CNS related 3' seq	1375	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1303	18.2	0.6	19	1	ABK71509	CNS related 3' seq	c1376	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1304	18.2	0.6	19	1	ABQ73231	Rabbit atheroscler	1377	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1305	18.2	0.6	19	1	ABQ73231	Rabbit atheroscler	c1378	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1306	18.2	0.6	19	1	AAD34663	PCR primer #4 used	1379	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1307	18.2	0.6	19	1	AAD34663	PCR primer #4 used	c1380	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1308	18.2	0.6	19	1	AAD40279	HOOK PCR primer us	1381	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1309	18.2	0.6	19	1	AAD40279	HOOK PCR primer us	c1382	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1310	18.2	0.6	19	1	ABZ68389	Reverse transcript	1383	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1311	18.2	0.6	19	1	ABZ68389	Reverse transcript	c1384	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1312	18.2	0.6	19	1	ACC79402	M13 sequencing pri	1385	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1313	18.2	0.6	19	1	ACC79402	M13 sequencing pri	c1386	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1314	18.2	0.6	19	1	AAD49149	3' sequencing prim	1387	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1315	18.2	0.6	19	1	AAD49149	3' sequencing prim	c1388	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1316	18.2	0.6	19	1	AAD50267	3' sequencing prim	1389	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1317	18.2	0.6	19	1	AAD50267	3' sequencing prim	c1390	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1318	18.2	0.6	19	1	ADC21495	3' sequencing prim	1391	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1319	18.2	0.6	19	1	ADC21495	Human PRDI-BF1 RT-	c1392	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1320	18.2	0.6	20	1	AAZ09197	Human PRDI-BF1 RT-	1393	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1321	18.2	0.6	20	1	AAZ09197	Oligonucleotide 9	c1394	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1322	18.2	0.6	20	1	AAQ45360	Oligonucleotide 9	1395	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1323	18.2	0.6	23	1	AAT37316	Human protein-tyro	c1396	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1324	18.2	0.6	23	1	AAZ28229	RT-PCR Primer for	1397	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1325	18.2	0.6	23	1	AAZ28229	Second round PCR p	c1398	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1326	18.2	0.6	23	1	AAZ29299	Second round prime	1399	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1327	18.2	0.6	23	1	ABA97431	Glycosyltransferas	c1400	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1328	18.2	0.6	24	1	ABA97997	Human mitochondria	1401	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1329	18.2	0.6	25	1	AAI72268	P4 primer used in	c1402	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1330	18.2	0.6	25	1	ACF79235	Calix(a)arene-olig	1403	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1331	18.2	0.6	25	1	AAC96079	16s rRNA gene PCR	c1404	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1332	18.2	0.6	25	1	AAT27193	Stem loop oligonuc	1405	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1333	18.2	0.6	25	1	AAC96418	HLA DQA1 gene PCR	c1406	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1334	18.2	0.6	25	1	AAC96060	16s rRNA gene PCR	1407	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1335	18.2	0.6	25	1	AAH38315	SNP specific SNPE	c1408	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1336	18.2	0.6	26	1	AAH89364	Chromosomal bindin	1409	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1337	18.2	0.6	26	1	ABS54659	Human p53 protein	c1410	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1338	18.2	0.6	27	1	ADC75075	Biosensor related	1411	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1339	18.2	0.6	27	1	AAT90275	Pyrimidine ring mo	c1412	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1340	18.2	0.6	27	1	ADC75076	Biosensor related	1413	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1341	18.2	0.6	28	1	AAF60450	RNA oligonucleotid	c1414	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1342	18.2	0.6	28	1	AAL45359	Puromycin linker D	1415	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1343	18.2	0.6	28	1	AAT70113	PolyAB primer 2.	c1416	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1344	18.2	0.6	28	1	AAD41903	Minority genome me	1417	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1345	18.2	0.6	29	1	AAA71176	ON-41 oligonucleot	c1418	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1346	18.2	0.6	29	1	AAA71193	Molecular interact	1419	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1347	18.2	0.6	29	1	AAA71193	Molecular interact	c1420	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
	18		18		AAQ34110	Sequence of a micr							

1421	18	0.6	19	1	AAQ75551	Reverse transcript	18	0.6	20	1	ABZ89719	Human oligonucleot
1422	18	0.6	19	1	AAQ75554	Reverse transcript	18	0.6	20	1	ADE52460	Stem cell factor (
c1423	18	0.6	19	1	AAQ75555	Reverse transcript	18	0.6	20	1	ADE52460	Stem cell factor (
c1424	18	0.6	19	1	AAQ75557	Reverse transcript	18	0.6	21	1	AAQ75692	Reverse transcript
1425	18	0.6	19	1	ABL51521	Tailing reaction r	18	0.6	21	1	AAQ75776	Reverse transcript
c1426	18	0.6	19	1	ABL51521	Tailing reaction r	18	0.6	21	1	AAQ75777	Reverse transcript
1427	18	0.6	19	1	ABZ75398	Synthetic nuclease	18	0.6	21	1	AAQ75693	Reverse transcript
c1428	18	0.6	19	1	ABZ75398	Synthetic nuclease	18	0.6	21	1	AAQ75694	Reverse transcript
1429	18	0.6	19	1	ABZ75399	Synthetic nuclease	18	0.6	21	1	AAQ75775	Reverse transcript
c1430	18	0.6	19	1	ABZ75399	Synthetic nuclease	18	0.6	21	1	AAQ75691	Reverse transcript
c1431	18	0.6	20	1	AAT04916	Mammalian stem cel	18	0.6	21	1	AAQ75735	Reverse transcript
1432	18	0.6	20	1	AAT04918	Mammalian stem cel	18	0.6	21	1	AAQ75738	Reverse transcript
c1433	18	0.6	20	1	AAAI3753	Stem cell factor u	18	0.6	21	1	AAQ75748	Reverse transcript
1434	18	0.6	20	1	AAAI3754	Stem cell factor u	18	0.6	21	1	AAQ75795	Reverse transcript
c1435	18	0.6	20	1	AAH41332	Universal stem cel	18	0.6	21	1	AAQ75671	Reverse transcript
1436	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75736	Reverse transcript
c1437	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75798	Reverse transcript
1438	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75674	Reverse transcript
c1439	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75674	Reverse transcript
1440	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75687	Reverse transcript
1441	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75793	Reverse transcript
c1442	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75794	Reverse transcript
1443	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75767	Reverse transcript
c1444	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75688	Reverse transcript
1445	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75713	Reverse transcript
c1446	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75747	Reverse transcript
1447	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75786	Reverse transcript
c1448	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75791	Reverse transcript
1449	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75743	Reverse transcript
c1450	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75769	Reverse transcript
1451	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75797	Reverse transcript
c1452	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75689	Reverse transcript
1453	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75703	Reverse transcript
1454	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75714	Reverse transcript
1455	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75705	Reverse transcript
1456	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75712	Reverse transcript
c1457	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75737	Reverse transcript
1458	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75672	Reverse transcript
c1459	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75706	Reverse transcript
1460	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75746	Reverse transcript
c1461	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75784	Reverse transcript
1462	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75785	Reverse transcript
1463	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75704	Reverse transcript
c1464	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75708	Reverse transcript
1465	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75673	Reverse transcript
c1466	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75768	Reverse transcript
1467	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75707	Reverse transcript
c1468	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75750	Reverse transcript
1469	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75710	Reverse transcript
1470	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75745	Reverse transcript
c1471	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75749	Reverse transcript
1472	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75770	Reverse transcript
c1473	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75709	Reverse transcript
1474	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75711	Reverse transcript
c1475	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75744	Reverse transcript
1476	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75783	Reverse transcript
c1477	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75792	Reverse transcript
1478	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ64706	2',5'-linked tetra
c1479	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ64706	2',5'-linked tetra
1480	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAA98276	Human mismatch rep
c1481	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75028	LCR oligo 2. Synt
1482	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
c1483	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
1484	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
c1485	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
1486	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
c1487	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
1488	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
c1489	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
1490	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
c1491	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
1492	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt
c1493	18	0.6	20	1	AAH41333	Universal stem cel	18	0.6	21	1	AAQ75029	LCR oligo 3. Synt

1567	18	0.6	24	1	ABQ79878	Nucleotide sequenc	c1640	17.8	0.6	21	1	AAQ75697	Reverse transcript
c1568	18	0.6	24	1	ABQ79878	Nucleotide sequenc	c1641	17.8	0.6	21	1	AAQ75637	Reverse transcript
1569	18	0.6	24	1	AAD333505	T7T18Apad_PS12-24-	c1642	17.8	0.6	21	1	AAQ75644	Reverse transcript
c1570	18	0.6	24	1	AAD333505	T7T18Apad_PS12-24-	1643	17.8	0.6	21	1	AAQ75761	Reverse transcript
1571	18	0.6	24	1	AAD333505	Biosensor related	c1644	17.8	0.6	21	1	AAQ75721	Reverse transcript
c1572	18	0.6	24	1	ADC75073	Biosensor related	1645	17.8	0.6	21	1	AAQ75762	Reverse transcript
c1573	18	0.6	24	1	ADC75073	Adapter sequence f	1646	17.8	0.6	21	1	AAQ75760	Reverse transcript
1574	18	0.6	25	1	AAA47833	BamT15G PCR primer	1647	17.8	0.6	21	1	AAQ75754	Reverse transcript
1575	18	0.6	25	1	ABK87633	BamT15A PCR primer	1648	17.8	0.6	21	1	AAQ75781	Reverse transcript
c1576	18	0.6	25	1	ABK87631	BamT15C PCR primer	c1649	17.8	0.6	21	1	AAQ75700	Reverse transcript
c1577	18	0.6	25	1	ABK87632	BamT15C PCR primer	1650	17.8	0.6	21	1	AAQ75742	Reverse transcript
c1578	18	0.6	25	1	AAD333507	T7T18Apad_PS11-25-	c1651	17.8	0.6	21	1	AAQ75716	Reverse transcript
c1579	18	0.6	25	1	AAD333507	T7T18Apad_PS11-25-	1652	17.8	0.6	21	1	AAQ75740	Reverse transcript
c1580	18	0.6	26	1	AAD12516	Thuja sp. pinoresi	c1653	17.8	0.6	21	1	AAQ75636	Reverse transcript
c1581	18	0.6	26	1	AAV35002	Human endothelin-b	1654	17.8	0.6	21	1	AAQ75790	Reverse transcript
c1582	18	0.6	26	1	AA88688	Oligo-dT-XhoI prim	c1655	17.8	0.6	21	1	AAQ75645	Reverse transcript
1583	18	0.6	26	1	AAC93128	Stephania tetrandr	1656	17.8	0.6	21	1	AAQ75662	Reverse transcript
1584	18	0.6	26	1	AAQ47178	MHC DR A intron bi	1657	17.8	0.6	21	1	AAQ75653	Reverse transcript
c1585	18	0.6	26	1	AAZ25387	Infectious pancrea	c1658	17.8	0.6	21	1	AAQ75677	Reverse transcript
c1586	18	0.6	26	1	AA91664	HCV(+)RNA oligonuc	c1659	17.8	0.6	21	1	AAQ75696	Reverse transcript
c1587	18	0.6	26	1	AAS01617	Human MINT31/CACNA	1660	17.8	0.6	21	1	AAQ75793	Reverse transcript
1588	18	0.6	26	1	AAS01577	Human T-type calci	c1661	17.8	0.6	21	1	AAQ75688	Reverse transcript
1589	18	0.6	26	1	AAS01670	Human MINT31/CACNA	c1662	17.8	0.6	21	1	AAQ75713	Reverse transcript
1590	18	0.6	26	1	ABK66615	Human gene specifi	1663	17.8	0.6	21	1	AAQ75769	Reverse transcript
c1591	18	0.6	26	1	AAD333509	T7T18Apad_PS10-26-	1664	17.8	0.6	21	1	AAQ75797	Reverse transcript
c1592	18	0.6	27	1	AAD333509	T7T18Apad_PS10-26-	c1665	17.8	0.6	21	1	AAQ75672	Reverse transcript
c1593	18	0.6	27	1	AAK15434	PCR primer used to	c1666	17.8	0.6	21	1	AAQ75708	Reverse transcript
c1594	18	0.6	27	1	AAT94842	PCR primer for hES	1667	17.8	0.6	21	1	AAQ75768	Reverse transcript
c1595	18	0.6	27	1	AA59740	Human ESF 1 3' PCR	1668	17.8	0.6	21	1	AAQ75745	Reverse transcript
c1596	18	0.6	27	1	AAF25224	3' primer for an e	1669	17.8	0.6	21	1	AAQ75749	Reverse transcript
c1597	18	0.6	27	1	ABL41793	Primer for human e	c1670	17.8	0.6	21	1	AAQ75709	Reverse transcript
c1598	18	0.6	27	1	ABX14927	hESF 1 amplifying	1671	17.8	0.6	21	1	AAQ75744	Reverse transcript
c1599	18	0.6	27	1	AA47309	Intracellular targ	1672	17.8	0.6	21	1	AAQ75792	Reverse transcript
c1600	18	0.6	27	1	AAK23568	Deletion sequence	1673	17.8	0.6	21	1	AAQ75633	Reverse transcript
1601	18	0.6	27	1	AAK23572	Deletion sequence	c1674	17.8	0.6	21	1	AAQ75620	Reverse transcript
c1602	18	0.6	27	1	AAD33510	T7T18Apad_PS9-27-0	c1675	17.8	0.6	21	1	AAQ75626	Reverse transcript
c1603	18	0.6	27	1	AAD33510	T7T18Apad_PS9-27-0	1676	17.8	0.6	21	1	AAQ75664	Reverse transcript
c1604	18	0.6	28	1	ACC83476	Oligo dT primer.	1677	17.8	0.6	21	1	AAQ75664	Reverse transcript
c1605	18	0.6	28	1	ADD35234	Potato gene PCR pr	c1678	17.8	0.6	21	1	AAQ75669	Reverse transcript
c1606	18	0.6	28	1	ADD35234	Mouse mitochondria	1679	17.8	0.6	21	1	AAQ75668	Reverse transcript
c1607	18	0.6	28	1	AAT70108	PolyTV primer 3.	c1680	17.8	0.6	21	1	AAQ75625	Reverse transcript
c1608	18	0.6	28	1	AAV61015	HS/HIP reverse tra	1681	17.8	0.6	21	1	AAQ75625	Reverse transcript
c1609	18	0.6	28	1	AAZ61254	Oligo dT primer fo	c1682	17.8	0.6	21	1	AAQ75634	Reverse transcript
1610	18	0.6	28	1	AAI71210	Single stranded DN	1683	17.8	0.6	21	1	AAQ75614	Reverse transcript
c1611	18	0.6	28	1	AAD33512	T7T18Apad_PS8-28-0	1684	17.8	0.6	21	1	AAQ75665	Reverse transcript
c1612	18	0.6	29	1	AA90025	PCR primer for fat	1685	17.8	0.6	21	1	AAQ75612	Reverse transcript
c1613	18	0.6	29	1	AAI69697	T7T18Apad_PS6-29-0	c1686	17.8	0.6	21	1	AAQ75612	Reverse transcript
1614	18	0.6	29	1	AAI69697	Hepatitis E virus	1687	17.8	0.6	21	1	AAQ75641	Reverse transcript
c1615	18	0.6	30	1	AAD33517	T7T18Apad_PS5-30-0	1688	17.8	0.6	21	1	AAQ75632	Reverse transcript
1616	18	0.6	30	1	AAV56638	Feline FLAF cDNA p	1689	17.8	0.6	21	1	AAQ75621	Reverse transcript
c1617	18	0.6	30	1	AAF74908	CD40L poly-A tract	1690	17.8	0.6	21	1	AAQ75656	Reverse transcript
c1618	18	0.6	31	1	AAD33519	T7T18Apad_PS4-31-0	c1691	17.8	0.6	21	1	AAQ75617	Reverse transcript
c1619	18	0.6	31	1	AAQ99582	Human TPO anti-sen	1692	17.8	0.6	21	1	AAQ75640	Reverse transcript
c1620	18	0.6	32	1	AAQ87894	Normalised library	1693	17.8	0.6	21	1	AAQ75640	Reverse transcript
c1621	18	0.6	32	1	AAD33521	T7T18Apad_PS3-32-0	c1694	17.8	0.6	21	1	AAQ75613	Reverse transcript
c1622	18	0.6	32	1	AAT94579	Antifungal polypep	c1695	17.8	0.6	21	1	AAQ75616	Reverse transcript
c1623	18	0.6	32	1	ADC87763	F. culmorum FCWP1	1696	17.8	0.6	21	1	AAQ75616	Reverse transcript
c1624	18	0.6	34	1	AAH28290	3' untranslated re	c1697	17.8	0.6	21	1	AAZ26563	Human polymorphic
c1625	18	0.6	34	1	AA90605	Tomato spotted wil	1698	17.8	0.6	22	1	AAF98936	Immunostimulatory
c1626	18	0.6	39	1	AAV12483	Oligonucleotide SE	1699	17.8	0.6	22	1	ABS77577	Angiogenesis inhib
1627	17.8	0.6	39	1	AAK30019	Multimer SEQ ID NO	1700	17.8	0.6	22	1	ACD99369	Immunostimulatory
c1628	17.8	0.6	19	1	AAT69640	Telomerase Oligo-d	1701	17.8	0.6	22	1	ADB36438	Immunostimulatory
c1629	17.8	0.6	19	1	AAT69640	Telomerase Oligo-d	1702	17.8	0.6	22	1	AAH91823	Human inflammatory
c1630	17.8	0.6	21	1	AAQ75733	Reverse transcript	1703	17.8	0.6	23	1	AAF98935	Human serine/threo
c1631	17.8	0.6	21	1	AAQ75732	Reverse transcript	1704	17.8	0.6	24	1	AAI64873	Human serine/threo
c1632	17.8	0.6	21	1	AAQ75648	Reverse transcript	c1705	17.8	0.6	24	1	AAI65187	Human gap connexin
c1633	17.8	0.6	21	1	AAQ75676	Reverse transcript	1706	17.8	0.6	24	1	ABS77576	Angiogenesis inhib
1634	17.8	0.6	21	1	AAQ75681	Reverse transcript	1707	17.8	0.6	24	1	ABA01048	Human sodium pump
1635	17.8	0.6	21	1	AAQ75780	Reverse transcript	1708	17.8	0.6	24	1	ABN86902	Human macroprotein
1636	17.8	0.6	21	1	AAQ75660	Reverse transcript	1709	17.8	0.6	24	1	ACD99368	Immunostimulatory
1637	17.8	0.6	21	1	AAQ75652	Reverse transcript	1710	17.8	0.6	24	1	ADB36437	Immunostimulatory
1638	17.8	0.6	21	1	AAQ75753	Reverse transcript	1711	17.8	0.6	24	1	AAV30657	Telomerase reverse
c1639	17.8	0.6	21	1	AAQ75788	Reverse transcript	c1712	17.8	0.6	25	1		

1713	17.8	0.6	25	1	1713	17.4	0.6	19	1	1713	Reverse transcript
c1714	17.8	0.6	25	1	1786	17.4	0.6	19	1	AAQ75557	Reverse transcript
1715	17.8	0.6	25	1	1787	17.4	0.6	19	1	AAQ75549	Reverse transcript
1716	17.8	0.6	25	1	c1788	17.4	0.6	19	1	AAQ75549	Reverse transcript
1717	17.8	0.6	25	1	1789	17.4	0.6	19	1	AAQ75548	Reverse transcript
1718	17.8	0.6	25	1	c1790	17.4	0.6	19	1	AAQ75548	Reverse transcript
1719	17.8	0.6	25	1	c1791	17.4	0.6	19	1	AAQ75550	Reverse transcript
1720	17.8	0.6	25	1	1792	17.4	0.6	19	1	ADE29541	Mitogen activated
1721	17.8	0.6	25	1	c1793	17.4	0.6	19	1	ADE29541	Mitogen activated
1722	17.8	0.6	25	1	1794	17.4	0.6	19	1	ADE29704	Mitogen activated
1723	17.8	0.6	25	1	c1795	17.4	0.6	19	1	ADE29704	Mitogen activated
1724	17.8	0.6	25	1	c1796	17.4	0.6	20	1	AAQ75582	Reverse transcript
1725	17.8	0.6	25	1	c1797	17.4	0.6	20	1	AAQ75579	Reverse transcript
1726	17.8	0.6	25	1	1798	17.4	0.6	20	1	AAQ75597	Reverse transcript
1727	17.8	0.6	25	1	1799	17.4	0.6	20	1	AAQ75595	Reverse transcript
1728	17.8	0.6	25	1	1800	17.4	0.6	20	1	AAA91207	Antisense IGFBP-5
1729	17.8	0.6	25	1	c1802	17.4	0.6	20	1	AAQ75566	Reverse transcript
1730	17.8	0.6	25	1	c1803	17.4	0.6	20	1	AAQ75569	Reverse transcript
c1731	17.8	0.6	25	1	c1804	17.4	0.6	20	1	AAQ75584	Reverse transcript
1732	17.8	0.6	25	1	c1805	17.4	0.6	20	1	AAQ75585	Reverse transcript
c1733	17.8	0.6	25	1	1806	17.4	0.6	20	1	AAQ75568	Reverse transcript
1734	17.8	0.6	25	1	c1807	17.4	0.6	20	1	AAQ75570	Reverse transcript
c1735	17.8	0.6	25	1	c1808	17.4	0.6	20	1	AAQ75589	Reverse transcript
1736	17.8	0.6	25	1	1809	17.4	0.6	20	1	AAQ75590	Reverse transcript
c1737	17.8	0.6	25	1	c1810	17.4	0.6	20	1	AAQ75602	Reverse transcript
1738	17.8	0.6	25	1	1811	17.4	0.6	20	1	ABZ85534	Human oligonucleot
c1739	17.8	0.6	25	1	c1812	17.4	0.6	20	1	ABZ88813	Human oligonucleot
1740	17.8	0.6	25	1	c1813	17.4	0.6	20	1	AAQ75583	Reverse transcript
c1741	17.8	0.6	26	1	c1814	17.4	0.6	20	1	AAQ75587	Reverse transcript
1742	17.8	0.6	27	1	1815	17.4	0.6	20	1	AAQ75599	Reverse transcript
1743	17.8	0.6	27	1	1816	17.4	0.6	20	1	ABZ89703	Human oligonucleot
c1744	17.8	0.6	27	1	c1817	17.4	0.6	20	1	AAQ75574	Reverse transcript
1745	17.6	0.6	24	1	1818	17.4	0.6	20	1	AAQ75563	Reverse transcript
1746	17.6	0.6	24	1	c1819	17.4	0.6	20	1	AAQ75563	Reverse transcript
1747	17.6	0.6	24	1	1820	17.4	0.6	20	1	AAQ75565	Reverse transcript
1748	17.6	0.6	24	1	c1821	17.4	0.6	20	1	AAQ75565	Reverse transcript
c1749	17.6	0.6	24	1	c1822	17.4	0.6	20	1	AAQ75573	Reverse transcript
1750	17.6	0.6	24	1	1823	17.4	0.6	20	1	AAQ75567	Reverse transcript
1751	17.6	0.6	24	1	c1824	17.4	0.6	20	1	AAQ75567	Reverse transcript
1752	17.6	0.6	25	1	c1825	17.4	0.6	20	1	AAQ75571	Reverse transcript
1753	17.6	0.6	25	1	c1826	17.4	0.6	20	1	AAQ75571	Reverse transcript
c1754	17.6	0.6	25	1	1827	17.4	0.6	20	1	AAF99943	Reverse transcript
c1755	17.6	0.6	25	1	c1828	17.4	0.6	20	1	ABA05917	Synthetic oligonuc
1756	17.6	0.6	25	1	c1829	17.4	0.6	20	1	Hepatitis B virus	Human oligonucleot
c1757	17.6	0.6	25	1	1830	17.4	0.6	20	1	ABZ88879	Human oligonucleot
c1758	17.6	0.6	25	1	c1831	17.4	0.6	20	1	ABZ85669	Human oligonucleot
c1759	17.6	0.6	25	1	c1832	17.4	0.6	20	1	ABZ90829	Human oligonucleot
c1760	17.6	0.6	25	1	c1833	17.4	0.6	20	1	ABZ89301	Human oligonucleot
c1761	17.6	0.6	25	1	c1834	17.4	0.6	21	1	ABZ89301	Human oligonucleot
c1762	17.6	0.6	25	1	c1835	17.4	0.6	21	1	AAQ75731	Reverse transcript
1763	17.6	0.6	25	1	c1836	17.4	0.6	21	1	AAQ75734	Reverse transcript
c1764	17.6	0.6	25	1	c1837	17.4	0.6	21	1	AAQ75649	Reverse transcript
1765	17.6	0.6	25	1	c1838	17.4	0.6	21	1	AAQ75701	Reverse transcript
c1766	17.6	0.6	26	1	c1839	17.4	0.6	21	1	AAF24290	Complementary nucl
c1767	17.6	0.6	26	1	1840	17.4	0.6	21	1	ABX79794	EST polymorphic DN
1768	17.6	0.6	26	1	c1841	17.4	0.6	21	1	AAQ75752	Reverse transcript
1769	17.6	0.6	26	1	c1842	17.4	0.6	21	1	AAQ75719	Reverse transcript
1770	17.6	0.6	26	1	1843	17.4	0.6	21	1	AAQ75722	Reverse transcript
c1771	17.6	0.6	26	1	c1844	17.4	0.6	21	1	AAQ75751	Reverse transcript
1772	17.6	0.6	26	1	1845	17.4	0.6	21	1	AAQ75759	Reverse transcript
c1773	17.6	0.6	27	1	c1846	17.4	0.6	21	1	AAQ75720	Reverse transcript
c1774	17.6	0.6	29	1	c1847	17.4	0.6	21	1	AAQ75651	Reverse transcript
c1775	17.6	0.6	29	1	c1848	17.4	0.6	21	1	AAQ75702	Reverse transcript
1776	17.6	0.6	29	1	c1849	17.4	0.6	21	1	AAQ75675	Reverse transcript
1777	17.6	0.6	29	1	c1850	17.4	0.6	21	1	AAQ75643	Reverse transcript
1778	17.6	0.6	29	1	c1851	17.4	0.6	21	1	AAQ75695	Reverse transcript
1779	17.6	0.6	29	1	c1852	17.4	0.6	21	1	AAQ75646	Reverse transcript
1780	17.6	0.6	31	1	c1853	17.4	0.6	21	1	AAQ75678	Reverse transcript
c1781	17.6	0.6	19	1	c1854	17.4	0.6	21	1	AAQ75779	Reverse transcript
c1782	17.4	0.6	19	1	c1855	17.4	0.6	21	1	AAQ75698	Reverse transcript
1783	17.4	0.6	19	1	c1856	17.4	0.6	21	1	AAQ75699	Reverse transcript
c1784	17.4	0.6	19	1	c1857	17.4	0.6	21	1	AAQ75782	Reverse transcript
c1785	17.4	0.6	19	1	c1858	17.4	0.6	21	1	AAQ75679	Reverse transcript
										AAQ75638	Reverse transcript

c1859	17.4	0.6	21	1	AAQ75647	Reverse transcript	c1932	17.4	0.6	28	1	AAQ36362	GL6anti, targeted
1860	17.4	0.6	21	1	AAQ75654	Reverse transcript	1933	17.4	0.6	28	1	AAQ70113	PolyAB primer 2
c1861	17.4	0.6	21	1	AAQ75671	Reverse transcript	c1934	17.4	0.6	30	1	ADA26181	Rice semi-dwarf (s
c1862	17.4	0.6	21	1	AAQ75674	Reverse transcript	c1935	17.4	0.6	30	1	ABL56893	Synthetic deoxyrib
c1863	17.4	0.6	21	1	AAQ75687	Reverse transcript	c1936	17.4	0.6	30	1	ABA97617	Poly f nucleotide
c1864	17.4	0.6	21	1	AAQ75690	Reverse transcript	c1937	17.4	0.6	30	1	ABL56894	Probe poly f for a
1865	17.4	0.6	21	1	AAQ75767	Reverse transcript	c1938	17.4	0.6	30	1	ABL56895	Synthetic deoxyrib
c1866	17.4	0.6	21	1	AAQ75689	Reverse transcript	c1939	17.4	0.6	30	1	ABL56896	Synthetic deoxyrib
c1867	17.4	0.6	21	1	AAQ75673	Reverse transcript	c1940	17.4	0.6	30	1	ABA97619	Poly h nucleotide
1868	17.4	0.6	21	1	AAQ75770	Reverse transcript	c1941	17.4	0.6	30	1	ABA97618	Poly g nucleotide
c1869	17.4	0.6	21	1	AAQ75626	Reverse transcript	c1942	17.4	0.6	30	1	ABL95891	Probe poly g for a
c1870	17.4	0.6	21	1	AAQ75669	Reverse transcript	c1943	17.4	0.6	30	1	ABL95892	Probe poly h for a
c1871	17.4	0.6	21	1	AAQ75634	Reverse transcript	c1944	17.4	0.6	30	1	ABL56888	Synthetic deoxyrib
c1872	17.4	0.6	21	1	AAQ75665	Reverse transcript	c1945	17.4	0.6	30	1	ABA97612	Poly a nucleotide
c1873	17.4	0.6	21	1	AAQ75641	Reverse transcript	c1946	17.4	0.6	30	1	ABL95885	Probe poly a for a
c1874	17.4	0.6	21	1	AAQ75632	Reverse transcript	c1947	17.4	0.6	30	1	ABL56892	Synthetic deoxyrib
c1875	17.4	0.6	21	1	AAQ75670	Reverse transcript	c1948	17.4	0.6	30	1	ABL56896	Synthetic deoxyrib
c1876	17.4	0.6	21	1	AAQ75657	Reverse transcript	c1949	17.4	0.6	30	1	ABL56890	Synthetic deoxyrib
1877	17.4	0.6	21	1	AAQ75631	Reverse transcript	c1950	17.4	0.6	30	1	ABL56891	Synthetic deoxyrib
c1878	17.4	0.6	21	1	AAQ75631	Reverse transcript	c1951	17.4	0.6	30	1	ABL56897	Synthetic deoxyrib
1879	17.4	0.6	21	1	AAQ75639	Reverse transcript	c1952	17.4	0.6	30	1	ABL56889	Synthetic deoxyrib
c1880	17.4	0.6	21	1	AAQ75639	Reverse transcript	c1953	17.4	0.6	30	1	ABA97613	Poly b nucleotide
c1881	17.4	0.6	21	1	AAQ75667	Reverse transcript	c1954	17.4	0.6	30	1	ABA97620	Poly i nucleotide
1882	17.4	0.6	21	1	AAQ75642	Reverse transcript	c1955	17.4	0.6	30	1	ABA97614	Poly c nucleotide
c1883	17.4	0.6	21	1	AAQ75642	Reverse transcript	c1956	17.4	0.6	30	1	ABA97615	Poly d nucleotide
c1884	17.4	0.6	21	1	AAQ75655	Reverse transcript	c1957	17.4	0.6	30	1	ABA97616	Poly e nucleotide
c1885	17.4	0.6	21	1	AAQ75663	Reverse transcript	c1958	17.4	0.6	30	1	ABL95886	Probe poly b for a
1886	17.4	0.6	21	1	AAQ75624	Reverse transcript	c1959	17.4	0.6	30	1	ABL95887	Probe poly c for a
c1887	17.4	0.6	21	1	AAQ75666	Reverse transcript	c1960	17.4	0.6	30	1	ABL95888	Probe poly j for a
c1888	17.4	0.6	21	1	AAQ75623	Reverse transcript	c1961	17.4	0.6	30	1	ABL95889	Probe poly d for a
1889	17.4	0.6	21	1	AAQ75623	Reverse transcript	c1962	17.4	0.6	30	1	ABL95889	Probe poly e for a
c1890	17.4	0.6	21	1	AAQ75623	Reverse transcript	c1963	17.4	0.6	30	1	ABL95893	Probe poly i for a
c1891	17.4	0.6	21	1	AAQ75658	Reverse transcript	1964	17.2	0.6	19	1	AAQ94431	Template mRNA poly
1892	17.4	0.6	21	1	ADE80976	Human papillomavir	c1965	17.2	0.6	19	1	AAQ94431	RT-PCR primer of t
1893	17.4	0.6	23	1	AAT33702	Primer #2 for tiss	1966	17.2	0.6	19	1	AAQ18390	RT-PCR primer of t
c1894	17.4	0.6	23	1	AAT33702	Primer #2 for tiss	c1967	17.2	0.6	19	1	AAQ18390	Oligonucleotide us
1895	17.4	0.6	23	1	AAV61555	Double-anchored ol	1968	17.2	0.6	22	1	ABV74140	Primer #3 for tiss
c1896	17.4	0.6	23	1	AAA07787	Structure of a fra	1969	17.2	0.6	23	1	AAV61556	Double-anchored ol
1897	17.4	0.6	23	1	AAA07786	Structure of a fra	1970	17.2	0.6	23	1	AAV61556	Oligonucleotide pr
1898	17.4	0.6	23	1	AAA08408	Oligonucleotide pr	1971	17.2	0.6	23	1	AAV61556	Neurofibromatosis
c1899	17.4	0.6	23	1	AAH08408	Human phosphatase	c1972	17.2	0.6	23	1	AAV74138	5' End of cDNA lib
c1900	17.4	0.6	24	1	AAH24266	Human FD 17 PCR pr	c1973	17.2	0.6	23	1	ABV74138	Oligonucleotide us
c1901	17.4	0.6	24	1	AAH44623	RT-PCR primer #2 f	1974	17.2	0.6	24	1	AAH75510	Human CCR4 related
c1902	17.4	0.6	24	1	ABK13715	Human cyclophilin-	c1975	17.2	0.6	24	1	AAH75510	Primer used to ide
c1903	17.4	0.6	24	1	AAH47515	Human amyloid prec	1976	17.2	0.6	24	1	AAV82670	Human neurotrophin
c1904	17.4	0.6	24	1	AAH76998	HLA DPAl gene PCR	c1977	17.2	0.6	24	1	AAI69702	Human DNA-PK inter
c1905	17.4	0.6	25	1	AAAC96267	CD40L poly-A tract	c1978	17.2	0.6	24	1	ABV77761	Human zinc finger
1906	17.4	0.6	25	1	AAAF74925	CD40L poly-A tract	1979	17.2	0.6	24	1	ABO78896	16s rRNA gene PCR
1907	17.4	0.6	25	1	AAAF74930	CD40L poly-A tract	c1980	17.2	0.6	25	1	AAAC96060	16s rRNA gene PCR
c1908	17.4	0.6	25	1	AAH38315	SNP specific SNPE	1981	17.2	0.6	25	1	AAAC96204	16s rRNA gene PCR
1909	17.4	0.6	25	1	AAAC95727	HLA DQA1 gene PCR	1982	17.2	0.6	25	1	AAAC96129	HLA HLA-B gene PCR
c1910	17.4	0.6	25	1	AAAC96201	16s rRNA gene PCR	c1983	17.2	0.6	25	1	AAAC96129	16s rRNA gene PCR
1911	17.4	0.6	25	1	AAAC96718	HLA HLA-A gene PCR	c1984	17.2	0.6	25	1	AAAC96115	16s rRNA gene PCR
1912	17.4	0.6	25	1	AAH39903	SNP specific SNPE	1985	17.2	0.6	25	1	AAAC96175	HLA HLA-B gene PCR
c1913	17.4	0.6	25	1	AAH39903	SNP specific SNPE	c1986	17.2	0.6	25	1	ACI84885	Human microarray D
c1914	17.4	0.6	25	1	AAAC90736	Human secretory pr	c1987	17.2	0.6	25	1	ACI81786	Human microarray D
1915	17.4	0.6	25	1	ADB04567	Human MDZ7 scannin	c1988	17.2	0.6	26	1	AAV61049	Primer Mt-2. Synt
c1916	17.4	0.6	25	1	ADB04567	Human MDZ7 scannin	1989	17.2	0.6	26	1	AAV07974	Helicobacter pylor
1917	17.4	0.6	25	1	ADB04568	Human MDZ7 scannin	c1990	17.2	0.6	26	1	AAAC92118	Human MLT gene int
c1918	17.4	0.6	25	1	ADB04568	Human MDZ7 scannin	c1991	17.2	0.6	28	1	AAAT13977	E. spinifera fumon
1919	17.4	0.6	26	1	AAF16616	Gastric acid produ	c1992	17.2	0.6	28	1	AAV65735	A. phoenices APOXD
1920	17.4	0.6	26	1	AAF74913	CD40L poly-A tract	c1993	17.2	0.6	28	1	AAV05727	E. spinifera fumon
1921	17.4	0.6	27	1	AAF74926	CD40L poly-A tract	c1994	17.2	0.6	28	1	ABZ70568	5' RACE primer Bam
1922	17.4	0.6	27	1	AAF74932	CD40L poly-A tract	c1995	17.2	0.6	35	1	AAQ52157	Breast cancer spec
1923	17.4	0.6	27	1	AAF74931	CD40L poly-A tract	1996	17	0.6	17	1	AAAC69800	Human flt1 VEGF re
1924	17.4	0.6	27	1	AAF74934	CD40L poly-A tract	c1997	17	0.6	17	1	AAAC69801	Human flt1 VEGF re
c1925	17.4	0.6	27	1	AAQ05023	Sequence binding t	1998	17	0.6	17	1	AAAC69801	RT-PCR primer of t
c1926	17.4	0.6	27	1	AAQ36361	GL6par, targeted	1999	17	0.6	17	1	AAAC69801	Oestrogen receptor
1927	17.4	0.6	28	1	AAF74906	CD40L poly-A tract	c2000	17	0.6	17	1	AAAC69801	Oestrogen receptor
1928	17.4	0.6	28	1	AAF74920	CD40L poly-A tract	2001	17	0.6	17	1	AAAC69801	Human retrovirus H
1929	17.4	0.6	28	1	AAF74916	CD40L poly-A tract	c2002	17	0.6	17	1	AAAC69801	Human retrovirus H
1930	17.4	0.6	28	1	AAF74927	CD40L poly-A tract	2003	17	0.6	17	1	AAAC69801	2'-Methoxyethoxy-m
c1931	17.4	0.6	28	1	AAQ52308	FKBP12C PCR primer	c2004	17	0.6	17	1	AAAC69801	2'-Methoxyethoxy-m

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c2151	17	0.6	23	1	AAT37316	RT-PCR primer for	2224	17	0.6	25	1	ACH03276	Immunostimulatory
c2152	17	0.6	23	1	ABA97431	Glycosyltransferas	c2225	17	0.6	25	1	ACH03276	Immunostimulatory
c2153	17	0.6	23	1	AAF85497	PCR primer for DNA	2226	17	0.6	25	1	ADB37240	Immunostimulatory
2154	17	0.6	23	1	ABL95973	Probe #48 for assa	c2227	17	0.6	25	1	ADB37240	Immunostimulatory
2155	17	0.6	23	1	ABQ96219	Tumour suppression	c2228	17	0.6	26	1	AAT99265	Human PUR-alpha ge
c2156	17	0.6	23	1	ABQ96219	Tumour suppression	c2229	17	0.6	26	1	AAV31721	Nucleotide sequenc
c2157	17	0.6	24	1	AAV48089	Oligonucleotide 25	c2230	17	0.6	26	1	AAX04087	PUR-alpha RACE rea
2158	17	0.6	24	1	AAT76905	S. glaucescens dTD	c2231	17	0.6	26	1	AAS01630	Human CACNA1G R6 3
2159	17	0.6	24	1	AAA63459	dNDP-glucose 4,6-d	2232	17	0.6	26	1	AAC92118	Human MLT gene int
2160	17	0.6	24	1	AAH75424	Human homo laminin	2233	17	0.6	26	1	AAT13051	cDNA primer. Synt
2161	17	0.6	24	1	AAD03811	S. galilaeus aClac	2234	17	0.6	26	1	AAT39393	Cotton fibre cDNA
2162	17	0.6	24	1	ABQ73254	Human macro protei	2235	17	0.6	26	1	AAT43363	Cotton fibre first
c2163	17	0.6	24	1	ABQ73254	Human macro protei	2236	17	0.6	26	1	AAT62627	Primer for cotton
2164	17	0.6	24	1	ABL40114	Human natriuretic	2237	17	0.6	26	1	AAT63663	Primer for cotton
c2165	17	0.6	25	1	AAZ99741	Primer used to rev	2238	17	0.6	26	1	AAT70058	Primer for cotton
c2166	17	0.6	25	1	AAC96419	HLA DQA1 gene PCR	c2239	17	0.6	26	1	AAZ59153	Oligonucleotide #1
c2167	17	0.6	25	1	AAC96289	HLA DPB1 gene PCR	c2240	17	0.6	26	1	AAH40741	SNP specific upper
2168	17	0.6	25	1	AAT38116	NotI-oligo primer.	c2241	17	0.6	26	1	ABL54492	GPCR protein BG37
2169	17	0.6	25	1	AAV06660	Unlabeled oligonuc	2242	17	0.6	27	1	ABK52620	Minority genome me
c2170	17	0.6	25	1	AAAX0404	Seq ID No:2 of WO9	c2243	17	0.6	28	1	AAT70107	PolyTV primer 1.
c2171	17	0.6	25	1	AAC95828	HLA HLA-A gene PCR	c2244	17	0.6	28	1	ABK52626	PolyTV primer 2.
c2172	17	0.6	25	1	AAC96374	HLA DPB1 gene PCR	c2245	17	0.6	28	1	ABK52626	Minority genome me
2173	17	0.6	25	1	AAC96624	HLA HLA-A gene PCR	c2246	17	0.6	29	1	AAQ49467	Oligo-dT primer "n
c2174	17	0.6	25	1	AAC96817	HLA HLA-C gene PCR	2247	17	0.6	29	1	AAF74917	CD40L poly-A tract
2175	17	0.6	25	1	AAC96343	HLA DPB1 gene PCR	2248	17	0.6	29	1	AAF74929	CD40L poly-A tract
2176	17	0.6	25	1	AAC95821	HLA HLA-A gene PCR	2249	16.8	0.6	29	1	ABZ22865	Human oligonucleot
c2177	17	0.6	25	1	AAC96433	HLA DQA1 gene PCR	2250	16.8	0.6	29	1	ABZ85669	Human oligonucleot
2178	17	0.6	25	1	AAC96784	HLA HLA-A gene PCR	c2251	16.8	0.6	29	1	AAV12302	Ribonucleotide red
2179	17	0.6	25	1	AAC96788	HLA HLA-A gene PCR	2252	16.8	0.6	29	1	AAV12302	Ribonucleotide red
c2180	17	0.6	25	1	AAC95789	HLA HLA-A gene PCR	2253	16.8	0.6	29	1	AAV12302	Ribonucleotide red
2181	17	0.6	25	1	AAC96182	HLA HLA-A gene PCR	2254	16.8	0.6	29	1	AAV12302	Ribonucleotide red
2182	17	0.6	25	1	AAC96171	HLA HLA-A gene PCR	2255	16.8	0.6	29	1	AAV12302	Ribonucleotide red
2183	17	0.6	25	1	AAC96172	HLA HLA-A gene PCR	2256	16.8	0.6	29	1	AAV12302	Ribonucleotide red
2184	17	0.6	25	1	AAC96172	HLA HLA-A gene PCR	2257	16.8	0.6	29	1	AAV12302	Ribonucleotide red
c2185	17	0.6	25	1	AAC96172	HLA HLA-A gene PCR	c2258	16.8	0.6	29	1	ABA91535	DNA oligonucleotid
2186	17	0.6	25	1	AAC96171	HLA HLA-A gene PCR	c2259	16.8	0.6	29	1	ABL94271	Human C/EBP beta p
c2187	17	0.6	25	1	AAC96171	HLA HLA-A gene PCR	c2260	16.8	0.6	29	1	ABZ88564	Human oligonucleot
c2188	17	0.6	25	1	AAC96219	HLA HLA-A gene PCR	2261	16.8	0.6	29	1	ABZ88564	Human oligonucleot
c2189	17	0.6	25	1	AAC96598	HLA DRB345 gene PC	c2262	16.8	0.6	29	1	ABZ85532	Human oligonucleot
2190	17	0.6	25	1	AAC96121	HLA HLA-A gene PCR	c2263	16.8	0.6	29	1	ABZ85535	Human oligonucleot
2191	17	0.6	25	1	AAC96156	HLA HLA-A gene PCR	c2264	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2192	17	0.6	25	1	AAC95962	HLA HLA-B gene PCR	2265	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2193	17	0.6	25	1	AAC96197	HLA HLA-A gene PCR	2266	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2194	17	0.6	25	1	AAC95728	HLA DQA1 gene PCR	2267	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2195	17	0.6	25	1	AAC96429	HLA DQA1 gene PCR	2268	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2196	17	0.6	25	1	AAC95855	HLA HLA-A gene PCR	2269	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2197	17	0.6	25	1	AAC95855	HLA HLA-A gene PCR	c2270	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2198	17	0.6	25	1	AAC96075	HLA HLA-A gene PCR	c2271	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2199	17	0.6	25	1	AAC96803	Protein kinase CDN	2272	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2200	17	0.6	25	1	AAF99738	Immunostimulatory	c2273	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2201	17	0.6	25	1	AAF99738	Immunostimulatory	2274	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2202	17	0.6	25	1	AAH39959	SNP specific SNPE	c2275	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2203	17	0.6	25	1	ABS78459	Angiogenesis inhib	2276	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2204	17	0.6	25	1	ABS78459	Angiogenesis inhib	c2277	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2205	17	0.6	25	1	ABQ94378	Tumour suppression	2278	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2206	17	0.6	25	1	ABQ94374	Tumour suppression	2279	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2207	17	0.6	25	1	ABQ94375	Tumour suppression	2280	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2208	17	0.6	25	1	ABS76278	Human PAPP-E exon	2281	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2209	17	0.6	25	1	ABS75770	Human PAPP-E exon	2282	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2210	17	0.6	25	1	ABS76277	Human PAPP-E exon	2283	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2211	17	0.6	25	1	ADB04575	Human MDZ7 scannin	2284	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2212	17	0.6	25	1	ADB04574	Human MDZ7 scannin	2285	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2213	17	0.6	25	1	ABV76902	Inverse-PCR primer	2286	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2214	17	0.6	25	1	ACI00609	Human microarray D	2287	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2215	17	0.6	25	1	ACI03338	Human microarray D	c2288	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2216	17	0.6	25	1	ACI61004	Human microarray D	2289	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2217	17	0.6	25	1	ACI89380	Human microarray D	2290	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2218	17	0.6	25	1	ACI62001	Human microarray D	c2291	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2219	17	0.6	25	1	ACI30406	Human microarray D	c2292	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
2220	17	0.6	25	1	ACK15478	Human microarray D	2293	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2221	17	0.6	25	1	ACI02702	Human microarray D	c2294	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2222	17	0.6	25	1	ACI83696	Human microarray D	c2295	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ
c2223	17	0.6	25	1	ACK11064	Human microarray D	2296	16.8	0.6	29	1	AAV76021	DEN-2 cloning/sequ

2297	16.8	0.6	25	1	ABS76271	Human PAPP-E exon
2298	16.8	0.6	25	1	ACD00129	G-protein coupled
2299	16.8	0.6	25	1	ACD00135	G-protein coupled
2300	16.6	0.6	23	1	AAA07787	Structure of a fra
2301	16.6	0.6	23	1	AAA07786	Structure of a fra
c2302	16.6	0.6	23	1	AAX23577	Deletion sequence
2303	16.6	0.6	24	1	ABN85224	Human translation
2304	16.6	0.6	24	1	AAT03687	Homopyrimidine pro
2305	16.6	0.6	24	1	AAX09351	Human biallelic po
2306	16.6	0.6	24	1	AAF84874	Sequence of the ac
c2307	16.6	0.6	24	1	ABA95669	Human zinc finger
2308	16.6	0.6	24	1	AAL42406	Human ORC413-64 PC
2309	16.6	0.6	24	1	ABV76657	Human EGF receptor
c2310	16.6	0.6	24	1	AAS18179	Human proliferatin
2311	16.6	0.6	24	1	ABN86867	Human macroprotein
c2312	16.6	0.6	24	1	ABL55230	Pax protein 11 RT-
2313	16.6	0.6	24	1	AAL51806	Short chain dehydr
c2314	16.6	0.6	24	1	ABQ79142	Primer #2 related
c2315	16.6	0.6	24	1	ABS56172	PCR primer #4 for
2316	16.6	0.6	25	1	AAC96201	16s rRNA gene PCR
2317	16.6	0.6	25	1	AAC96219	16s rRNA gene PCR
2318	16.6	0.6	25	1	AAC95968	HLA HLA-B gene PCR
2319	16.6	0.6	25	1	AAQ55856	Fragile X probe.
2320	16.6	0.6	25	1	AAQ85271	Probe for Fragile
c2321	16.6	0.6	25	1	AAV81177	Antisense fragment
2322	16.6	0.6	25	1	AAX07505	Synthetic IDDMK1.2
2323	16.6	0.6	25	1	AAX07482	Synthetic IDDMK1.2
2324	16.6	0.6	25	1	AAX05267	Fragile X chromoso
2325	16.6	0.6	25	1	AAX07199	IDDM-associated re
2326	16.6	0.6	25	1	AAX07220	Retroviral R-poly(
2327	16.6	0.6	25	1	AAZ49618	PCR primer-2 for s
c2328	16.6	0.6	25	1	AAC96779	HLA HLA-A gene PCR
c2329	16.6	0.6	25	1	AAC96092	16s rRNA gene PCR
2330	16.6	0.6	25	1	AAC96449	HLA DQB1 gene PCR
2331	16.6	0.6	25	1	AAC95730	HLA DQB1 gene PCR
2332	16.6	0.6	25	1	AAC96753	HLA HLA-A gene PCR
2333	16.6	0.6	25	1	AAC96394	HLA DPB1 gene PCR
c2334	16.6	0.6	25	1	AAC96353	HLA DPB1 gene PCR
2335	16.6	0.6	25	1	AAC96041	16s rRNA gene PCR
2336	16.6	0.6	25	1	AAC96099	16s rRNA gene PCR
c2337	16.6	0.6	25	1	AAC96245	HLA DPB1 gene PCR
c2338	16.6	0.6	25	1	AAC96396	HLA DPB1 gene PCR
c2339	16.6	0.6	25	1	AAC96089	16s rRNA gene PCR
2340	16.6	0.6	25	1	AAC96423	HLA DQA1 gene PCR
2341	16.6	0.6	25	1	AAD03602	Human IAP-like pro
2342	16.6	0.6	25	1	AAH28308	3' untranslated re
2343	16.6	0.6	25	1	AAS20313	Human Gamma gene
2344	16.6	0.6	25	1	ABN15565	Human GDMPLP-1 25-m
2345	16.6	0.6	25	1	ABN15567	Human GDMPLP-1 25-m
2346	16.6	0.6	25	1	ABN15566	Human GDMPLP-1 25-m
c2347	16.6	0.6	25	1	ABL43221	Human chromosome 1
2348	16.6	0.6	25	1	ABS75946	Human PAPP-Ea asso
2349	16.6	0.6	25	1	ABS75944	Human PAPP-Ea asso
2350	16.6	0.6	25	1	ABS75945	Human PAPP-Ea asso
2351	16.6	0.6	25	1	ABK90953	PCR primer, 25657,
c2352	16.6	0.6	25	1	ABZ83992	Toxicologically re
2353	16.6	0.6	25	1	AAD53331	Probe used in huma
c2354	16.6	0.6	25	1	AAL61680	Oligonucleotide #3
c2355	16.6	0.6	25	1	ACI99045	Human microarray D
c2356	16.6	0.6	25	1	ACI22395	Human microarray D
c2357	16.6	0.6	25	1	ACK13084	Human microarray D
c2358	16.6	0.6	25	1	ACI81508	Human microarray D
2359	16.6	0.6	25	1	ACI27529	Human microarray D
c2360	16.6	0.6	27	1	ADC75076	Biosensor related
c2361	16.4	0.6	18	1	AAX18372	RT-PCR primer of t
2362	16.4	0.6	18	1	AAF75598	Binary encoded seq
c2363	16.4	0.6	18	1	AAX18373	RT-PCR primer of t
2364	16.4	0.6	18	1	AAN30173	Sequence derived f
2365	16.4	0.6	18	1	AAN92257	SS probe #300. Sy
c2366	16.4	0.6	18	1	AAQ20109	Cross-linking olig
c2367	16.4	0.6	18	1	AAQ20108	Cross-linking olig
2368	16.4	0.6	18	1	AAQ30446	Oligomer TNFR941 f
c2369	16.4	0.6	18	1	AAQ25501	Purine rich HUMNFR

c2370	16.4	0.6	18	1	AAQ30448	Oligomer TNFR943 f
c2371	16.4	0.6	18	1	AAQ30447	Oligomer TNFR942 f
c2372	16.4	0.6	18	1	AAF75596	Binary encoded seq
2373	16.4	0.6	18	1	AAF75597	Binary encoded seq
c2374	16.4	0.6	18	1	AAF75597	Binary encoded seq
2375	16.4	0.6	20	1	AAF99943	Synthetic oligonuc
2376	16.4	0.6	20	1	ABZ91658	Human oligonucleot
2377	16.4	0.6	20	1	ABZ89872	Human oligonucleot
2378	16.4	0.6	20	1	AAV12302	Ribonucleotide red
2379	16.4	0.6	20	1	AAX32010	MSH2 gene specific
2380	16.4	0.6	20	1	AAC82913	Human beta-actin d
2381	16.4	0.6	20	1	ABZ72190	Gene 216 SSCP sequ
2382	16.4	0.6	20	1	ABA05916	Hepatitis B virus
c2383	16.4	0.6	20	1	ABA05916	Hepatitis B virus
2384	16.4	0.6	20	1	ABZ87902	Human oligonucleot
2385	16.4	0.6	20	1	ABX75043	Human gene 216 pol
2386	16.4	0.6	20	1	ADA45251	Human MSH2 gene PC
2387	16.4	0.6	21	1	AAX226563	Human polymorphic
2388	16.4	0.6	21	1	AAX226584	Human polymorphic
2389	16.4	0.6	21	1	AAZ226142	Human polymorphic
c2390	16.4	0.6	21	1	AAZ226142	Human polymorphic
2391	16.4	0.6	21	1	AAZ226268	Human polymorphic
c2392	16.4	0.6	21	1	AAZ226268	Human polymorphic
2393	16.4	0.6	21	1	AAZ226141	Human polymorphic
c2394	16.4	0.6	21	1	AAZ226141	Human polymorphic
2395	16.4	0.6	21	1	ABK15655	Anchored oligo-dt
c2396	16.4	0.6	21	1	ABK99283	Hepatitis C virus
2397	16.4	0.6	21	1	ADE80960	Human papillomavir
2398	16.4	0.6	22	1	AAT28053	3'-primer K for hu
2399	16.4	0.6	22	1	AAT58493	First primer #10 f
2400	16.4	0.6	22	1	AAZ47351	PCR primer K used
2401	16.4	0.6	22	1	AAH22194	Human hepatocyte a
c2402	16.4	0.6	23	1	AAV61555	Double-anchored ol
2403	16.4	0.6	23	1	AAX23577	Deletion sequence
2404	16.4	0.6	23	1	AAV35580	STS probe GV10 gen
2405	16.4	0.6	23	1	AAZ87324	Maize cytochrome P
c2406	16.4	0.6	23	1	AAZ87324	Maize cytochrome P
c2407	16.4	0.6	23	1	AAA10767	Primer CayOR110D u
c2408	16.4	0.6	23	1	AAZ50028	Oligo dt primer 3'
c2409	16.4	0.6	23	1	AAZ50028	Oligo dt primer 3'
c2410	16.4	0.6	24	1	ABA01048	Human sodium pump
2411	16.4	0.6	24	1	AAC96428	HLA DQA1 gene PCR
c2412	16.4	0.6	24	1	AAA94317	RNA-protein fusion
c2413	16.4	0.6	24	1	ABL57074	Molecular beacon o
2414	16.4	0.6	24	1	ABX92831	Borrelia burgdofer
2415	16.4	0.6	24	1	ADC51227	Brassica defensin
2416	16.4	0.6	25	1	AAC96214	16s rRNA gene PCR
c2417	16.4	0.6	25	1	AAC96549	HLA DRB345 gene PC
c2418	16.4	0.6	25	1	AAC96718	HLA HLA-A gene PCR
c2419	16.4	0.6	25	1	AAC96830	HLA HLA-C gene PCR
c2420	16.4	0.6	25	1	AAC96121	16s rRNA gene PCR
c2421	16.4	0.6	25	1	ADB04575	Human MDZ7 scannin
2422	16.4	0.6	25	1	AAC96251	HLA DPB1 gene PCR
c2423	16.4	0.6	25	1	AAC95851	HLA HLA-A gene PCR
2424	16.4	0.6	25	1	AAC96884	HLA HLA-C gene PCR
c2425	16.4	0.6	25	1	AAC95722	HLA DQA1 gene PCR
2426	16.4	0.6	25	1	AAC96511	HLA DQB1 gene PCR
2427	16.4	0.6	25	1	AAC95684	HLA DPB1 gene PCR
c2428	16.4	0.6	25	1	AAC96213	16s rRNA gene PCR
2429	16.4	0.6	25	1	AAC96504	HLA DQB1 gene PCR
2430	16.4	0.6	25	1	AAC96618	HLA DRB345 gene PC
2431	16.4	0.6	25	1	AAC96321	HLA DPB1 gene PCR
2432	16.4	0.6	25	1	AAC95753	HLA DQB1 gene PCR
c2433	16.4	0.6	25	1	AAC95751	HLA DQB1 gene PCR
2434	16.4	0.6	25	1	AAC96028	HLA HLA-C gene PCR
c2435	16.4	0.6	25	1	AAC96424	HLA DQA1 gene PCR
c2436	16.4	0.6	25	1	ABL57069	Molecular beacon o
c2437	16.4	0.6	25	1	ABL57077	Molecular beacon o
c2438	16.4	0.6	25	1	ADE64628	Recombinant blood
2439	16.4	0.6	25	1	ADB04566	Human MDZ7 scannin
c2440	16.4	0.6	25	1	ADB04566	Human MDZ7 scannin
2441	16.4	0.6	25	1	ADB04576	Human MDZ7 scannin
c2442	16.4	0.6	25	1	ADB04576	Human MDZ7 scannin

C2443	16.4	0.6	25	1	ACI83927	Human microarray D	2516	16	0.6	16	1	AAH42481	Oligonucleotide us
C2444	16.4	0.6	25	1	ADA14835	Hairpin oligonucle	C2517	16	0.6	16	1	AAH42481	Oligonucleotide us
C2445	16.4	0.6	25	1	AAD57902	Oligonucleotide us	2518	16	0.6	16	1	ABA02556	HCCS-1 differentia
2446	16.4	0.6	25	1	AAD57848	Oligonucleotide re	2519	16	0.6	16	1	ABK87148	Scarlet runner bea
C2447	16.4	0.6	25	1	AAD57848	Oligonucleotide re	2520	16	0.6	16	1	ABK87148	Mouse E2 cDNA ampl
2448	16.4	0.6	25	1	ACF04465	Real time PCR targ	2521	16	0.6	16	1	ABL57075	Molecular beacon t
C2449	16.4	0.6	26	1	AAT93819	Antitumoural phosp	2522	16	0.6	16	1	ABA97402	Nucleotide sequenc
2450	16.4	0.6	27	1	AAX23568	Deletion sequence	C2523	16	0.6	16	1	ABA97402	Nucleotide sequenc
2451	16.4	0.6	30	1	ABL35101	Phosphorothioate s	2524	16	0.6	16	1	ABK90584	Target cDNA PCR pr
C2452	16.4	0.6	35	1	AAT93816	Antitumoural phosp	2525	16	0.6	16	1	ABK32157	H-T11-G PCR primer
2453	16.2	0.6	18	1	AAX18389	RT-PCR primer of t	2526	16	0.6	16	1	ABK12623	Mouse E4 protein,
C2454	16.2	0.6	18	1	AAX18389	RT-PCR primer of t	2527	16	0.6	16	1	ABK12623	PTTG cDNA isolatin
2455	16.2	0.6	21	1	AAX26249	Human polymorphic	2528	16	0.6	16	1	AAD30090	Rat PTTG1 cDNA amp
2456	16.2	0.6	21	1	AAZ09196	Oligonucleotide 8	2529	16	0.6	16	1	ABZ21814	Anti-cancer drug r
2457	16.2	0.6	21	1	AAZ73804	Human biallelic ma	2530	16	0.6	16	1	ABN87395	PTTG isolation rel
2458	16.2	0.6	21	1	AAA62856	PCR primer used fo	2531	16	0.6	16	1	ABA98029	Human PTTG2 cDNA c
C2459	16.2	0.6	21	1	AAH89080	Human polymorphic	2532	16	0.6	16	1	ACC58340	MMLV-RT PCR; prime
C2460	16.2	0.6	21	1	ABX79739	EST polymorphic DN	2533	16	0.6	16	1	ABX16054	RNA differential d
2461	16.2	0.6	22	1	AAA26585	Human HPC1 mutatio	2534	16	0.6	16	1	ABZ58394	H-T11G anchored ol
C2462	16.2	0.6	22	1	AAC86203	Primer #3 used to	2535	16	0.6	16	1	AAD56451	2'-F-ANA antisense
2463	16.2	0.6	23	1	AAT08689	CRH related G-prot	C2536	16	0.6	16	1	AAD56451	2'-F-ANA antisense
C2464	16.2	0.6	23	1	AAH45458	PCR primer specifi	2537	16	0.6	16	1	AAL54078	Oligo-homodeoxyrib
2465	16.2	0.6	23	1	AAL46192	Human liver cancer	C2538	16	0.6	16	1	AAL54078	Oligo-homodeoxyrib
2466	16.2	0.6	24	1	ABK91269	Leukaemia related	2539	16	0.6	16	1	AAD57845	Target oligonucleo
C2467	16.2	0.6	24	1	ABA98547	Insulin-like growt	2540	16	0.6	16	1	ADB68519	DNA hybridisation
2468	16.2	0.6	24	1	ABV77761	Human DNA-PK inter	C2541	16	0.6	16	1	ADB68519	DNA hybridisation
2469	16.2	0.6	24	1	AAV48089	Oligonucleotide 25	C2542	16	0.6	16	1	AAK69800	Human flt1 VEGF re
C2470	16.2	0.6	24	1	AAL51806	Short chain dehydr	2543	16	0.6	17	1	AAK69801	Human flt1 VEGF re
C2471	16.2	0.6	24	1	AZ07017	Murine alpha-L-idu	2544	16	0.6	17	1	ABK13941	5'-PCR primer used
2472	16.2	0.6	24	1	AAF70467	Human DRD2 exon 5	C2545	16	0.6	17	1	ADB04271	Human MDZ7 scannin
2473	16.2	0.6	24	1	ABS57731	Human zinc finger	2546	16	0.6	17	1	ACF36345	Nucleotide sequenc
C2474	16.2	0.6	24	1	ABS57731	Human zinc finger	2547	16	0.6	17	1	ACF36370	Nucleotide sequenc
C2475	16.2	0.6	24	1	ABV74853	Protein 16.17 PCR	2548	16	0.6	17	1	AAK69799	Human flt1 VEGF re
2476	16.2	0.6	24	1	ABK67211	Human gene specifi	C2549	16	0.6	17	1	AAK69802	Human flt1 VEGF re
C2477	16.2	0.6	24	1	ABQ77631	Human Hsmari prote	C2550	16	0.6	17	1	AAV37934	Primer of the spec
2478	16.2	0.6	24	1	ABL56411	PCR primer F used	2551	16	0.6	17	1	AAV49503	Human eosinophil c
2479	16.2	0.6	24	1	AAK99651	Human alpha 2, 3-s	2552	16	0.6	17	1	AAK18371	RT-PCR primer of t
2480	16.2	0.6	24	1	ABZ21302	DNA binding protei	2553	16	0.6	17	1	AAA30179	PCR primer GT15A u
2481	16.2	0.6	24	1	ABQ77543	Human red blood ce	C2554	16	0.6	17	1	AAA30180	PCR primer GT15C u
C2482	16.2	0.6	24	1	ABQ77543	Human red blood ce	C2555	16	0.6	17	1	AAK82722	Human Iga nephropa
C2483	16.2	0.6	24	1	AAS19218	Kringle protein 14	2556	16	0.6	17	1	AAK82722	Human Iga nephropa
C2484	16.2	0.6	24	1	ABL58652	Human development	2557	16	0.6	17	1	AAZ36739	Anchored oligo (dT)
2485	16.2	0.6	24	1	ABZ25620	Human zinc finger	2558	16	0.6	17	1	AAA25449	Oestrogen receptor
C2486	16.2	0.6	24	1	AAL57131	RT-PCR primer 2 re	C2559	16	0.6	17	1	AAA25449	Oestrogen receptor
C2487	16.2	0.6	24	1	ADC10360	Human NOVX polypep	2560	16	0.6	17	1	AAA25451	Oestrogen receptor
C2488	16.2	0.6	25	1	AAV57477	Cytochrome P450ox	C2561	16	0.6	17	1	AAA25451	Oestrogen receptor
C2489	16.2	0.6	25	1	ABA03917	Human connexin 9 P	2562	16	0.6	17	1	AAC64202	PCR anchor primer,
C2490	16.2	0.6	25	1	AAC96118	16S rRNA gene PCR	C2563	16	0.6	17	1	AAC64203	PCR anchor primer,
2491	16.2	0.6	25	1	AAH38027	SNP specific SNPE	2564	16	0.6	17	1	AAC64181	PCR anchor primer,
2492	16.2	0.6	25	1	AAC95728	HLA DQA1 gene PCR	C2565	16	0.6	17	1	AAC64182	PCR anchor primer,
2493	16.2	0.6	25	1	AAC96429	HLA DQA1 gene PCR	2566	16	0.6	17	1	AAC64171	PCR anchor primer,
C2494	16.2	0.6	25	1	AAC96256	HLA DPA1 gene PCR	C2567	16	0.6	17	1	AAC64172	PCR anchor primer,
2495	16.2	0.6	25	1	AAC96779	HLA HLA-A gene PCR	2568	16	0.6	17	1	AAC64161	PCR anchor primer,
2496	16	0.6	16	1	AAT75139	Arbitrary anchor p	C2569	16	0.6	17	1	AAC64162	PCR anchor primer,
2497	16	0.6	16	1	AAV36965	Rat pituitary-tumo	2570	16	0.6	17	1	AAC64213	PCR anchor primer,
2498	16	0.6	16	1	AAK57361	P. obesus beacon p	C2571	16	0.6	17	1	AAC64214	PCR anchor primer,
2499	16	0.6	16	1	AAK24309	Differential displ	C2572	16	0.6	17	1	AAC64231	PCR anchor primer,
2500	16	0.6	16	1	AAK19462	Human senescence f	2573	16	0.6	17	1	AAC64230	PCR anchor primer,
C2501	16	0.6	16	1	AAK18362	RT-PCR primer of t	2574	16	0.6	17	1	AAC92292	Human pollinosis-a
2502	16	0.6	16	1	AAK07568	Homo sapiens fetal	C2575	16	0.6	17	1	AAC92293	Human pollinosis-a
C2503	16	0.6	16	1	AAK07568	Homo sapiens fetal	2576	16	0.6	17	1	AAS06655	Human cDNA synthes
2504	16	0.6	16	1	AAC66068	DNA chip primer #4	C2577	16	0.6	17	1	AAC91720	PCR anchor primer,
C2505	16	0.6	16	1	AAC66068	DNA chip primer #4	2578	16	0.6	17	1	AAC91719	PCR anchor primer,
2506	16	0.6	16	1	AAC87710	MMLV reverse trans	C2579	16	0.6	17	1	AAC82875	Human pollinosis-a
2507	16	0.6	16	1	AAA94101	Fruit-associated b	2580	16	0.6	17	1	AAC82874	Human pollinosis-a
2508	16	0.6	16	1	ABA04585	Oligonucleotide #5	C2581	16	0.6	17	1	AAH47127	Nucleotide sequenc
C2509	16	0.6	16	1	ABA04585	Oligonucleotide #5	2582	16	0.6	17	1	AAH47126	Nucleotide sequenc
2510	16	0.6	16	1	AAF83580	B. gymnorhiza sal	2583	16	0.6	17	1	ABK49634	Human Acetyltransf
2511	16	0.6	16	1	AAS06651	Human cDNA synthes	C2584	16	0.6	17	1	ABK49635	Human Acetyltransf
2512	16	0.6	16	1	AAF30895	Oligonucleotide-mi	2585	16	0.6	17	1	ABL59038	Nucleotide sequenc
C2513	16	0.6	16	1	AAF30895	Oligonucleotide-mi	C2586	16	0.6	17	1	ABL59039	Nucleotide sequenc
2514	16	0.6	16	1	AAF30880	Oligonucleotide po	2587	16	0.6	17	1	ABN99829	Human allergic dis
C2515	16	0.6	16	1	AAF30880	Oligonucleotide po	C2588	16	0.6	17	1	ABN99830	Human allergic dis

2589	16	0.6	17	1	16	2662	16	0.6	24	1	1	ABQ79142	Primer #2 related
c2590	16	0.6	17	1	16	2663	16	0.6	24	1	1	AAQ43999	HIV-1 LTR region a
2591	16	0.6	17	1	16	c2664	16	0.6	24	1	1	AAAX26962	PCR primer used to
c2592	16	0.6	17	1	16	2665	16	0.6	24	1	1	AAZ49466	Gene specific sens
c2593	16	0.6	17	1	16	c2666	16	0.6	24	1	1	AAAC70288	Single nucleotide
2594	16	0.6	17	1	16	c2667	16	0.6	24	1	1	AAAC67230	Fibrosis modulator
c2595	16	0.6	17	1	16	2668	16	0.6	24	1	1	AAH44680	Human Kazal type i
2596	16	0.6	17	1	16	c2669	16	0.6	24	1	1	AAF30562	Human Factor V gen
2597	16	0.6	17	1	16	2670	16	0.6	24	1	1	AAAL47095	Human proliferatin
c2598	16	0.6	17	1	16	2671	16	0.6	24	1	1	ABV74361	Signalase 10.01 PC
2599	16	0.6	17	1	16	c2672	16	0.6	24	1	1	ABV74361	Signalase 10.01 PC
2600	16	0.6	17	1	16	2673	16	0.6	24	1	1	ABL56688	PCR primer #2 for
c2601	16	0.6	17	1	16	2674	16	0.6	24	1	1	AAD26271	Human caspase-12 c
c2602	16	0.6	17	1	16	2675	16	0.6	24	1	1	AAD33504	T7T18Apad_PS23-24-
2603	16	0.6	17	1	16	c2676	16	0.6	24	1	1	AAD33504	T7T18Apad_PS23-24-
c2604	16	0.6	17	1	16	2677	16	0.6	24	1	1	ABN86391	Basophilic nucleop
2605	16	0.6	18	1	16	c2678	16	0.6	24	1	1	ABZ57032	Human kinesin ligh
2606	16	0.6	18	1	16	c2679	16	0.6	24	1	1	ABZ23085	Human GPCR 10823 P
2607	16	0.6	18	1	16	2680	16	0.6	24	1	1	ACD27468	Human LTBP 1 bindi
c2608	16	0.6	18	1	16	2681	16	0.6	24	1	1	ADE86193	Ret gene chair qua
2609	16	0.6	18	1	16	c2682	16	0.6	25	1	1	AAC95686	HLA DPB1 gene PCR
2610	16	0.6	18	1	16	c2683	16	0.6	25	1	1	AAC96367	HLA DPB1 gene PCR
c2611	16	0.6	18	1	16	2684	16	0.6	25	1	1	ABK87632	BamT15C PCR primer
2612	16	0.6	18	1	16	c2685	16	0.6	25	1	1	AAC96038	16s rRNA gene PCR
c2613	16	0.6	18	1	16	c2686	16	0.6	25	1	1	AAC96204	16s rRNA gene PCR
c2614	16	0.6	18	1	16	2687	16	0.6	25	1	1	AAC95828	HLA HLA-A gene PCR
2615	16	0.6	18	1	16	2688	16	0.6	25	1	1	AAH39959	SNP specific SNPE
c2616	16	0.6	18	1	16	c2689	16	0.6	25	1	1	AAC96753	HLA HLA-A gene PCR
2617	16	0.6	18	1	16	c2690	16	0.6	25	1	1	AAC96423	HLA HLA-A gene PCR
c2618	16	0.6	18	1	16	2691	16	0.6	25	1	1	AAC95851	HLA HLA-A gene PCR
2619	16	0.6	18	1	16	c2692	16	0.6	25	1	1	AAC96884	HLA HLA-C gene PCR
c2620	16	0.6	18	1	16	2693	16	0.6	25	1	1	AAC96213	16s rRNA gene PCR
2621	16	0.6	18	1	16	c2694	16	0.6	25	1	1	AAC96028	HLA HLA-C gene PCR
c2622	16	0.6	18	1	16	c2695	16	0.6	26	1	1	AAA62140	HLA HLA-C gene PCR
2623	16	0.6	18	1	16	c2696	16	0.6	26	1	1	AZ225387	A. auricalliformis
c2624	16	0.6	18	1	16	2697	16	0.6	27	1	1	AAZ23572	Infectious pancrea
c2625	16	0.6	18	1	16	2698	16	0.6	27	1	1	AAZ49491	Deletion sequence
2626	16	0.6	18	1	16	2699	16	0.6	28	1	1	AAZ33514	Oligonucleotide #2
c2627	16	0.6	18	1	16	2700	16	0.6	29	1	1	AAZ33516	T7T18Apad_PS19-28-
2628	16	0.6	20	1	16	c2701	16	0.6	34	1	1	ADC65905	T7T18Apad_PS18-29-
c2629	16	0.6	20	1	16	2702	15.8	0.6	19	1	1	ADE27346	DNA oligonucleotid
c2630	16	0.6	20	1	16	c2703	15.8	0.6	19	1	1	ADE27636	Stearoyl-CoA desat
2631	16	0.6	20	1	16	c2704	15.8	0.6	20	1	1	AAZ05713	Stearoyl-CoA desat
c2632	16	0.6	20	1	16	c2705	15.8	0.6	20	1	1	AAF83959	Polypyrimidine Cri
c2633	16	0.6	20	1	16	c2706	15.8	0.6	20	1	1	ABZ88564	BAP28 gene fragmen
2634	16	0.6	20	1	16	2707	15.8	0.6	20	1	1	ABZ85535	Human oligonucleot
c2635	16	0.6	20	1	16	c2708	15.8	0.6	20	1	1	AAQ37797	Human oligonucleot
c2636	16	0.6	20	1	16	c2709	15.8	0.6	20	1	1	AAQ48269	Antisense oligonuc
2637	16	0.6	20	1	16	c2710	15.8	0.6	20	1	1	AAQ68872	Glucocerebrosidase
c2638	16	0.6	20	1	16	c2711	15.8	0.6	20	1	1	AAQ44565	Oligonucleotide (S
c2639	16	0.6	20	1	16	c2712	15.8	0.6	20	1	1	AAAT44565	Antisense oligo OL
c2640	16	0.6	20	1	16	c2713	15.8	0.6	20	1	1	AAAT93630	Human p53 oncogene
c2641	16	0.6	21	1	16	2714	15.8	0.6	20	1	1	AAAT88465	Phosphorothioate l
2642	16	0.6	21	1	16	c2715	15.8	0.6	20	1	1	AAV47686	Unmethylated CpG d
c2643	16	0.6	21	1	16	2716	15.8	0.6	20	1	1	AAV18923	Phosphorothioate o
2644	16	0.6	21	1	16	2717	15.8	0.6	20	1	1	AAV22438	Antisense oligonuc
c2645	16	0.6	21	1	16	c2718	15.8	0.6	20	1	1	AAV74243	Human p53 antisens
2646	16	0.6	22	1	16	c2719	15.8	0.6	20	1	1	AAAX27854	Antisense oligonuc
c2647	16	0.6	22	1	16	2720	15.8	0.6	20	1	1	AAA39400	Human biallelic ma
c2648	16	0.6	23	1	16	c2721	15.8	0.6	20	1	1	AAZ77398	Antisense IGFBP-5
c2649	16	0.6	23	1	16	2722	15.8	0.6	20	1	1	AAA91253	Human cDNA clone-s
c2650	16	0.6	23	1	16	2723	15.8	0.6	20	1	1	AAK95078	Human cDNA clone-s
c2651	16	0.6	23	1	16	2724	15.8	0.6	20	1	1	AAAF99116	Immunostimulatory
c2652	16	0.6	23	1	16	2725	15.8	0.6	20	1	1	AAH91454	Human inflammatory
c2653	16	0.6	23	1	16	c2726	15.8	0.6	20	1	1	AAH44608	20-mer p53 phospho
c2654	16	0.6	23	1	16	c2727	15.8	0.6	20	1	1	ABK90841	p53 antisense olig
2655	16	0.6	23	1	16	c2728	15.8	0.6	20	1	1	ABN84654	p53 antisense olig
c2656	16	0.6	23	1	16	c2729	15.8	0.6	20	1	1	ABN84654	Angiogenesis inhib
c2657	16	0.6	23	1	16	2730	15.8	0.6	20	1	1	ABT07490	Rat protein phosph
c2658	16	0.6	24	1	16	c2731	15.8	0.6	20	1	1	ABL39008	Immunostimulatory
c2659	16	0.6	24	1	16	2732	15.8	0.6	20	1	1	ABL39008	Humulus lupulus fa
c2660	16	0.6	24	1	16	c2733	15.8	0.6	20	1	1	ABL42562	Tumour suppression
c2661	16	0.6	24	1	16	c2734	15.8	0.6	20	1	1	ABQ96037	

c2735	15.8	0.6	20	1	ABA97643	probe n. Unidenti
c2736	15.8	0.6	20	1	ABZ91981	Human oligonucleot
2737	15.8	0.6	20	1	ABZ85436	Human oligonucleot
2738	15.8	0.6	20	1	ABZ85668	Human oligonucleot
2739	15.8	0.6	20	1	ABZ92287	Human oligonucleot
c2740	15.8	0.6	20	1	ABZ89545	Human oligonucleot
c2741	15.8	0.6	20	1	ABZ22859	Clonal T cell rece
2742	15.8	0.6	20	1	ACD99549	Immunostimulatory
c2743	15.8	0.6	20	1	ADA24235	Human p53 oncogene
2744	15.8	0.6	20	1	ADB36618	Immunostimulatory
2745	15.8	0.6	21	1	ABS97317	Aryl hydrocarbon n
c2745	15.8	0.6	21	1	AAT80586	Anti-p53 phosphoro
c2747	15.8	0.6	21	1	AAV67330	Nucleotide fragmen
c2748	15.8	0.6	21	1	AAZ18450	Polymorphic fragme
c2749	15.8	0.6	21	1	AAZ58827	Human MUC12 gene s
2750	15.8	0.6	21	1	AAZ44349	Protein kinase inh
2751	15.8	0.6	21	1	AAF95374	Human gene single
2752	15.8	0.6	21	1	AAH91825	Human inflammatory
c2753	15.8	0.6	21	1	AAF75035	Primer #7. Homo s
c2754	15.8	0.6	21	1	ABK99279	Hepatitis C virus
2755	15.8	0.6	21	1	ABS98381	Human multidrug re
2756	15.8	0.6	21	1	ABS66998	Human MRP-1 polymo
c2757	15.8	0.6	21	1	ABS66997	Human MRP-1 polymo
c2758	15.8	0.6	22	1	AAF98936	Immunostimulatory
c2759	15.8	0.6	22	1	ABS77577	Angiogenesis inhib
c2760	15.8	0.6	22	1	ACD99369	Immunostimulatory
c2761	15.8	0.6	22	1	ADB36438	Immunostimulatory
c2762	15.8	0.6	22	1	ABV74140	Oligonucleotide us
2763	15.8	0.6	22	1	AAA66932	Dog genomic marker
2764	15.8	0.6	22	1	ABL35690	Immunostimulatory
2765	15.8	0.6	23	1	ABV74138	5' End of cDNA lib
c2766	15.8	0.6	23	1	ABV74139	Oligonucleotide us
2767	15.8	0.6	23	1	AAT60786	Subtelomeric prime
c2768	15.8	0.6	23	1	AAT60790	Subtelomeric prime
c2769	15.8	0.6	23	1	AAV62118	Telomere length an
2770	15.8	0.6	23	1	AAV62114	Telomere length an
2771	15.8	0.6	23	1	AAF60331	Human liver RNA re
2772	15.8	0.6	23	1	ABQ81205	Human endostatin c
c2773	15.8	0.6	23	1	ABT16546	Ethylene insensiti
c2774	15.8	0.6	24	1	AAF98935	Immunostimulatory
c2775	15.8	0.6	24	1	ABS77576	Angiogenesis inhib
c2776	15.8	0.6	24	1	ACD99368	Immunostimulatory
c2777	15.8	0.6	24	1	ADB36437	Immunostimulatory
2778	15.8	0.6	24	1	ABV74853	Protein 16.17 PCR
c2779	15.8	0.6	24	1	AAZ75929	Human interleukin
2780	15.8	0.6	24	1	AAZ24999	Sense probe to Fra
c2781	15.8	0.6	24	1	AAZ24998	Antisense probe to
c2782	15.8	0.6	24	1	AAZ95163	Forward primer #9
2783	15.8	0.6	24	1	AAC96274	HLA DPB1 gene PCR
2784	15.8	0.6	24	1	AAC61624	Reporter probe for
2785	15.8	0.6	24	1	ABA04964	Human FD14 PCR pri
c2786	15.8	0.6	24	1	AAD46030	Human UGT2B7 DNA s
c2787	15.8	0.6	24	1	ABK53197	Bacillus subtilis
c2788	15.8	0.6	24	1	ABL60935	Human nucleotide r
2789	15.8	0.6	24	1	ABQ76045	Human actin simila
c2790	15.8	0.6	24	1	ABQ76045	Human actin simila
2791	15.8	0.6	25	1	ABL45245	Human chromosome 1
c2792	15.8	0.6	25	1	AAC96268	HLA DPB1 gene PCR
c2793	15.8	0.6	25	1	AAH38199	SNP specific SNPE
c2794	15.8	0.6	25	1	AAC95727	HLA DQA1 gene PCR
c2795	15.8	0.6	25	1	AAC96129	16s rRNA gene PCR
c2796	15.8	0.6	25	1	AAQ98161	Hind III primer/ad
c2797	15.8	0.6	25	1	AAC96249	HLA DPB1 gene PCR
c2798	15.8	0.6	25	1	AAC95664	HLA DQA1 gene PCR
2799	15.8	0.6	25	1	AAC96421	HLA DQA1 gene PCR
2800	15.8	0.6	25	1	AAC95706	HLA DQA1 gene PCR
2801	15.8	0.6	25	1	AAC96550	HLA DRB345 gene PC
c2802	15.8	0.6	26	1	AAQ47178	MHC DR A intron bi
2803	15.8	0.6	27	1	AAF74933	CD40L poly-A tract
c2804	15.8	0.6	29	1	AAQ85070	Oligonucleotide cl
c2805	15.8	0.6	29	1	AAQ83933	Oligonucleotide cl
c2806	15.8	0.6	34	1	AAV12929	Oligonucleotide SE
c2807	15.8	0.6	34	1	AAV59243	Small synthetic DN

c2808	15.6	0.6	17	1	AAV19118	Anchored oligo(T)
2809	15.6	0.6	17	1	AAZ89372	RNA detecting prim
c2810	15.6	0.6	17	1	AAZ89372	RNA detecting prim
2811	15.6	0.6	22	1	AAI19021	Caltravirus PCR pri
c2812	15.6	0.6	22	1	AAI67259	B533S forward prim
2813	15.6	0.6	22	1	AAF55172	Probe used to iden
c2814	15.6	0.6	22	1	AAS21990	Human COL1A1 PCR p
2815	15.6	0.6	22	1	ADA45284	Human MLH1 gene PC
c2816	15.6	0.6	22	1	ADD21919	Protein translatio
2817	15.6	0.6	23	1	AAT28017	Primer (B5LFr4) fo
c2818	15.6	0.6	23	1	AAT76235	Human IL6 antisens
c2819	15.6	0.6	23	1	AAZ54065	Human IL-6 antisen
c2820	15.6	0.6	23	1	AAZ81611	PCR primer used to
c2821	15.6	0.6	23	1	AAAF19631	Low adenosine anti
c2822	15.6	0.6	23	1	AAAF19631	Human IL6 polynucl
c2823	15.6	0.6	23	1	ABZ95325	Human IL-6 antisen
2824	15.6	0.6	24	1	AAA94317	RNA-protein fusion
2825	15.6	0.6	24	1	ABQ77631	Human Hsmar1 prote
2826	15.6	0.6	24	1	ABL58652	Human development
2827	15.6	0.6	24	1	AAT39969	Minimal motif codi
c2828	15.6	0.6	24	1	AAD12863	Human CASB765 cDNA
2829	15.6	0.6	24	1	AAC91733	Human pollinosis-a
2830	15.6	0.6	24	1	AAC91993	T-box binding site
2831	15.6	0.6	24	1	ABL40063	DNA-cysteine methy
2832	15.6	0.6	24	1	ABK13945	RT-PCR primer #2 f
c2833	15.6	0.6	24	1	ABQ78172	Plant related PCR
2834	15.6	0.6	24	1	AAD35583	Human hscd5 cDNA a
2835	15.6	0.6	24	1	ABV74368	Ubiquitin specific
2836	15.6	0.6	24	1	AAD38971	Human GDD DNA ampl
2837	15.6	0.6	24	1	ABS62457	Analyte sorting ta
2838	15.6	0.6	24	1	ABS61625	Capture oligonucle
2839	15.6	0.6	24	1	ABI89287	Capture oligonucle
c2840	15.6	0.6	24	1	ABA97546	Cancer cell discr
2841	15.6	0.6	24	1	ABS55785	Human Sailor trans
2842	15.6	0.6	24	1	ABV93379	Bacillus thuringie
2843	15.6	0.6	24	1	ABV93349	B. thuringiensis t
2844	15.6	0.6	25	1	AAC96427	HLA DQA1 gene PCR
2845	15.6	0.6	25	1	AAC95726	HLA DQA1 gene PCR
2846	15.6	0.6	25	1	AAC96039	16s rRNA gene PCR
c2847	15.6	0.6	25	1	AAC96245	HLA DPB1 gene PCR
2848	15.6	0.6	25	1	AAC96245	Oligonucleotide #1
2849	15.6	0.6	26	1	AAZ59153	SNP specific upper
2850	15.6	0.6	26	1	AAH40741	RT-PCR primer of t
c2851	15.4	0.5	17	1	AAZ18370	RT-PCR primer of t
c2852	15.4	0.5	17	1	AAZ18371	Human MDZ7 scannin
c2853	15.4	0.5	17	1	ADB04270	Human flt1 VEGF re
2854	15.4	0.5	17	1	AAZ69798	Human flt1 VEGF re
c2855	15.4	0.5	17	1	AAZ69804	Human flt1 VEGF re
c2856	15.4	0.5	17	1	AAZ69796	Human flt1 VEGF re
2857	15.4	0.5	17	1	AAZ69797	Human flt1 VEGF re
2858	15.4	0.5	17	1	AAZ25453	Oestrogen receptor
2859	15.4	0.5	17	1	AAA25452	Oestrogen receptor
2860	15.4	0.5	17	1	AAA25452	DNA-RNA-DNA oligon
c2861	15.4	0.5	17	1	ABA91530	DNA-RNA-DNA oligon
2862	15.4	0.5	17	1	ABA91530	Oligo-AT PCR prime
c2863	15.4	0.5	17	1	ABA91530	Oligo-AT PCR prime
c2864	15.4	0.5	17	1	AAD44151	Tumour suppression
c2865	15.4	0.5	17	1	AAD44151	Tumour suppression
2866	15.4	0.5	17	1	ABT38816	Tumour suppression
2867	15.4	0.5	17	1	ABT34888	Human MDZ7 scannin
2868	15.4	0.5	17	1	ADB04269	Human MDZ7 scannin
c2869	15.4	0.5	17	1	ADB04269	Human MDZ7 scannin
c2870	15.4	0.5	17	1	ADB04273	Human MDZ7 scannin
c2871	15.4	0.5	17	1	ADB04273	Tumour suppression
2872	15.4	0.5	17	1	ADB43022	Tumour suppression
c2873	15.4	0.5	18	1	AAV54164	Nucleotide sequenc
2874	15.4	0.5	18	1	AAV54166	Nucleotide sequenc
2875	15.4	0.5	18	1	AAZ90648	Human adipose tiss
c2876	15.4	0.5	18	1	AAZ90646	Human adipose tiss
2877	15.4	0.5	18	1	AAQ20109	Cross-linking olig
2878	15.4	0.5	18	1	AAQ20108	Cross-linking olig
c2879	15.4	0.5	18	1	AAQ30446	Oligomer TNFR941 f
2880	15.4	0.5	18	1	AAQ25501	Purine rich HUMNFR

1	AAV19118	Anchored oligo(T)
1	AAZ89372	RNA detecting prim
1	AAZ89372	RNA detecting prim
1	AAI19021	Caltravirus PCR pri
1	AAI67259	B533S forward prim
1	AAF55172	Probe used to iden
1	AAS21990	Human COL1A1 PCR p
1	ADA45284	Human MLH1 gene PC
1	ADD21919	Protein translatio
1	AAT28017	Primer (B5LFr4) fo
1	AAT76235	Human IL6 antisens
1	AAZ54065	Human IL-6 antisen
1	AAZ81611	PCR primer used to
1	AAAF19631	Low adenosine anti
1	AAAF19631	Human IL6 polynucl
1	ABZ95325	Human IL-6 antisen
1	AAA94317	RNA-protein fusion
1	ABQ77631	Human Hsmar1 prote
1	ABL58652	Human development
1	AAT39969	Minimal motif codi
1	AAD12863	Human CASB765 cDNA
1	AAC91733	Human pollinosis-a
1	AAC91993	T-box binding site
1	ABL40063	DNA-cysteine methy
1	ABK13945	RT-PCR primer #2 f
1	ABQ78172	Plant related PCR
1	AAD35583	Human hscd5 cDNA a
1	ABV74368	Ubiquitin specific
1	AAD38971	Human GDD DNA ampl
1	ABS62457	Analyte sorting ta
1	ABS61625	Capture oligonucle
1	ABI89287	Capture oligonucle
1	ABA97546	Cancer cell discr
1	ABS55785	Human Sailor trans
1	ABV93379	Bacillus thuringie
1	ABV93349	B. thuringiensis t
1	AAC96427	HLA DQA1 gene PCR
1	AAC95726	HLA DQA1 gene PCR
1	AAC96039	16s rRNA gene PCR
1	AAC96245	HLA DPB1 gene PCR
1	AAC96245	Oligonucleotide #1
1	AAZ59153	SNP specific upper
1	AAH40741	RT-PCR primer of t
1	AAZ18370	RT-PCR primer of t
1	AAZ18371	Human MDZ7 scannin
1	ADB04270	Human flt1 VEGF re
1	AAZ69798	Human flt1 VEGF re
1	AAZ69804	Human flt1 VEGF re
1	AAZ69796	Human flt1 VEGF re
1	AAZ69797	Human flt1 VEGF re
1	AAZ25453	Oestrogen receptor
1	AAA25452	Oestrogen receptor
1	AAA25452	DNA-RNA-DNA oligon
1	ABA91530	DNA-RNA-DNA oligon
1	ABA91530	Oligo-AT PCR prime
1	AAD44151	Oligo-AT PCR prime
1	AAD44151	Tumour suppression
1	ABT38816	Tumour suppression
1	ABT34888	Human MDZ7 scannin
1	ADB04269	Human MDZ7 scannin
1	ADB04269	Human MDZ7 scannin
1	ADB04273	Human MDZ7 scannin
1	ADB04273	Tumour suppression
1	ADB43022	Tumour suppression
1	AAV54164	Nucleotide sequenc
1	AAV54166	Nucleotide sequenc
1	AAZ90648	Human adipose tiss
1	AAZ90646	Human adipose tiss
1	AAQ20109	Cross-linking olig
1	AAQ20108	Cross-linking olig
1	AAQ30446	Oligomer TNFR941 f
1	AAQ25501	Purine rich HUMNFR

2881	15.4	0.5	18	1	AAQ30448	Oligomer TNFR943 f
2882	15.4	0.5	18	1	AAQ30447	Oligomer TNFR942 f
2883	15.4	0.5	18	1	AAV54173	Nucleotide sequenc
2884	15.4	0.5	18	1	AAV54169	Nucleotide sequenc
2885	15.4	0.5	18	1	AAV54167	Nucleotide sequenc
2886	15.4	0.5	18	1	AAZ90649	Human adipose tiss
2887	15.4	0.5	18	1	AAZ90645	Human adipose tiss
2888	15.4	0.5	18	1	AAZ90643	Human adipose tiss
2889	15.4	0.5	18	1	AAV54168	Nucleotide sequenc
2890	15.4	0.5	18	1	AAV54168	Nucleotide sequenc
2891	15.4	0.5	18	1	AAV54174	Nucleotide sequenc
2892	15.4	0.5	18	1	AAV54165	Nucleotide sequenc
2893	15.4	0.5	18	1	AAV54165	Nucleotide sequenc
2894	15.4	0.5	18	1	AAV16014	PCR primer G-R use
2895	15.4	0.5	18	1	AAZ90644	Human adipose tiss
2896	15.4	0.5	18	1	AAZ90644	Human adipose tiss
2897	15.4	0.5	18	1	AAZ90644	Human adipose tiss
2898	15.4	0.5	18	1	AAZ90650	Human adipose tiss
2899	15.4	0.5	18	1	AAZ90647	Human adipose tiss
2900	15.4	0.5	18	1	AAZ90647	Human adipose tiss
2901	15.4	0.5	18	1	AAZ43273	Murine Sox3 gene P
2902	15.4	0.5	18	1	AAAO5258	PCR primer G-R use
2903	15.4	0.5	18	1	AAAF5305	Human mGluR1alpha
2904	15.4	0.5	18	1	ACF36862	Human lactoferrin
2905	15.4	0.5	18	1	ADA27361	Human microsatelli
2906	15.4	0.5	18	1	ADD20088	Oreochromis niloti
2907	15.4	0.5	19	1	AAV44628	Human uncoupling p
2908	15.4	0.5	20	1	ABZ85436	Human oligonucleot
2909	15.4	0.5	20	1	AAT73291	Primer 1 for pUC19
2910	15.4	0.5	20	1	AAT73292	Primer 2 for pUC19
2911	15.4	0.5	20	1	AAT76100	Human histidine de
2912	15.4	0.5	20	1	AAV44626	Human uncoupling p
2913	15.4	0.5	20	1	AAAX53905	Histidine decarbox
2914	15.4	0.5	20	1	AAA33348	Low adenosine anti
2915	15.4	0.5	20	1	AAF19470	Human histidine de
2916	15.4	0.5	20	1	AAF99302	Immunostimulatory
2917	15.4	0.5	20	1	AAL40102	Pathogenic microor
2918	15.4	0.5	20	1	ABS77947	Angiogenesis inhib
2919	15.4	0.5	20	1	ABL39308	Immunostimulatory
2920	15.4	0.5	20	1	ABK99977	Human CADPKL DNA P
2921	15.4	0.5	20	1	ABA05915	Hepatitis B virus
2922	15.4	0.5	20	1	ABI94179	Capture oligonucle
2923	15.4	0.5	20	1	ABT23594	Stabilising reagen
2924	15.4	0.5	20	1	ABZ89676	Human oligonucleot
2925	15.4	0.5	20	1	ABZ89676	Human oligonucleot
2926	15.4	0.5	20	1	ABZ89720	Human oligonucleot
2927	15.4	0.5	20	1	ABZ89440	Human oligonucleot
2928	15.4	0.5	20	1	ABZ89119	Human oligonucleot
2929	15.4	0.5	20	1	ABZ95164	Human histidine de
2930	15.4	0.5	20	1	ABZ90648	Human oligonucleot
2931	15.4	0.5	20	1	ACC47638	Human IGFBP5 phosp
2932	15.4	0.5	20	1	ACD99727	Immunostimulatory
2933	15.4	0.5	20	1	ADB36804	Immunostimulatory
2934	15.4	0.5	21	1	ABK99283	Hepatitis C virus
2935	15.4	0.5	21	1	AAQ71626	Primer to amplify
2936	15.4	0.5	21	1	AAZ26573	Human polymorphic
2937	15.4	0.5	21	1	AAZ26500	Human polymorphic
2938	15.4	0.5	21	1	AAZ57386	Human polymorphic
2939	15.4	0.5	21	1	AAZ57386	Factor VII mutagen
2940	15.4	0.5	21	1	AAC80381	Oligonucleotide pr
2941	15.4	0.5	21	1	AAF57100	Forward primer #15
2942	15.4	0.5	21	1	ABS97681	Human Factor VII m
2943	15.4	0.5	21	1	ABS97669	Histamine N-methyl
2944	15.4	0.5	21	1	ABT06086	Histamine N-methyl
2945	15.4	0.5	21	1	ABT23595	Human IGM heavy ch
2946	15.4	0.5	22	1	ABT28050	Stabilising reagen
2947	15.4	0.5	22	1	AAT28051	3'-primer G for hu
2948	15.4	0.5	22	1	AAT28051	3'-primer H for hu
2949	15.4	0.5	22	1	AAT58492	3'-primer J for hu
2950	15.4	0.5	22	1	AAT58490	First primer #9 fo
2951	15.4	0.5	22	1	AAT58491	First primer #7 fo
2952	15.4	0.5	22	1	AAZ47348	First primer #8 fo
2953	15.4	0.5	22	1	AAZ47349	PCR primer G used
						PCR primer H used

2954	15.4	0.5	22	1	AAZ47350	PCR primer I used
2955	15.4	0.5	22	1	AAA90070	Bovine lysosomal t
2956	15.4	0.5	22	1	AAA88330	Bovine lysosomal t
2957	15.4	0.5	22	1	AAC80382	Forward primer #15
2958	15.4	0.5	22	1	AAH22191	Human hepatocyte a
2959	15.4	0.5	22	1	AAH22192	Human hepatocyte a
2960	15.4	0.5	22	1	AAH22193	Human hepatocyte a
2961	15.4	0.5	22	1	ADC10242	Human NOVX polypep
2962	15.4	0.5	23	1	AAC80383	Forward primer #15
2963	15.4	0.5	23	1	ABL51554	Human NSAID regula
2964	15.4	0.5	23	1	ADC66134	Human CFTR exon 21
2965	15.4	0.5	24	1	ABL57074	Molecular beacon o
2966	15.4	0.5	24	1	ADC51227	Brassica defensin
2967	15.4	0.5	24	1	AAH44680	Human Kazal type i
2968	15.4	0.5	24	1	AAZ95163	Forward primer #9
2969	15.4	0.5	24	1	AAD46030	Human UGT2B7 DNA s
2970	15.4	0.5	25	1	AAC96418	HLA DQA1 gene PCR
2971	15.4	0.5	25	1	AAC96237	16s rRNA gene PCR
2972	15.4	0.5	25	1	AAC96175	16s rRNA gene PCR
2973	15.4	0.5	25	1	AAC96624	HLA HLA-A gene PCR
2974	15.4	0.5	25	1	AAC95821	HLA HLA-A gene PCR
2975	15.4	0.5	25	1	AAC95722	HLA DQA1 gene PCR
2976	15.4	0.5	25	1	AAC96424	HLA DQA1 gene PCR
2977	15.4	0.5	25	1	ABL57069	Molecular beacon o
2978	15.4	0.5	25	1	ABL57077	Molecular beacon o
2979	15.4	0.5	25	1	ADA14835	Hairpin oligonucle
2980	15.4	0.5	25	1	AAD57902	Oligonucleotide us
2981	15.4	0.5	29	1	AAH28298	3' untranslated re
2982	15.4	0.5	29	1	ADA26182	Rice semi-dwarf (s
2983	15.4	0.5	33	1	AAV06769	Oligonucleotide co
2984	15.2	0.5	16	1	AAF82119	Human TSA7005 gene
2985	15.2	0.5	16	1	AAF82119	Human TSA7005 gene
2986	15.2	0.5	16	1	AAH27758	Primer used in hum
2987	15.2	0.5	16	1	AAH27758	Primer used in hum
2988	15.2	0.5	16	1	AAD44145	Oligo-dT PCR prime
2989	15.2	0.5	17	1	AAH18388	RT-PCR primer of t
2990	15.2	0.5	17	1	AAH18388	RT-PCR primer of t
2991	15.2	0.5	17	1	AAS06666	Human differential
2992	15.2	0.5	17	1	AAS14174	Modified Poly-T Pr
2993	15.2	0.5	17	1	AAS14174	Modified Poly-T Pr
2994	15.2	0.5	20	1	ABA05917	Hepatitis B virus
2995	15.2	0.5	20	1	ABZ88879	Human oligonucleot
2996	15.2	0.5	20	1	AAC82913	Human beta-actin d
2997	15.2	0.5	20	1	AAQ95389	Primer A (Group 2,
2998	15.2	0.5	20	1	AAT10129	Sequence #1 used i
2999	15.2	0.5	20	1	AAT50899	Probe #13 for inte
3000	15.2	0.5	20	1	AAT91100	Bovine lysosomal a
3001	15.2	0.5	20	1	AAV47995	Human B7-1 targett
3002	15.2	0.5	20	1	AAZ37559	Human mdm2 phospho
3003	15.2	0.5	20	1	AAZ36657	PCR primer for mar
3004	15.2	0.5	20	1	AAZ06095	PCR primer used to
3005	15.2	0.5	20	1	AAZ04917	PCR primer used to
3006	15.2	0.5	20	1	AAX96826	PCR primer used to
3007	15.2	0.5	20	1	AAF32837	Human B7-1 mRNA an
3008	15.2	0.5	20	1	AAF32944	Human B7-1 antisen
3009	15.2	0.5	20	1	AAF80713	Human mdm2 phospho
3010	15.2	0.5	20	1	AAC84794	Human TLR4 gene ex
3011	15.2	0.5	20	1	AAC82910	Human beta-actin d
3012	15.2	0.5	20	1	AAC82909	Human beta-actin d
3013	15.2	0.5	20	1	AAC82914	Human beta-actin d
3014	15.2	0.5	20	1	AAF99949	Synthetic oligonuc
3015	15.2	0.5	20	1	AAS29328	Human mdm2 antisen
3016	15.2	0.5	20	1	AAH80594	Oligonucleotide hy
3017	15.2	0.5	20	1	ABA91532	DNA oligonucleotid
3018	15.2	0.5	20	1	ABA91537	DNA oligonucleotid
3019	15.2	0.5	20	1	ABA91534	DNA oligonucleotid
3020	15.2	0.5	20	1	ABA02210	Human/mouse C/EBP
3021	15.2	0.5	20	1	ABL45622	Human chromosome 2
3022	15.2	0.5	20	1	ABL94262	Human C/EBP beta p
3023	15.2	0.5	20	1	ABX04655	Human endogenous r
3024	15.2	0.5	20	1	ABZ85316	Human oligonucleot
3025	15.2	0.5	20	1	ABZ90374	Human oligonucleot
3026	15.2	0.5	20	1	ABZ85667	Human oligonucleot

PCR primer I used
Bovine lysosomal t
Bovine lysosomal t
Forward primer #15
Human hepatocyte a
Human hepatocyte a
Human hepatocyte a
Human NOVX polypep
Forward primer #15
Human NSAID regula
Human CFTR exon 21
Molecular beacon o
Brassica defensin
Human Kazal type i
Forward primer #9
Human UGT2B7 DNA s
HLA DQA1 gene PCR
16s rRNA gene PCR
16s rRNA gene PCR
HLA HLA-A gene PCR
HLA HLA-A gene PCR
HLA DQA1 gene PCR
HLA DQA1 gene PCR
Molecular beacon o
Molecular beacon o
Hairpin oligonucle
Oligonucleotide us
3' untranslated re
Rice semi-dwarf (s
Oligonucleotide co
Human TSA7005 gene
Human TSA7005 gene
Primer used in hum
Primer used in hum
Oligo-dT PCR prime
RT-PCR primer of t
RT-PCR primer of t
Human differential
Modified Poly-T Pr
Modified Poly-T Pr
Hepatitis B virus
Human oligonucleot
Human beta-actin d
Primer A (Group 2,
Sequence #1 used i
Probe #13 for inte
Bovine lysosomal a
Human B7-1 targett
Human mdm2 phospho
PCR primer for mar
PCR primer used to
PCR primer used to
PCR primer used to
Human B7-1 mRNA an
Human B7-1 antisen
Human mdm2 phospho
Human TLR4 gene ex
Human beta-actin d
Human beta-actin d
Human beta-actin d
Synthetic oligonuc
Human mdm2 antisen
Oligonucleotide hy
DNA oligonucleotid
DNA oligonucleotid
DNA oligonucleotid
Human/mouse C/EBP
Human chromosome 2
Human C/EBP beta p
Human endogenous r
Human oligonucleot
Human oligonucleot
Human oligonucleot

3027	15.2	0.5	20	1	ABZ85670	Human oligonucleot	c3100	15.2	0.5	26	1	AAx89364	Chromosomal bindin
3028	15.2	0.5	20	1	ABZ88438	Human oligonucleot	c3101	15.2	0.5	26	1	ABS54659	Human p53 protein
3029	15.2	0.5	20	1	ABZ90373	Human oligonucleot	3102	15	0.5	15	1	AAQ79185	Nuclease resistant
3030	15.2	0.5	20	1	ABZ91225	Human oligonucleot	c3103	15	0.5	15	1	AAQ79185	Nuclease resistant
3031	15.2	0.5	20	1	ABX12581	Human cytochrome P	3104	15	0.5	15	1	AAQ79184	Nuclease resistant
3032	15.2	0.5	20	1	ACC49194	Human ribonuclease	c3105	15	0.5	15	1	AAQ79184	Nuclease resistant
3033	15.2	0.5	20	1	AAL53968	DNA mutation detec	3106	15	0.5	15	1	AAQ79184	Nuclease resistant
3034	15.2	0.5	20	1	AAL61401	Human FXR antisense	c3107	15	0.5	15	1	AAT52136	Human ICAM hammerh
3035	15.2	0.5	20	1	ADC98404	ITGA12 polymorphis	3108	15	0.5	15	1	AAT52136	Human ICAM hammerh
3036	15.2	0.5	20	1	ADD21524	Human mdm2 antisense	c3109	15	0.5	15	1	AAT52138	Human ICAM hammerh
3037	15.2	0.5	20	1	ADD81485	HIV PRT antisense	c3110	15	0.5	15	1	AAT52140	Human ICAM hammerh
3038	15.2	0.5	20	1	ADE27772	Human B7-1 mRNA ta	c3111	15	0.5	15	1	AAT52142	Human ICAM hammerh
3039	15.2	0.5	20	1	ADE27879	Human B7-1 targete	3112	15	0.5	15	1	AAV01604	Oligonucleotide co
3040	15.2	0.5	21	1	AAZ26235	Human polymorphic	c3113	15	0.5	15	1	AAV01604	Oligonucleotide co
3041	15.2	0.5	21	1	ABK15655	Anchored oligo-dt	3114	15	0.5	15	1	AAV01603	Oligonucleotide co
3042	15.2	0.5	21	1	AAZ25989	Human polymorphic	c3115	15	0.5	15	1	AAV01603	Oligonucleotide co
3043	15.2	0.5	21	1	AAZ25672	Human endogenous r	3116	15	0.5	15	1	AAV07431	Synthetic peptide-
3044	15.2	0.5	21	1	AAAX14731	Triple helix third	c3117	15	0.5	15	1	AAV07431	Synthetic peptide-
3045	15.2	0.5	21	1	AAA11484	Human dysferlin PC	3118	15	0.5	15	1	AAT86675	Oligonucleotide li
3046	15.2	0.5	21	1	AAA11497	Human dysferlin PC	c3119	15	0.5	15	1	AAT86675	Oligonucleotide li
3047	15.2	0.5	21	1	AAA36939	Human dysferlin ex	3120	15	0.5	15	1	AAT86605	Oligonucleotide se
3048	15.2	0.5	21	1	AAA36952	Human dysferlin ex	c3121	15	0.5	15	1	AAT86605	Oligonucleotide se
3049	15.2	0.5	21	1	AAZ52058	5'PCR primer L1-5	3122	15	0.5	15	1	AAX00787	N3-P5 phosphoramid
3050	15.2	0.5	21	1	AAZ75737	Human biallelic ma	c3123	15	0.5	15	1	AAX00787	N3-P5 phosphoramid
3051	15.2	0.5	21	1	AAZ75372	Human biallelic ma	3124	15	0.5	15	1	AAX00788	N3-P5 phosphoramid
3052	15.2	0.5	21	1	AAC72800	Single nucleotide	c3125	15	0.5	15	1	AAX00788	N3-P5 phosphoramid
3053	15.2	0.5	21	1	AAC72803	Single nucleotide	3126	15	0.5	15	1	AAX55056	C/EBP-beta antisen
3054	15.2	0.5	21	1	AAA80353	Human A5TH1 5' re	3127	15	0.5	15	1	AAA34503	Human adenosine re
3055	15.2	0.5	21	1	AAF29175	DNA encoding an E-	3128	15	0.5	15	1	AAZ61854	HCV 3' non core re
3056	15.2	0.5	21	1	AAH88904	Human polymorphic	c3129	15	0.5	15	1	AAZ61854	HCV 3' non core re
3057	15.2	0.5	21	1	AAF81140	Primer used for se	3130	15	0.5	15	1	AAZ64910	Substrate for HH r
3058	15.2	0.5	21	1	ABK37488	Packaged vector pl	c3131	15	0.5	15	1	AAZ64910	Substrate for HH r
3059	15.2	0.5	21	1	ABK37472	Packaging signal a	3132	15	0.5	15	1	AAA46502	PCR primer used to
3060	15.2	0.5	21	1	ABL44934	Human chromosome 1	c3133	15	0.5	15	1	AAA46502	PCR primer used to
3061	15.2	0.5	21	1	ABS97218	Human CYP4502E1 pr	3134	15	0.5	15	1	AAA75048	Primer used to rev
3062	15.2	0.5	21	1	ABK89936	Virus like particl	c3135	15	0.5	15	1	AAA75048	Primer used to rev
3063	15.2	0.5	21	1	ABZ69339	Human SLC11A3 codi	3136	15	0.5	15	1	AAA07792	Nucleic acid seque
3064	15.2	0.5	21	1	ADC16521	Short interfering	c3137	15	0.5	15	1	AAA07792	Nucleic acid seque
3065	15.2	0.5	22	1	AAT78995	Mouse Huntington's	3138	15	0.5	15	1	AAA07794	Nucleic acid seque
3066	15.2	0.5	22	1	AAV81783	Rat ALK-7 PCR prim	c3139	15	0.5	15	1	AAA07794	Nucleic acid seque
3067	15.2	0.5	22	1	AAC61618	Probe specific for	3140	15	0.5	15	1	AAA07828	Nucleic acid seque
3068	15.2	0.5	22	1	AAD14545	Arabidopsis thalia	c3141	15	0.5	15	1	AAA07828	Nucleic acid seque
3069	15.2	0.5	22	1	AAS03330	ABRE binding facto	3142	15	0.5	15	1	AAA07790	Nucleic acid seque
3070	15.2	0.5	22	1	AAS01584	Human fibrillin-1	c3143	15	0.5	15	1	AAA07790	Nucleic acid seque
3071	15.2	0.5	22	1	AAS01637	Human fibrillin-1	3144	15	0.5	15	1	AAA07789	Nucleic acid seque
3072	15.2	0.5	22	1	AAS07849	Abcsic acid resp	c3145	15	0.5	15	1	AAA07789	Nucleic acid seque
3073	15.2	0.5	22	1	AAD08919	Arabidopsis thalia	3146	15	0.5	15	1	AAA07795	Nucleic acid seque
3074	15.2	0.5	22	1	AAS00383	5' PCR primer #2 u	c3147	15	0.5	15	1	AAA07795	Nucleic acid seque
3075	15.2	0.5	22	1	ABL44301	Human chromosome 1	3148	15	0.5	15	1	AAA07797	Nucleic acid seque
3076	15.2	0.5	22	1	ABX97353	Human NOV-associat	c3149	15	0.5	15	1	AAA07797	Nucleic acid seque
3077	15.2	0.5	22	1	ACF42669	Human ALMS1 PCR pr	3150	15	0.5	15	1	AAA07799	Nucleic acid seque
3078	15.2	0.5	22	1	ABZ58799	Cinnamycin cina ge	c3151	15	0.5	15	1	AAA07799	Nucleic acid seque
3079	15.2	0.5	22	1	ABT33591	NOV reverse PCR pr	3152	15	0.5	15	1	AAA07802	Nucleic acid seque
3080	15.2	0.5	23	1	AAQ10627	HLA Class I locus-	c3153	15	0.5	15	1	AAA07802	Nucleic acid seque
3081	15.2	0.5	23	1	AAV27967	Ataxia telangiecta	3154	15	0.5	15	1	AAA07825	Nucleic acid seque
3082	15.2	0.5	23	1	AAA39504	Human Factor V sta	c3155	15	0.5	15	1	AAA07825	Nucleic acid seque
3083	15.2	0.5	23	1	AAA28111	Human androgen shu	3156	15	0.5	15	1	AAA07831	Nucleic acid seque
3084	15.2	0.5	23	1	AAH56004	Human SCN2A PCR-SS	c3157	15	0.5	15	1	AAA07831	Nucleic acid seque
3085	15.2	0.5	23	1	AAF70491	Human DRD2 fragmen	3158	15	0.5	15	1	AAA07803	Nucleic acid seque
3086	15.2	0.5	23	1	ABK90968	PCR primer, 22164,	c3159	15	0.5	15	1	AAA07803	Nucleic acid seque
3087	15.2	0.5	23	1	ACC47485	PCR primer for det	3160	15	0.5	15	1	AAA07834	Nucleic acid seque
3088	15.2	0.5	23	1	ADC42610	Human FANCD2 PCR p	c3161	15	0.5	15	1	AAA07834	Nucleic acid seque
3089	15.2	0.5	23	1	ADD28129	HIV-1 LTR region D	3162	15	0.5	15	1	AAA07796	Nucleic acid seque
3090	15.2	0.5	24	1	AAS18179	Human proliferatin	c3163	15	0.5	15	1	AAA07796	Nucleic acid seque
3091	15.2	0.5	24	1	AAL57131	Rt-PCR primer 2 re	3164	15	0.5	15	1	AAA07800	Nucleic acid seque
3092	15.2	0.5	25	1	AAT27193	Stem loop oligonuc	c3165	15	0.5	15	1	AAA07800	Nucleic acid seque
3093	15.2	0.5	25	1	AAC96817	HLA HLA-C gene PCR	3166	15	0.5	15	1	AAA07793	Nucleic acid seque
3094	15.2	0.5	25	1	AAC96075	16s rRNA gene PCR	c3167	15	0.5	15	1	AAA07793	Nucleic acid seque
3095	15.2	0.5	25	1	AAC96447	HLA DQA1 gene PCR	3168	15	0.5	15	1	AAA07798	Nucleic acid seque
3096	15.2	0.5	25	1	AAC96434	HLA DQA1 gene PCR	c3169	15	0.5	15	1	AAA07798	Nucleic acid seque
3097	15.2	0.5	25	1	AAC96448	HLA DQA1 gene PCR	3170	15	0.5	15	1	AAA07788	Nucleic acid seque
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 3174 15 AAA07801 1 0.5 Nucleic acid seque
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 3176 15 AAF20625 1 0.5 Human C/EBP polynu
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 3183 15 AAH20308 1 0.5 Oligo dT15 EDTA la
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 3185 15 AAF30882 1 0.5 Oligonucleotide po
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 3187 15 AAH20511 1 0.5 Oligonucleotide b)
 c3188 15 AAH20511 1 0.5 Oligonucleotide b)
 3189 15 AAF16603 1 0.5 Gastric acid produ
 3190 15 AAH49243 1 0.5 PNA-forming oligon
 c3191 15 AAH49243 1 0.5 PNA-forming oligon
 3192 15 ABL40743 1 0.5 Chicken heparanase
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 3194 15 ABA97403 1 0.5 Nucleotide sequenc
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 3196 15 AAL49453 1 0.5 Mutation detection
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 c3199 15 AAD29506 1 0.5 Primer used for th
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 c3201 15 AAD2531 1 0.5 Retroviral reverse
 3202 15 AAD2531 1 0.5 Retroviral reverse
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 3204 15 ABQ82140 1 0.5 Acceptor vector pH
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 3228 15 ABX98184 1 0.5 Triple helix formi
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 3230 15 ABZ96319 1 0.5 Human C/EBP antise
 c3231 15 ABZ37501 1 0.5 Oligonucleotide SE
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 3243 15 ADC18592 1 0.5 Annealing control
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 3245 15 ABL57075 1 0.5 Molecular beacon t

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 3247 15 AAT75138 1 0.5 Arbitrary anchor p
 3248 15 AAX89227 1 0.5 PCR primer H-T11A.
 3249 15 AAX55055 1 0.5 C/EBP-beta antisen
 3250 15 AAX19464 1 0.5 Human senescence f
 3251 15 AAX19463 1 0.5 Human senescence f
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 3253 15 AAX18369 1 0.5 RT-PCR primer of t
 3254 15 AAX18368 1 0.5 RT-PCR primer of t
 c3255 15 AAX18363 1 0.5 RT-PCR primer of t
 3256 15 AAA99205 1 0.5 Human apoptosis re
 3257 15 AAA99206 1 0.5 Human apoptosis re
 3258 15 AAA34502 1 0.5 Reverse transcript
 3259 15 AAA97561 1 0.5 Rapid analysis of
 3260 15 AAA60992 1 0.5 Rabbit KKIAMRE kin
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 3262 15 AAF20624 1 0.5 Fruit-associated b
 3263 15 AAA94103 1 0.5 Fruit-associated b
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 3265 15 AAF82230 1 0.5 B. gymnorhiza sal
 3266 15 AAF83581 1 0.5 B. gymnorhiza sal
 3267 15 AAF83582 1 0.5 Human cDNA synthe
 3268 15 AAS06650 1 0.5 Human cDNA synthe
 3269 15 AAS06649 1 0.5 Scarlet runner bea
 3270 15 ABK87149 1 0.5 Mouse E2 CDNA ampl
 3271 15 AAD34283 1 0.5 Mouse E2 CDNA ampl
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 3273 15 AAD32156 1 0.5 H-T11-C PCR primer
 3274 15 AAD32155 1 0.5 H-T11-A PCR primer
 3275 15 ABK12621 1 0.5 Mouse E4 protein,
 3276 15 ABK12622 1 0.5 Mouse E4 protein,
 3277 15 ABK87933 1 0.5 Anchored oligo-dr
 3278 15 ABK87932 1 0.5 Anchored oligo-dr
 3279 15 AAD30092 1 0.5 PTTG CDNA isolatin
 3280 15 AAD30916 1 0.5 Rat PTTG1 cDNA amp
 3281 15 ABZ221815 1 0.5 Anti-cancer drug r
 3282 15 ABZ221816 1 0.5 Anti-cancer drug r
 3283 15 ABN87397 1 0.5 PTTG isolation rel
 3284 15 ABA98031 1 0.5 Human PTTG4 encodi
 3285 15 ABZ96318 1 0.5 Human C/EBP antise
 3286 15 ACC69782 1 0.5 Human cervical can
 3287 15 ABZ70966 1 0.5 Human cervical can
 3288 15 ADB68508 1 0.5 PNA-HypNA hybridis
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 3290 15 ADD26193 1 0.5 Primer relating to
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 3292 15 ADE48126 1 0.5 Oligo-dT primer of
 c3293 15 ADE86353 1 0.5 Human PTPN11 PCR p
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 3296 15 AAV37934 1 0.5 Primer of the spec
 c3297 15 AAV49503 1 0.5 Human eosinophil c
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 3300 15 AAX82722 1 0.5 Human IgA nephropa
 c3301 15 AAX82720 1 0.5 Human IgA nephropa
 c3302 15 AAZ36739 1 0.5 Anchored oligo(dT)
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 3317 15 AAC91720 1 0.5 PCR anchor primer,
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3319	15	0.5	17	1	1	AAC82875	Human pollinosis-a	3392	15	0.5	17	1	1	AAL47236	Allergic disease e
3320	15	0.5	17	1	1	AAC82874	Human pollinosis-a	3393	15	0.5	17	1	1	ABK49758	Human atopic derma
3321	15	0.5	17	1	1	AAH47127	Nucleotide sequenc	3394	15	0.5	17	1	1	ABK49758	Human atopic derma
3322	15	0.5	17	1	1	AAH47126	Nucleotide sequenc	3395	15	0.5	17	1	1	ABK49758	Human C/EBP antise
3323	15	0.5	17	1	1	ABK49634	Human Acetyltransf	3396	15	0.5	17	1	1	ABK49634	Murine oligonucleo
3324	15	0.5	17	1	1	ABK49635	Human Acetyltransf	3397	15	0.5	17	1	1	ADC84470	PCR primer for amp
3325	15	0.5	17	1	1	ABL59038	Nucleotide sequenc	3398	15	0.5	17	1	1	ADC84470	PCR primer for amp
3326	15	0.5	17	1	1	ABL59039	Nucleotide sequenc	3399	15	0.5	18	1	1	AAV54170	Nucleotide sequenc
3327	15	0.5	17	1	1	ABN99829	Human allergic dis	3400	15	0.5	18	1	1	AAV54175	Nucleotide sequenc
3328	15	0.5	17	1	1	ABN99830	Human allergic dis	3401	15	0.5	18	1	1	AAV54172	HIV-1 gag protein
3329	15	0.5	17	1	1	AAH49948	Human B1153 expres	3402	15	0.5	18	1	1	AAV35391	Human adipose tiss
3330	15	0.5	17	1	1	AAH49949	Human B1153 expres	3403	15	0.5	18	1	1	AAZ90642	Human adipose tiss
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3333	15	0.5	17	1	1	ABK49757	Human atopic derma	3406	15	0.5	18	1	1	AAV54174	Nucleotide sequenc
3334	15	0.5	17	1	1	ABK49756	Human atopic derma	3407	15	0.5	18	1	1	AAV54174	Nucleotide sequenc
3335	15	0.5	17	1	1	ABX79793	EST polymorphic DN	3408	15	0.5	18	1	1	AAZ90650	Nucleotide sequenc
3336	15	0.5	17	1	1	ADC84469	PCR primer for amp	3409	15	0.5	18	1	1	AAV54171	Nucleotide sequenc
3337	15	0.5	17	1	1	ADC84468	PCR primer for amp	3410	15	0.5	18	1	1	AAV54171	Nucleotide sequenc
3338	15	0.5	17	1	1	ADE77745	DNA oligo (SeqID 5	3411	15	0.5	18	1	1	AAV55053	C/EBP-beta antisen
3339	15	0.5	17	1	1	AAV19118	Anchored oligo(r)	3412	15	0.5	18	1	1	AAV55053	Reverse transcript
3340	15	0.5	17	1	1	AAK69437	Human flt1 VEGF re	3413	15	0.5	18	1	1	AAV55053	Human adenosine re
3341	15	0.5	17	1	1	AAK69436	Human flt1 VEGF re	3414	15	0.5	18	1	1	AAZ90641	Human adipose tiss
3342	15	0.5	17	1	1	AAK69435	Human flt1 VEGF re	3415	15	0.5	18	1	1	AAZ90641	Human adipose tiss
3343	15	0.5	17	1	1	AAK69435	C/EBP-beta antisen	3416	15	0.5	18	1	1	AAZ90641	Polynucleotide # 2
3344	15	0.5	17	1	1	AAK69435	PCR primer G15G u	3417	15	0.5	18	1	1	AAZ90641	Polynucleotide # 2
3345	15	0.5	17	1	1	AAK69435	PCR primer G15G u	3418	15	0.5	18	1	1	AAZ90641	Human biallelic ma
3346	15	0.5	17	1	1	AAK69435	Human adenosine re	3419	15	0.5	18	1	1	AAZ90641	Human C/EBP polynu
3347	15	0.5	17	1	1	AAK69435	Murine gene anchor	3420	15	0.5	18	1	1	AAZ90641	DNA sequence of ca
3348	15	0.5	17	1	1	AAK69435	Murine gene anchor	3421	15	0.5	18	1	1	AAZ90641	Rifampicin resista
3349	15	0.5	17	1	1	AAK69435	Human Iga nephropa	3422	15	0.5	18	1	1	AAZ90641	Human C/EBP antise
3350	15	0.5	17	1	1	AAK69435	Human Iga nephropa	3423	15	0.5	18	1	1	AAZ90641	DNA mutation detec
3351	15	0.5	17	1	1	AAK69435	Anchored oligo(dT)	3424	15	0.5	18	1	1	AAZ90641	Camellia sinensis
3352	15	0.5	17	1	1	AAK69435	Anchored oligo(dT)	3425	15	0.5	18	1	1	AAZ90641	Camellia sinensis
3353	15	0.5	17	1	1	AAK69435	Human C/EBP polynu	3426	15	0.5	18	1	1	AAZ90641	Camellia sinensis
3354	15	0.5	17	1	1	AAK69435	Oestrogen receptor	3427	15	0.5	18	1	1	AAZ90641	C/EBP-beta antisen
3355	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3428	15	0.5	19	1	1	AAZ90641	Human adenosine re
3356	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3429	15	0.5	19	1	1	AAZ90641	Human C/EBP polynu
3357	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3430	15	0.5	19	1	1	AAZ90641	Human MLH1 DNA mis
3358	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3431	15	0.5	19	1	1	AAZ90641	Human C/EBP antise
3359	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3432	15	0.5	20	1	1	AAZ90641	Primer for pUC19 D
3360	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3433	15	0.5	20	1	1	AAZ90641	Human oligonucleot
3361	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3434	15	0.5	20	1	1	AAZ90641	Hepatitis B virus
3362	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3435	15	0.5	20	1	1	AAZ90641	Human oligonucleot
3363	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3436	15	0.5	20	1	1	AAZ90641	Human beta-actin d
3364	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3437	15	0.5	20	1	1	AAZ90641	Oligonucleotide 7
3365	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3438	15	0.5	20	1	1	AAZ90641	Oligonucleotide 7
3366	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3439	15	0.5	20	1	1	AAZ90641	C/EBP-beta antisen
3367	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3440	15	0.5	20	1	1	AAZ90641	MSH2 gene specific
3368	15	0.5	17	1	1	AAK69435	Human pollinosis-a	3441	15	0.5	20	1	1	AAZ90641	Human adenosine re
3369	15	0.5	17	1	1	AAK69435	Human pollinosis-a	3442	15	0.5	20	1	1	AAZ90641	Human C/EBP polynu
3370	15	0.5	17	1	1	AAK69435	Human cDNA synthe	3443	15	0.5	20	1	1	AAZ90641	Forward primer #14
3371	15	0.5	17	1	1	AAK69435	Human cDNA synthe	3444	15	0.5	20	1	1	AAZ90641	Human S-9 derived
3372	15	0.5	17	1	1	AAK69435	Human cDNA synthe	3445	15	0.5	20	1	1	AAZ90641	Human S-9 derived
3373	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3446	15	0.5	20	1	1	AAZ90641	Human S-9 derived
3374	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3447	15	0.5	20	1	1	AAZ90641	Human beta-actin d
3375	15	0.5	17	1	1	AAK69435	PCR anchor primer,	3448	15	0.5	20	1	1	AAZ90641	Human beta-actin d
3376	15	0.5	17	1	1	AAK69435	Human pollinosis-a	3449	15	0.5	20	1	1	AAZ90641	Human S-9 derived
3377	15	0.5	17	1	1	AAK69435	Nucleotide sequenc	3450	15	0.5	20	1	1	AAZ90641	Human beta-actin d
3378	15	0.5	17	1	1	AAH47128	Nucleotide sequenc	3451	15	0.5	20	1	1	AAZ90641	Human S-9 derived
3379	15	0.5	17	1	1	AAH47128	Nucleotide sequenc	3452	15	0.5	20	1	1	AAZ90641	Human S-9 derived
3380	15	0.5	17	1	1	ABK49636	Human Acetyltransf	3453	15	0.5	20	1	1	AAZ90641	Human glutathione
3381	15	0.5	17	1	1	ABK49636	Human Acetyltransf	3454	15	0.5	20	1	1	AAZ90641	Molecular beacon t
3382	15	0.5	17	1	1	ABQ64253	Human KTOM1a porti	3455	15	0.5	20	1	1	AAZ90641	Molecular beacon t
3383	15	0.5	17	1	1	ABQ64253	Human KTOM1a porti	3456	15	0.5	20	1	1	AAZ90641	Human oligonucleot
3384	15	0.5	17	1	1	ABQ64255	Human KTOM1a porti	3457	15	0.5	20	1	1	AAZ90641	Human oligonucleot
3385	15	0.5	17	1	1	ABQ64255	Human KTOM1a porti	3458	15	0.5	20	1	1	AAZ90641	Human oligonucleot
3386	15	0.5	17	1	1	ABL59040	Nucleotide sequenc	3459	15	0.5	20	1	1	AAZ90641	Human MSH2 gene PC
3387	15	0.5	17	1	1	ABN99831	Nucleotide sequenc	3460	15	0.5	20	1	1	AAZ90641	Target oligonucleo
3388	15	0.5	17	1	1	ABN99831	Human allergic dis	3461	15	0.5	20	1	1	AAZ90641	Target oligonucleo
3389	15	0.5	17	1	1	AAH49950	Human allergic dis	3462	15	0.5	20	1	1	AAZ90641	Molecular beacon t
3390	15	0.5	17	1	1	AAH49950	Human B1153 expres	3463	15	0.5	21	1	1	ABL57071	Molecular beacon t
3391	15	0.5	17	1	1	AAH49950	Allergic disease e	3464	15	0.5	21	1	1	ABS97681	Histamine N-methyl

3465 ABS97669 21 0.5 15 Histamine N-methyl
3466 AAZ26619 21 0.5 15 Human polymorphic
3467 AAZ26366 21 0.5 15 Human polymorphic
3468 AAX55050 21 0.5 15 C/EBP-beta antisen
3469 AAA34497 21 0.5 15 Human adenosine re
3470 AAF20619 21 0.5 15 Human C/EBP polynu
c3471 AAH62016 21 0.5 15 IL8 hairpin/hammer
3472 ABZ96313 21 0.5 15 Human C/EBP antise
c3473 ADB88602 22 0.5 15 Frizzled-4 (FZD4)
3474 AAT28045 22 0.5 15 3'-primer B for hu
3475 AAT28046 22 0.5 15 3'-primer C for hu
3476 AAT28048 22 0.5 15 3'-primer E for hu
3477 AAT28049 22 0.5 15 3'-primer F for hu
3478 AAT28054 22 0.5 15 3'-primer L for hu
3479 AAT28055 22 0.5 15 3'-primer M for hu
3480 AAT28047 22 0.5 15 3'-primer D for hu
3481 AAT28044 22 0.5 15 3'-primer A for hu
3482 AAT58488 22 0.5 15 First primer #5 fo
3483 AAT58489 22 0.5 15 First primer #11 f
3484 AAT58487 22 0.5 15 First primer #6 fo
3485 AAT58485 22 0.5 15 First primer #4 fo
3486 AAT58495 22 0.5 15 First primer #12 f
3487 AAT58484 22 0.5 15 First primer #1 fo
3488 AAT58485 22 0.5 15 First primer #2 fo
3489 AAT58486 22 0.5 15 First primer #3 fo
3490 AAV58375 22 0.5 15 Biotinylated prime
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3492 AAX55049 22 0.5 15 C/EBP-beta antisen
3493 AAX77101 22 0.5 15 GC6 Gene 3' primer
3494 AAA34496 22 0.5 15 Human adenosine re
3495 AAZ47353 22 0.5 15 PCR primer M used
3496 AAZ47347 22 0.5 15 PCR primer F used
3497 AAZ47346 22 0.5 15 PCR primer E used
3498 AAZ47352 22 0.5 15 PCR primer L used
3499 AAZ47342 22 0.5 15 PCR primer A used
3500 AAZ47344 22 0.5 15 PCR primer C used
3501 AAZ47343 22 0.5 15 PCR primer B used
3502 AAZ47345 22 0.5 15 PCR primer D used
3503 AAA99617 22 0.5 15 (T)-primer for fir
3504 AAF20618 22 0.5 15 Human C/EBP polynu
3505 AAH22185 22 0.5 15 Human hepatocyte a
3506 AAH22189 22 0.5 15 Human hepatocyte a
3507 AAH22187 22 0.5 15 Human hepatocyte a
3508 AAH22188 22 0.5 15 Human hepatocyte a
3509 AAH22190 22 0.5 15 Human hepatocyte a
3510 AAH22195 22 0.5 15 Human hepatocyte a
3511 AAH22186 22 0.5 15 Human hepatocyte a
3512 ABZ96312 22 0.5 15 Human C/EBP antise
3513 AAL56810 22 0.5 15 T(13) bio-primer o
c3514 AAZ99839 23 0.5 15 Nucleotide sequenc
c3515 AAQ36059 23 0.5 15 HIV-2 detection se
c3516 AAV30513 23 0.5 15 Sunflower ORF522 p
3517 AAX55048 23 0.5 15 C/EBP-beta antisen
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3520 AAZ47417 23 0.5 15 Probe 1 used to co
3521 AAZ49423 23 0.5 15 Human Galectin 11
3522 AAZ55321 23 0.5 15 Neisseria species
3523 AAF10628 23 0.5 15 PCR primer #2 used
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3525 AAA53817 23 0.5 15 Primer BTU1-75 hyb
c3526 AAC66214 23 0.5 15 Galectin 11 PCR pr
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3528 AAC92334 23 0.5 15 Human hTmPT27 PCR
3529 AAH13613 23 0.5 15 3' untranslated re
c3530 AAS13613 23 0.5 15 Forward PCR primer
3531 ABT05505 23 0.5 15 NOVX related probe
3532 ABV74137 23 0.5 15 Human C/EBP antise
c3533 ABV74137 23 0.5 15 Oligonucleotide us
c3534 AAH75424 24 0.5 15 Human homo laminin
3535 ABL60935 24 0.5 15 Human nucleotide r
c3536 ABV93494 24 0.5 15 Bacillus thuringie
c3537 ABV93779 24 0.5 15 B. thuringiensis t

c3538 15 0.5 25 1 ABK87633
c3539 15 0.5 25 1 ABK87631
3540 15 0.5 25 1 AAC96446
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3589 14.8 0.5 20 1 ABQ96037
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3602 14.8 0.5 20 1 AAT44460
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3605 14.8 0.5 20 1 AAT73396
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c3607 14.8 0.5 20 1 AAZ46525
3608 14.8 0.5 20 1 AAA55739
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c3610 14.8 0.5 20 1 AAA60341

BamT15G PCR primer
BamT15A PCR primer
HLA DQA1 gene PCR
NotI-oligo primer.
Seq ID No:2 of WO9
HLA DPB1 gene PCR
HLA DQA1 gene PCR
PCR primer EcoR1-d
16s rRNA gene PCR
cDNA primer. Synt
Cotton fibre cDNA
Cotton fibre first
Primer for cotton
Primer for cotton
Primer for cotton
Nucleotide sequenc
Sequence of probe
Duplex target sequ
Human G-alpha-13 a
PCR primer used to
TRAF1 antisense ol
Primer 4 for casei
Antisense oligonuc
Multiple repeated
DNA-RNA-DNA oligon
DNA-RNA-DNA oligon
Stearoyl-CoA desat
Stearoyl-CoA desat
Human MLH1 DNA mis
Cross-linking olig
Oligomer HUM beta
Oligomer HUM beta
Triple helix-formi
Rat type L pyruvat
Oligonucleotide #4
Oligonucleotide GA
Triple helix formi
Tumour necrosis fa
cdk-we-hu ribozyme
Mutant E. coli J g
Cdk-we-hu ribozyme
5' end of endochit
Triple helix formi
RNA/DNA hybrid com
HCV coding region-
HCV coding region-
Human c-fos transc
Human c-fos siNA l
Oligonucleotide (S
Antisense oligonuc
Human inflammatory
Tumour suppression
Human oligonucleot
Human oligonucleot
Human oligonucleot
Human beta-actin d
Human S-9 derived
Human beta-actin d
Human beta-actin d
Cross-linking olig
Oligomer HUM beta
Oligomer HUM beta
Multiplex vector 1
Self paired oligon
5' primer for lami
PCR primer (TSK8B)
Seq ID No: 13 of U
S. pneumoniae HSP7
Primer2 for mutant
Mouse CACNA1F exon
TRAF1 antisense ol
Human HPC2 cDNA ex
Human HPC2 cDNA ex

3903	14.4	0.5	20	1	ADD20414	Oreochromis niloti
3904	14.4	0.5	20	1	ADD81484	HIV PRT antisense
3905	14.4	0.5	20	1	ADD81483	HIV PRT antisense
3906	14.4	0.5	20	1	ADD81482	HIV PRT antisense
3907	14.4	0.5	20	1	ADD81481	HIV PRT antisense
3908	14.4	0.5	21	1	AAZ26619	Human polymorphic
3909	14.4	0.5	21	1	AAT94317	Human DPC4 sequenc
3910	14.4	0.5	21	1	AAZ26572	Human polymorphic
3911	14.4	0.5	21	1	AAA11454	Human dysferlin PC
3912	14.4	0.5	21	1	AAA36909	Human dysferlin ex
3913	14.4	0.5	21	1	AAZ30231	Human housekeeping
3914	14.4	0.5	21	1	AAF95557	Human gene single
3915	14.4	0.5	21	1	AAF95571	Human gene single
3916	14.4	0.5	21	1	AAF87033	Anchored 3' oligo
3917	14.4	0.5	21	1	AAF80105	Nucleotide sequenc
3918	14.4	0.5	21	1	ABL57072	Molecular beacon t
3919	14.4	0.5	21	1	ABX11284	Mouse P0 gene 5' U
3920	14.4	0.5	21	1	ABS58234	Sequence surroundi
3921	14.4	0.5	21	1	ABQ80008	SiRNA duplex antis
3922	14.4	0.5	22	1	AAQ90036	Human SMP30 gene P
3923	14.4	0.5	22	1	AAQ82287	Chromosome 11 (loc
3924	14.4	0.5	22	1	AAT62686	Primer for human s
3925	14.4	0.5	22	1	AAV51724	Zea mays genome re
3926	14.4	0.5	22	1	AAA72031	Human cathepsin Y
3927	14.4	0.5	22	1	ABS52173	Human forward prim
3928	14.4	0.5	22	1	ABV73127	N-acetyltransferas
3929	14.4	0.5	22	1	ABV74921	NAT1*14 allele spe
3930	14.4	0.5	22	1	ABQ78653	Nucleotide sequenc
3931	14.4	0.5	22	1	ABA00253	NAT1 A560G mutatio
3932	14.4	0.5	22	1	AAD54260	NAT1 mutant allele
3933	14.4	0.5	22	1	ABZ75815	NAT1 allele NAT1*1
3934	14.4	0.5	22	1	AAD50983	NAT1 allele specif
3935	14.4	0.5	22	1	ABZ20529	Human NAT1 genotyp
3936	14.4	0.5	22	1	ABZ23147	PCR primer used to
3937	14.4	0.5	22	1	ABV72580	Primer used to det
3938	14.4	0.5	22	1	AAL53876	Gastroesophageal r
3939	14.4	0.5	22	1	AAD51319	N-acetyl transfera
3940	14.4	0.5	22	1	ABZ23435	Primer used to amp
3941	14.4	0.5	22	1	AAD54568	Human M2-PK gene a
3942	14.4	0.5	22	1	AAD47697	N-acetyltransferas
3943	14.4	0.5	22	1	ABV76236	N-acetyltransferas
3944	14.4	0.5	22	1	ACF05573	N-acetyltransferas
3945	14.4	0.5	22	1	ACC79724	N-acetyltransferas
3946	14.4	0.5	22	1	ACC83560	N-acetyltransferas
3947	14.4	0.5	22	1	ACF04612	Human NAT1 NAT1*14
3948	14.4	0.5	24	1	ABA05517	Human Tre carcinog
3949	14.4	0.5	24	1	ABA99264	Human tra oncogene
3950	14.4	0.5	24	1	ABZ57032	Human kinesin ligh
3951	14.4	0.5	24	1	ADE86193	Ret gene chair qua
3952	14.4	0.5	25	1	AAC95684	HLA DPB1 gene PCR
3953	14.4	0.5	25	1	AAC96504	HLA DQB1 gene PCR
3954	14.4	0.5	25	1	AAC96321	HLA DPB1 gene PCR
3955	14.4	0.5	25	1	AAC95753	HLA DQB1 gene PCR
3956	14.4	0.5	28	1	ADD41445	Hepatitis C virus
3957	14.2	0.5	15	1	AAA47676	Oligo d(T) primer
3958	14.2	0.5	15	1	AAA47676	Oligo d(T) primer
3959	14.2	0.5	15	1	AAD44150	Oligo-AT PCR prime
3960	14.2	0.5	15	1	AAD44150	Oligo-AT PCR prime
3961	14.2	0.5	16	1	AAX18387	RT-PCR primer of t
3962	14.2	0.5	16	1	AAX18387	RT-PCR primer of t
3963	14.2	0.5	16	1	AAD44147	Oligo-dT PCR prime
3964	14.2	0.5	16	1	AAD44149	Oligo-dT PCR prime
3965	14.2	0.5	19	1	AAT65892	Primer #1 to ampli
3966	14.2	0.5	19	1	AAZ00090	Primer LCF used fo
3967	14.2	0.5	19	1	AAZ87035	RBP-7 microsequenc
3968	14.2	0.5	19	1	AAA86471	PCBA HH ribozyme b
3969	14.2	0.5	19	1	AAA85728	Cyclin B1 ribozyme
3970	14.2	0.5	19	1	AAA84722	Cyclin E ribozyme
3971	14.2	0.5	19	1	AAA86468	PCBA HH ribozyme b
3972	14.2	0.5	19	1	AAC60721	CYP2D1 gene partia
3973	14.2	0.5	19	1	AAZ71872	Human biallelic ma
3974	14.2	0.5	19	1	AAC67521	Alzheimer's diseas
3975	14.2	0.5	19	1	AAC83562	DNA synthesis meth

c3976	14.2	0.5	19	1	AAH888897	Human polymorphic
c3977	14.2	0.5	19	1	AAH61633	PCNA HH ribozyme b
c3978	14.2	0.5	19	1	AAH59884	Cyclin E ribozyme
c3979	14.2	0.5	19	1	AAH61630	PCNA HH ribozyme b
c3980	14.2	0.5	19	1	AAH60890	Cyclin B1 ribozyme
3981	14.2	0.5	19	1	ABA91528	DNA-RNA-DNA oligon
c3982	14.2	0.5	19	1	ABA91528	DNA-RNA-DNA oligon
3983	14.2	0.5	19	1	ABX13088	Hantavirus gene re
c3984	14.2	0.5	19	1	AAD34425	Barley chymotrypsi
c3985	14.2	0.5	19	1	ABL40490	Nucleotide sequenc
c3986	14.2	0.5	19	1	ABA97625	Probe d. Unidenti
c3987	14.2	0.5	19	1	ABT13058	Human apolipoprote
3988	14.2	0.5	19	1	ADD43444	Human mitochondria
3989	14.2	0.5	19	1	ADE65656	Human c-fos transc
c3990	14.2	0.5	19	1	ADE65772	Human c-fos siNA 1
3991	14.2	0.5	19	1	ADE27175	Stearoyl-CoA desat
c3992	14.2	0.5	19	1	ADE27465	Stearoyl-CoA desat
3993	14.2	0.5	19	1	ADE27307	Stearoyl-CoA desat
c3994	14.2	0.5	19	1	ADE27597	Stearoyl-CoA desat
3995	14.2	0.5	20	1	ABZ89873	Human oligonucleot
3996	14.2	0.5	20	1	AAT10129	Sequence #1 used i
c3997	14.2	0.5	20	1	AAF99949	Synthetic oligonuc
3998	14.2	0.5	20	1	ABA91537	DNA oligonucleotid
c3999	14.2	0.5	20	1	ABX04655	Human endogenous r
4000	14.2	0.5	20	1	ABZ90374	Human oligonucleot
c4001	14.2	0.5	20	1	ABZ85670	Human oligonucleot
c4002	14.2	0.5	20	1	ABZ88438	Human oligonucleot
c4003	14.2	0.5	20	1	ABZ91225	Human oligonucleot
4004	14.2	0.5	20	1	AAL53968	DNA mutation detec
c4005	14.2	0.5	20	1	ADC98404	ITGA12 polymorphis
c4006	14.2	0.5	20	1	AAQ22135	Primer G corresp.
c4007	14.2	0.5	20	1	AAQ51661	ADV primer (II)a.
c4008	14.2	0.5	20	1	AAQ62025	Mutant Ki-ras 5'-U
c4009	14.2	0.5	20	1	AAT41033	Human gene signatu
c4010	14.2	0.5	20	1	AAT41311	Human gene signatu
c4011	14.2	0.5	20	1	AAQ79844	K-ras modulating s
c4012	14.2	0.5	20	1	AAT86501	S-adenosylmethioni
4013	14.2	0.5	20	1	AAV37666	Allelic variant M4
4014	14.2	0.5	20	1	AAV69993	Mouse c-jun protei
c4015	14.2	0.5	20	1	AAV11765	Nucleic acid-polym
4016	14.2	0.5	20	1	AAZ11062	PCR primer for clo
4017	14.2	0.5	20	1	AAZ00584	Human glypican seq
c4018	14.2	0.5	20	1	AAV84024	Antisense oligonuc
c4019	14.2	0.5	20	1	AAZ21620	Human Ki-ras speci
c4020	14.2	0.5	20	1	AAZ56984	Ras gene modulator
4021	14.2	0.5	20	1	AAZ01454	PCR primer used to
c4022	14.2	0.5	20	1	AAZ05484	PCR primer used to
c4023	14.2	0.5	20	1	AAZ21925	Human B-raf kinase
4024	14.2	0.5	20	1	AAZ92436	PCR primer used to
c4025	14.2	0.5	20	1	AAZ95694	PCR primer used to
4026	14.2	0.5	20	1	AAZ29320	JNK1-specific prob
4027	14.2	0.5	20	1	AAZ57332	Human interferon a
c4028	14.2	0.5	20	1	AAA46210	Primer IPM18R for
c4029	14.2	0.5	20	1	AAA95858	Human Ki-ras antis
4030	14.2	0.5	20	1	AAZ47296	Enterohaemorrhagic
c4031	14.2	0.5	20	1	AAZ70845	Human biallelic ma
4032	14.2	0.5	20	1	AAZ71898	Human biallelic ma
4033	14.2	0.5	20	1	AAZ76242	Human biallelic ma
c4034	14.2	0.5	20	1	AAA09679	Human SHP-1 antise
4035	14.2	0.5	20	1	AAA11880	Human MDMX antisen
4036	14.2	0.5	20	1	AAZ59002	Escherichia coli s
c4037	14.2	0.5	20	1	AAC60557	Human fra-1 mRNA a
4038	14.2	0.5	20	1	AAC62863	JNK antisense olig
c4039	14.2	0.5	20	1	AAC65597	Human uteroglobin
4040	14.2	0.5	20	1	AAC66295	Primer P13 used in
4041	14.2	0.5	20	1	AAC60958	Interleukin 2 shor
4042	14.2	0.5	20	1	AAS02211	A. thaliana phosph
c4043	14.2	0.5	20	1	AAD14811	Human glycogen syn
4044	14.2	0.5	20	1	AAS45779	Mouse PARP-2 antis
4045	14.2	0.5	20	1	AAH00614	Staphylococcus det
c4046	14.2	0.5	20	1	AAF62926	Human PEPCK-cytoso
4047	14.2	0.5	20	1	AAS04459	Human DAXX gene pr
4048	14.2	0.5	20	1	AAF28352	DNA oligomer #2.

c4049	14.2	0.5	20	1	AAAF28352	DNA oligomer #2.
4050	14.2	0.5	20	1	AAS03670	PCR primer re012,
c4051	14.2	0.5	20	1	AAF27109	Human MEKK1 phosph
4052	14.2	0.5	20	1	AAH45579	Enterohaemorrhagic
4053	14.2	0.5	20	1	AAS23808	Primer B #61 used
4054	14.2	0.5	20	1	AAF91339	Human E2F transcri
c4055	14.2	0.5	20	1	AAS08770	Human PD-ABC form
c4056	14.2	0.5	20	1	AAS08861	Human PD-ABC form
4057	14.2	0.5	20	1	ABL96288	Primer #1 related
4058	14.2	0.5	20	1	AAH80595	Oligonucleotide hy
4059	14.2	0.5	20	1	ABA01567	HLA class I micros
c4060	14.2	0.5	20	1	ABK96703	Interleukin-3 (IL-
c4061	14.2	0.5	20	1	ABQ78576	RT-PCR primer used
4062	14.2	0.5	20	1	AAD41796	Human RECQL2 antis
4063	14.2	0.5	20	1	AAL43954	Polynucleotide sep
4064	14.2	0.5	20	1	ABK99983	Human CADPKL DNA P
4065	14.2	0.5	20	1	ABL45623	Human chromosome 2
c4066	14.2	0.5	20	1	AAL45626	Human serine/threo
c4067	14.2	0.5	20	1	ABK94489	Human BRCA1 gene f
c4068	14.2	0.5	20	1	ABA03194	Human KRGF1 PCR pr
c4069	14.2	0.5	20	1	ABX24613	EIF2AK3 gene seque
4070	14.2	0.5	20	1	ABL58300	Human GLUT 10 SSCP
4071	14.2	0.5	20	1	ABZ30568	Candida albicans G
4072	14.2	0.5	20	1	ABZ30869	Candida albicans G
c4073	14.2	0.5	20	1	ABA97642	probe m. Unidenti
c4074	14.2	0.5	20	1	ABA97644	probe o. Unidenti
4075	14.2	0.5	20	1	ABN80890	Human caspase 7 ph
4076	14.2	0.5	20	1	ABQ74654	STEAP gene sense P
c4077	14.2	0.5	20	1	AAD44809	Human B-raf kinase
4078	14.2	0.5	20	1	ABL30917	Human HLA genotypi
c4079	14.2	0.5	20	1	ABI94721	Capture Ots2-B9 forw
4080	14.2	0.5	20	1	ABK47121	Mouse Ots2-B9 forw
4081	14.2	0.5	20	1	ABS65064	Human casein kinas
c4082	14.2	0.5	20	1	AAL53492	Signal transducer
c4083	14.2	0.5	20	1	ABX78222	Human bifunctional
4084	14.2	0.5	20	1	ABZ98046	Human MCP4 oligonu
c4085	14.2	0.5	20	1	ABZ90034	Human oligonucleot
c4086	14.2	0.5	20	1	ABZ88602	Human oligonucleot
4087	14.2	0.5	20	1	ABZ98097	Human MCP4 oligonu
c4088	14.2	0.5	20	1	ABZ98729	Human tryptase a o
c4089	14.2	0.5	20	1	ABZ99386	Human PDE4C oligon
c4090	14.2	0.5	20	1	ABZ85859	Human oligonucleot
4091	14.2	0.5	20	1	ABZ87871	Human oligonucleot
c4092	14.2	0.5	20	1	ABZ92871	Human oligonucleot
4093	14.2	0.5	20	1	ABZ88203	Human oligonucleot
4094	14.2	0.5	20	1	ABZ98593	Human tryptase a o
c4095	14.2	0.5	20	1	ABZ91192	Human oligonucleot
4096	14.2	0.5	20	1	ABZ88600	Human oligonucleot
c4097	14.2	0.5	20	1	ABZ90510	Human oligonucleot
c4098	14.2	0.5	20	1	ABZ85536	Human oligonucleot
4099	14.2	0.5	20	1	ABZ88781	Human oligonucleot
c4100	14.2	0.5	20	1	ABZ88781	Human oligonucleot
c4101	14.2	0.5	20	1	ABZ90942	Human oligonucleot
c4102	14.2	0.5	20	1	ABZ85566	Human oligonucleot
4103	14.2	0.5	20	1	ABZ89197	Human oligonucleot
c4104	14.2	0.5	20	1	ABZ86102	Human oligonucleot
c4105	14.2	0.5	20	1	ABZ87395	Human oligonucleot
c4106	14.2	0.5	20	1	ABZ87364	Human oligonucleot
4107	14.2	0.5	20	1	ABZ89513	Human oligonucleot
c4108	14.2	0.5	20	1	ABZ91731	Human oligonucleot
c4109	14.2	0.5	20	1	ABZ98830	Human oligonucleot
c4110	14.2	0.5	20	1	ABZ76530	Human tryptase b o
4111	14.2	0.5	20	1	ADA55771	Lactobacillus brev
c4112	14.2	0.5	20	1	ABX33988	Human protein-rela
c4113	14.2	0.5	20	1	ABX34004	Human interleukin
c4114	14.2	0.5	20	1	ABQ84614	Human interleukin
4115	14.2	0.5	20	1	ACC82913	DPP10 related PSQ
c4116	14.2	0.5	20	1	ACD42192	Human TRIP6 antis
c4117	14.2	0.5	20	1	ACA92581	Antisense oligonuc
c4118	14.2	0.5	20	1	ADA44763	Human Ki-ras antis
c4119	14.2	0.5	20	1	ADA44762	Antisense oligonuc
4120	14.2	0.5	20	1	ACC58274	Vascular endotheli
c4121	14.2	0.5	20	1	ACC49680	Human KSR chimeric
1	ABZ76424	0.5	20	1	c4122	PRRSV polymerase p
1	ABZ74905	0.5	20	1	4123	Human acyl coenzym
1	ADA26567	0.5	20	1	4124	Human Jun N-termin
1	ABX95044	0.5	20	1	4125	Human RAK mutagen
1	ACH66530	0.5	20	1	4126	Antisense PCR prim
1	ADAL4704	0.5	20	1	c4127	PCR primer #1 for
1	ADC20037	0.5	20	1	4128	Synthetic oligonuc
1	AAD61385	0.5	20	1	c4129	Primer #12 used to
1	ADD81486	0.5	20	1	4130	HIV PRT antisense
1	ADE15814	0.5	20	1	c4131	Human PKR exon 13
1	ADE43612	0.5	20	1	c4132	Human KNSL1 sequen
1	ADE43690	0.5	20	1	c4133	Triple helix third
1	AAX14731	0.5	21	1	c4134	3' primer #1087-11
1	AAT42561	0.5	21	1	c4135	Pyruvate decarboxy
1	AAT46179	0.5	21	1	c4136	Human beta-globin
1	AAT48456	0.5	21	1	4137	Human beta-globin
1	AAT48456	0.5	21	1	c4138	Third-strand oligo
1	AAT48459	0.5	21	1	c4139	Primer #2 for the
1	AAV60859	0.5	21	1	c4140	Zea mays genome fo
1	AAV51661	0.5	21	1	4141	Antisense primer u
1	AAV05205	0.5	21	1	c4142	Human TSC gene exo
1	AAV40600	0.5	21	1	c4143	Human polymorphic
1	AAZ26264	0.5	21	1	4144	Human polymorphic
1	AAZ26012	0.5	21	1	4145	Human STE20-relate
1	AAZ40513	0.5	21	1	4146	Human TFIIID gene c
1	AAZ27494	0.5	21	1	c4147	Triple helix third
1	AAX14729	0.5	21	1	4148	Triple helix third
1	AAX14730	0.5	21	1	4149	Triple helix formi
1	AAX14730	0.5	21	1	c4150	Triple helix formi
1	AAZ23796	0.5	21	1	4151	HSV RNA fragment 1
1	AAZ18469	0.5	21	1	c4152	Polymorphic fragme
1	AAZ18390	0.5	21	1	c4153	Polymorphic fragme
1	AAZ01252	0.5	21	1	c4154	PCR primer for PGI
1	AAZ00468	0.5	21	1	4155	Human MINT1 clone
1	AAZ59336	0.5	21	1	4156	Human STP2 intron
1	AAZ14463	0.5	21	1	4157	AUTUA RNA target s
1	AAZ69623	0.5	21	1	c4158	Human biallelic ma
1	AAZ73890	0.5	21	1	c4159	Human biallelic ma
1	AAZ75985	0.5	21	1	4160	Primer PAD4.5 to s
1	AAZ00964	0.5	21	1	c4161	Rat opsin gene spe
1	AAZ46461	0.5	21	1	c4162	Human ASTH1J trans
1	AAA80291	0.5	21	1	c4163	Human ASTH1J 5' re
1	AAA80375	0.5	21	1	c4164	Rat hepatocyte car
1	AAAF7655	0.5	21	1	c4165	Human gene single
1	AAF97089	0.5	21	1	c4166	Human gene single
1	AAF96485	0.5	21	1	c4167	Human gene single
1	AAF96326	0.5	21	1	4168	Mouse ISF PCR prim
1	AAC92911	0.5	21	1	c4169	Transcription fact
1	AAH62338	0.5	21	1	c4170	PCR primer used in
1	AAH20432	0.5	21	1	4171	Primer A #35 used
1	AAS23721	0.5	21	1	4172	Bovine CVM disease
1	ABS58442	0.5	21	1	c4173	TGF-beta type II r
1	AAD33350	0.5	21	1	c4174	Human single nucle
1	ABK65500	0.5	21	1	4175	Human single nucle
1	ABK65490	0.5	21	1	c4176	Human single nucle
1	ABT13236	0.5	21	1	c4177	Fanconi anaemia FA
1	ABK41517	0.5	21	1	c4178	Human CTNNA3 exon-
1	ABS55055	0.5	21	1	4179	R. Obamensis DNA p
1	ABZ229935	0.5	21	1	4180	Candida albicans G
1	ABS98382	0.5	21	1	4181	Human multidrug re
1	ABS98479	0.5	21	1	c4182	Human orphan nucle
1	ABS56153	0.5	21	1	4183	Sperm formation re
1	ABK14355	0.5	21	1	c4184	Human interleukin-
1	ABK37957	0.5	21	1	c4185	Forward RT-PCR pri
1	AAL40172	0.5	21	1	4186	Isoprenoid related
1	ABK94369	0.5	21	1	4187	Endothelin convert
1	ABK94370	0.5	21	1	c4188	Endothelin convert
1	AAL50228	0.5	21	1	4189	Human ARE-mRNA seq
1	ABZ24198	0.5	21	1	c4190	Humanised R. renif
1	AAL53707	0.5	21	1	4191	Adenylate Uridylat
1	AAD49639	0.5	21	1	4192	Human adenylate ur
1	ACC83520	0.5	21	1	4193	AU rich element (A
1	ADC42473	0.5	21	1	c4194	FANCD2 PCR primer

C4195	14.2	0.5	21	1	ADD14366	Human src biomarke	C4268	14	0.5	15	1	ABK98168	Triple helix formi
C4196	14.2	0.5	21	1	AAD61847	Mouse MORC exon 1	4269	14	0.5	15	1	ABK98167	Triple helix formi
4197	14.2	0.5	21	1	ADE86000	AU-rich element mo	C4270	14	0.5	15	1	ABK98167	Triple helix formi
C4198	14.2	0.5	22	1	ABL35690	Immunostimulatory	4271	14	0.5	15	1	ABK98186	Triple helix formi
C4199	14.2	0.5	22	1	AAT28054	3'-primer L for hu	C4272	14	0.5	15	1	ABK98186	Triple helix formi
C4200	14.2	0.5	22	1	AAT58494	First primer #11 f	4273	14	0.5	15	1	ABX79833	EST polymorphic DN
C4201	14.2	0.5	22	1	AZA47352	PCR primer L used	C4274	14	0.5	15	1	ABX79833	EST polymorphic DN
C4202	14.2	0.5	22	1	AAH22195	Human hepatocyte a	C4275	14	0.5	16	1	AAD44145	Oligo-dt PCR prime
C4203	14.2	0.5	22	1	AAH28299	3' untranslated re	4276	14	0.5	16	1	AAX18360	RT-PCR primer of t
C4204	14.2	0.5	22	1	AAH28297	3' untranslated re	C4277	14	0.5	16	1	AAX18368	RT-PCR primer of t
C4205	14.2	0.5	23	1	ADD28129	HIV-1 LTR region D	4278	14	0.5	16	1	AAX18365	RT-PCR primer of t
C4206	14.2	0.5	24	1	ABQ73262	Human ribosomal pr	C4279	14	0.5	16	1	AAD44147	Oligo-dt PCR prime
4207	14.2	0.5	24	1	ABL55230	Pax protein 11 RT-	C4280	14	0.5	16	1	AAX33896	Oligo-dt PCR prime
C4208	14.2	0.5	24	1	ABZ21302	DNA binding protei	4281	14	0.5	16	1	AAX33896	PCR primer #6 for
4209	14.2	0.5	25	1	AAC95960	HLA HLA-B gene PCR	C4282	14	0.5	17	1	AAX69798	Human flt1 VEGF re
C4210	14.2	0.5	25	1	AAV06660	Unlabeled oligonuc	4283	14	0.5	17	1	AAX69803	Human flt1 VEGF re
4211	14	0.5	14	1	AAQ33508	Sequence of micros	4284	14	0.5	17	1	AAX70117	Human flt1 VEGF re
C4212	14	0.5	14	1	AAQ33508	3' poly(T) primer	4285	14	0.5	17	1	AAX70116	Human flt1 VEGF re
4213	14	0.5	14	1	AAV09230	3' poly(T) primer	4286	14	0.5	17	1	AAX69438	Human flt1 VEGF re
C4214	14	0.5	14	1	AAV09234	Poly(T) oligonucle	4287	14	0.5	17	1	AAX69434	Human flt1 VEGF re
4215	14	0.5	14	1	AAV12222	Poly(T) oligonucle	4288	14	0.5	17	1	AAA20469	Integrin alpha 6 s
C4216	14	0.5	14	1	AAT95552	Oligo-dt primer us	4289	14	0.5	17	1	AAA25447	Oestrogen receptor
C4217	14	0.5	14	1	AAX02696	Barley HPPD primer	C4291	14	0.5	17	1	AAA25447	Oestrogen receptor
C4218	14	0.5	14	1	AAV09234	C/EBP-beta antisen	4292	14	0.5	17	1	AAF03225	Hammerhead ribozym
4219	14	0.5	14	1	AAV14689	Triple helix third	4293	14	0.5	17	1	AAF03223	Hammerhead ribozym
C4220	14	0.5	14	1	AAV14689	Triple helix third	C4294	14	0.5	17	1	AAF07018	Hammerhead ribozym
4221	14	0.5	14	1	AAV14688	Triple helix formi	4295	14	0.5	17	1	AAF03224	Hammerhead ribozym
C4222	14	0.5	14	1	AAV14688	Triple helix formi	4296	14	0.5	17	1	AAF03226	Hammerhead ribozym
C4223	14	0.5	14	1	AAV14688	Triple helix formi	C4297	14	0.5	17	1	ABK02792	Human CD20 Hammerh
4224	14	0.5	14	1	AAV14688	Triple helix formi	C4298	14	0.5	17	1	ABK02791	Human CD20 Hammerh
C4225	14	0.5	14	1	AAV14688	Triple helix formi	C4299	14	0.5	17	1	ABQ64252	Human KTOM1a porti
4226	14	0.5	14	1	AAV14688	Triple helix formi	C4300	14	0.5	17	1	ABQ64256	Human KTOM1a porti
C4227	14	0.5	14	1	AAV14688	Triple helix formi	C4301	14	0.5	17	1	ABQ99687	Murine Ikbkap exon
4228	14	0.5	14	1	AAV14688	Triple helix formi	4302	14	0.5	17	1	ABS76198	Human PAPP-Eb asso
C4229	14	0.5	14	1	AAV14688	Triple helix formi	4303	14	0.5	17	1	ABS76197	Human PAPP-Eb asso
4230	14	0.5	14	1	AAV14688	Triple helix formi	4304	14	0.5	17	1	ACD55508	HBV amberyzyme subs
C4231	14	0.5	14	1	AAV14688	Triple helix formi	4305	14	0.5	17	1	ACD55509	HBV amberyzyme subs
4232	14	0.5	14	1	AAV14688	Triple helix formi	C4306	14	0.5	17	1	ACD50744	HBV amberyzyme subs
C4233	14	0.5	14	1	AAV14688	Triple helix formi	4307	14	0.5	17	1	ACD63827	HCV minus strand D
4234	14	0.5	14	1	AAV14688	Triple helix formi	C4308	14	0.5	17	1	ACD58843	HCV DNazyme substr
C4235	14	0.5	14	1	AAV14688	Triple helix formi	4309	14	0.5	17	1	ACD58843	Murine oligonucleo
4236	14	0.5	14	1	AAV14688	Triple helix formi	C4310	14	0.5	17	1	ACD58843	Murine oligonucleo
C4237	14	0.5	14	1	AAV14688	Triple helix formi	4311	14	0.5	17	1	ADB40646	Tumour suppression
4238	14	0.5	14	1	AAV14688	Triple helix formi	C4312	14	0.5	17	1	ADB40646	Tumour suppression
C4239	14	0.5	14	1	AAV14688	Triple helix formi	4313	14	0.5	18	1	AAH74930	Tumour suppression
4240	14	0.5	14	1	AAV14688	Triple helix formi	C4314	14	0.5	18	1	ADC64942	DNA sequence of ca
C4241	14	0.5	14	1	AAV14688	Triple helix formi	4315	14	0.5	18	1	AAV48547	Camellia sinensis
4242	14	0.5	14	1	AAV14688	Triple helix formi	C4316	14	0.5	18	1	AAV48548	p53 gene antisense
C4243	14	0.5	14	1	AAV14688	Triple helix formi	4317	14	0.5	18	1	AAV48548	p53 gene antisense
4244	14	0.5	14	1	AAV14688	Triple helix formi	C4318	14	0.5	18	1	AAZ70573	Human biallelic ma
C4245	14	0.5	14	1	AAV14688	Triple helix formi	4319	14	0.5	18	1	ABX95294	Human ABCA7 associ
4246	14	0.5	14	1	AAV14688	Triple helix formi	C4320	14	0.5	19	1	ADE27175	Stearoyl-CoA desat
C4247	14	0.5	14	1	AAV14688	Triple helix formi	4321	14	0.5	19	1	ADE27465	Forward PCR primer
4248	14	0.5	14	1	AAV14688	Triple helix formi	C4322	14	0.5	19	1	AAZ59379	Cdc 25 hs ribozyme
C4249	14	0.5	14	1	AAV14688	Triple helix formi	4323	14	0.5	19	1	AAA86064	Cdc 25 hs ribozyme
4250	14	0.5	15	1	AAV14688	Triple helix formi	C4324	14	0.5	19	1	AAA86065	Cdc 25 hs ribozyme
C4251	14	0.5	15	1	AAV14688	Triple helix formi	4325	14	0.5	19	1	AAH61226	Cdc25 hs ribozyme
4252	14	0.5	15	1	AAV14688	Triple helix formi	C4326	14	0.5	20	1	AAH61227	Primer 1 for pUC19
C4253	14	0.5	15	1	AAV14688	Triple helix formi	4327	14	0.5	20	1	AAT73291	Primer 2 for pUC19
4254	14	0.5	15	1	AAV14688	Triple helix formi	C4328	14	0.5	20	1	AAT73292	Immunostimulatory
C4255	14	0.5	15	1	AAV14688	Triple helix formi	4329	14	0.5	20	1	ABF77947	Angiogenesis inhib
4256	14	0.5	15	1	AAV14688	Triple helix formi	C4330	14	0.5	20	1	ABL39308	Immunostimulatory
C4257	14	0.5	15	1	AAV14688	Triple helix formi	4331	14	0.5	20	1	ACD99727	Immunostimulatory
4258	14	0.5	15	1	AAV14688	Triple helix formi	C4332	14	0.5	20	1	ADB36804	Immunostimulatory
C4259	14	0.5	15	1	AAV14688	Triple helix formi	4333	14	0.5	20	1	AAQ97488	M. sexta alaserpin
4260	14	0.5	15	1	AAV14688	Triple helix formi	C4334	14	0.5	20	1	AAQ97488	PEBP2 alpha A gene
C4261	14	0.5	15	1	AAV14688	Triple helix formi	4335	14	0.5	20	1	AAQ97488	PEBP2 alpha A gene
4262	14	0.5	15	1	AAV14688	Triple helix formi	C4336	14	0.5	20	1	AAQ97488	PEBP2 alpha A gene
C4263	14	0.5	15	1	AAV14688	Triple helix formi	4337	14	0.5	20	1	AAQ97488	Human caspase 3 an
4264	14	0.5	15	1	AAV14688	Triple helix formi	C4338	14	0.5	20	1	AAQ97488	Human hDPP PCR pri
C4265	14	0.5	15	1	AAV14688	Triple helix formi	4339	14	0.5	20	1	AAQ97488	Human PTP1B antise
4266	14	0.5	15	1	AAV14688	Triple helix formi	4340	14	0.5	20	1	AAQ97488	Human PTP1B antise
C4267	14	0.5	15	1	AAV14688	Triple helix formi							

4487	13.8	0.5	17	1	ADB41005	Tumour suppression
4488	13.8	0.5	17	1	ADB42684	Tumour suppression
C4489	13.8	0.5	17	1	ADB44777	Tumour suppression
C4490	13.8	0.5	17	1	ADB44262	Tumour suppression
C4491	13.8	0.5	17	1	ADD20961	Human GAP N DNA 17
4492	13.8	0.5	17	1	ADE25221	Plant growth assoc
C4493	13.8	0.5	17	1	ADE25221	Plant growth assoc
4494	13.8	0.5	17	1	ADE30707	Cholesterol homeos
4495	13.8	0.5	18	1	AAQ20007	Oligonucleotide #3
C4496	13.8	0.5	18	1	AAQ20007	Oligonucleotide #3
4497	13.8	0.5	18	1	AAQ36431	GRP-R primer (EXT)
4498	13.8	0.5	18	1	AAQ34456	DQA1 probe AG2.3,
4499	13.8	0.5	18	1	AAQ15198	Triple helix formi
C4500	13.8	0.5	18	1	AAQ15198	Triple helix formi
4501	13.8	0.5	18	1	AAT36431	Human papillomavir
4502	13.8	0.5	18	1	AAT93487	DQA1 allele determ
C4503	13.8	0.5	18	1	AAT93488	DQA1 allele determ
C4504	13.8	0.5	18	1	AAQ71708	Human KDR VEGF rec
C4505	13.8	0.5	18	1	AAQ13864	Oligonucleotide-cy
C4506	13.8	0.5	18	1	AAQ63292	Delta-9 desaturase
C4507	13.8	0.5	18	1	AAT98144	Primer V-alpha(16)
C4508	13.8	0.5	18	1	AAV54725	Primer used to det
4509	13.8	0.5	18	1	AAV16008	PCR primer D-R use
C4510	13.8	0.5	18	1	AAQ85987	PCR primer used to
4511	13.8	0.5	18	1	AAQ25592	Human RhoG antisen
C4512	13.8	0.5	18	1	AAQ88163	T cell receptor al
4513	13.8	0.5	18	1	AAQ90266	DQA1 gene PCR prim
C4514	13.8	0.5	18	1	AAQ90267	DQA1 gene PCR prim
4515	13.8	0.5	18	1	AAQ00540	Human adenine nucl
C4516	13.8	0.5	18	1	AAQ275194	Human biallelic ma
4517	13.8	0.5	18	1	AAQ43267	Murine Sox3 gene P
4518	13.8	0.5	18	1	AAQ05252	PCR primer D-R use
C4519	13.8	0.5	18	1	AAQ293440	TRADD antisense ol
4520	13.8	0.5	18	1	AAQ293475	TRADD antisense ol
4521	13.8	0.5	18	1	AAH27102	Heltest4 cleavage
C4522	13.8	0.5	18	1	AAH27102	Heltest4 cleavage
4523	13.8	0.5	18	1	AAH56578	S. pneumoniae groE
4524	13.8	0.5	18	1	AAQ08670	BsgI-AFLP primer/M
4525	13.8	0.5	18	1	AAQ94740	Rho G antisense ph
4526	13.8	0.5	18	1	AAQ05922	Human ANT-3 sequen
C4527	13.8	0.5	18	1	AAQ11767	Human AAG6 DNA exo
4528	13.8	0.5	18	1	AAH91840	Human inflammatory
C4529	13.8	0.5	18	1	ABZ72262	Gene 216 SSCP sequ
4530	13.8	0.5	18	1	ABL54126	Cleavage product o
C4531	13.8	0.5	18	1	ABL54126	Cleavage product o
4532	13.8	0.5	18	1	AAQ97605	Murine SAC1 gene-s
4533	13.8	0.5	18	1	ABL44451	Human chromosome 1
4534	13.8	0.5	18	1	ABQ78689	Cleavage product o
C4535	13.8	0.5	18	1	ABQ78689	Cleavage product o
C4536	13.8	0.5	18	1	ABS52682	mRNA display splin
4537	13.8	0.5	18	1	AAQ95764	Human adenine nucl
4538	13.8	0.5	18	1	ABK94050	Cardiovascular reg
4539	13.8	0.5	18	1	AAQ41291	Human C6ST gene am
4540	13.8	0.5	18	1	ABK87302	FEN 1 nuclease cle
C4541	13.8	0.5	18	1	ABK87302	FEN 1 nuclease cle
C4542	13.8	0.5	18	1	ABK98126	Triple helix formi
C4543	13.8	0.5	18	1	ABX75115	Human gene 216 seq
C4544	13.8	0.5	18	1	ABV75014	Nucleotide sequenc
4545	13.8	0.5	18	1	ADE39920	Human Midkine intr
4546	13.8	0.5	19	1	AAQ20028	Cross-linking olig
4547	13.8	0.5	19	1	AAQ20029	Cross-linking olig
4548	13.8	0.5	19	1	AAQ30375	Oligomer HUM beta
4549	13.8	0.5	19	1	AAQ30374	Oligomer HUM beta
4550	13.8	0.5	19	1	AAQ39059	S. nodosus 2634bp
4551	13.8	0.5	19	1	AAT492298	5' end fragment of
4552	13.8	0.5	19	1	AAT74905	5' end fragment of
4553	13.8	0.5	19	1	AAT47271	Capped RNA influen
4554	13.8	0.5	19	1	AAT47276	Capped RNA influen
4555	13.8	0.5	19	1	AAT47269	Capped RNA influen
4556	13.8	0.5	19	1	AAT47279	Capped RNA influen
4557	13.8	0.5	19	1	AAT47277	Capped RNA influen
4558	13.8	0.5	19	1	AAT47273	Capped RNA influen
4559	13.8	0.5	19	1	AAT47264	5' fragment of alf

4560	13.8	0.5	19	1	AAT47272	Capped RNA influen
4561	13.8	0.5	19	1	AAT47278	Capped RNA influen
4562	13.8	0.5	19	1	AAT47267	Capped RNA influen
4563	13.8	0.5	19	1	AAT47270	Capped RNA influen
4564	13.8	0.5	19	1	AAT50897	Probe #11 for inte
4565	13.8	0.5	19	1	AAQ32232	Probe specific for
4566	13.8	0.5	19	1	AAZ00903	Primer for PGI bia
4567	13.8	0.5	19	1	AAZ01223	PCR primer for PGI
C4568	13.8	0.5	19	1	AAA35512	Myrtaceae microsat
4569	13.8	0.5	19	1	AAZ37261	PCR primer for AV3
C4570	13.8	0.5	19	1	AAA86469	PCBA HH ribozyme b
C4571	13.8	0.5	19	1	AAA84405	Cyclin D3 ribozyme
C4572	13.8	0.5	19	1	AAA84723	Cyclin E ribozyme
C4573	13.8	0.5	19	1	AAA86472	PCBA HH ribozyme b
4574	13.8	0.5	19	1	AAZ70580	Human biallelic ma
4575	13.8	0.5	19	1	AAZ73500	Human biallelic ma
4576	13.8	0.5	19	1	AAA75956	PCR primer used to
C4577	13.8	0.5	19	1	AAH61634	PCNA HH ribozyme b
C4578	13.8	0.5	19	1	AAH61631	PCNA HH ribozyme b
C4579	13.8	0.5	19	1	AAH59885	Cyclin E ribozyme
C4580	13.8	0.5	19	1	AAH59567	Cyclin D3 ribozyme
4581	13.8	0.5	19	1	ABK41301	Human prostate can
4582	13.8	0.5	19	1	AAH42341	Novel sand pear mi
4583	13.8	0.5	19	1	ABK49173	F. oxysporum tryps
4584	13.8	0.5	19	1	ABK90099	Oestrogen response
4585	13.8	0.5	19	1	ACD06509	Forward RT-PCR pri
4586	13.8	0.5	19	1	ACD06722	Forward RT-PCR pri
C4587	13.8	0.5	19	1	ADA25723	Human REL-A short
4588	13.8	0.5	19	1	ADA26072	Human REL-A short
4589	13.8	0.5	19	1	ADA45472	Human BAP1 DNA pro
C4590	13.8	0.5	19	1	ACD99555	Immunostimulatory
4591	13.8	0.5	19	1	ACD07875	F. oxysporum tryps
4592	13.8	0.5	19	1	ADD00126	HCV coding region-
4593	13.8	0.5	19	1	ADD00278	HCV coding region-
4594	13.8	0.5	19	1	ADD19509	Salmo salar SNP PC
4595	13.8	0.5	19	1	ABE65619	Human c-fos transc
C4596	13.8	0.5	19	1	ABE65735	Human c-fos siNA 1
C4597	13.8	0.5	19	1	ADE36637	Human ERG gene PCR
4598	13.8	0.5	19	1	ADE43577	Human IDE sequenci
4599	13.8	0.5	19	1	ADE29797	Mitogen activated
C4600	13.8	0.5	19	1	ADE29902	Mitogen activated
C4601	13.8	0.5	20	1	AAQ4537	Antisense oligonuc
4602	13.8	0.5	20	1	ABZ89720	Human oligonucleot
C4603	13.8	0.5	20	1	AAQ32003	MSH2 gene specific
C4604	13.8	0.5	20	1	AAQ82921	Human S-9 derived
C4605	13.8	0.5	20	1	ADA45244	Human MSH2 gene PC
4606	13.8	0.5	20	1	AAQ20027	Cross-linking olig
4607	13.8	0.5	20	1	AAQ30372	Oligomer HUM beta
C4608	13.8	0.5	20	1	AAA94534	Antisense oligonuc
C4609	13.8	0.5	20	1	ABZ89084	Human oligonucleot
C4610	13.8	0.5	20	1	ACF57337	Human atlastin exo
C4611	13.8	0.5	20	1	AAA55978	Human G713 PCR pri
4612	13.8	0.5	20	1	ABZ89489	Human oligonucleot
4613	13.8	0.5	20	1	AAQ43126	HCV type 2 NS-4 se
C4614	13.8	0.5	20	1	AAQ41528	Antisense oligomer
C4615	13.8	0.5	20	1	AAQ47650	Mouse jun-B MUSJUN
C4616	13.8	0.5	20	1	AAQ56662	Bacteriophage lamb
4617	13.8	0.5	20	1	AAQ64082	NANBHV NS1/NS2 (EN
C4618	13.8	0.5	20	1	AAQ45269	Primer to amplify
4619	13.8	0.5	20	1	AAQ98982	H1 extra exon reve
C4620	13.8	0.5	20	1	AAT41105	HEV ORF2.0 PCR 5'
4621	13.8	0.5	20	1	AAQ86599	Antisense oligonuc
4622	13.8	0.5	20	1	AAQ86829	Maize acetyl CoA c
C4623	13.8	0.5	20	1	AAT39924	Primer 5 for ampli
C4624	13.8	0.5	20	1	AAT44306	Mouse gut RNA ampli
C4625	13.8	0.5	20	1	AAV06314	Detector probe 1 f
C4626	13.8	0.5	20	1	AAT88934	5' fragment #2 of
4627	13.8	0.5	20	1	AAT47265	Primer Sf MI -25+
4628	13.8	0.5	20	1	AAV20640	Nucleotide sequenc
4629	13.8	0.5	20	1	AAV07136	Primer Sf MI -25+
4630	13.8	0.5	20	1	AAV16787	Nucleotide sequenc
4631	13.8	0.5	20	1	AAV53579	Retroviral DNA bas
4632	13.8	0.5	20	1	AAV19518	

C4633	13.8	0.5	20	1	AAV68581	Nucleotide sequenc
C4634	13.8	0.5	20	1	AAV28931	Bovine Nramp1 clon
4635	13.8	0.5	20	1	AAV36926	S. cereale microsa
4636	13.8	0.5	20	1	AAV74259	CpG-N motif oligon
C4637	13.8	0.5	20	1	AAV74259	CpG-N motif oligon
C4638	13.8	0.5	20	1	AAZ02544	PCR primer used to
C4639	13.8	0.5	20	1	AAZ02339	PCR primer used to
4640	13.8	0.5	20	1	AAZ03397	PCR primer used to
4641	13.8	0.5	20	1	AAZ02828	PCR primer used to
4642	13.8	0.5	20	1	AAZ26623	PCR primer used to
4643	13.8	0.5	20	1	AAZ23851	Rye mircrosatellit
C4644	13.8	0.5	20	1	AAZ93392	PCR primer used to
4645	13.8	0.5	20	1	AAZ95000	PCR primer used to
4646	13.8	0.5	20	1	AAZ81592	PCR primer used to
4647	13.8	0.5	20	1	AAZ29455	Rat JNK3-specific
C4648	13.8	0.5	20	1	AAZ86719	Antisense inhibito
C4649	13.8	0.5	20	1	AAZ49841	PCR primer 28sst-1
C4650	13.8	0.5	20	1	AAA40867	Murine TNFalpha an
C4651	13.8	0.5	20	1	AAZ28947	PCR primer cl14 fo
C4652	13.8	0.5	20	1	AAZ59205	Forward PCR primer
C4653	13.8	0.5	20	1	AAZ59204	Second strand cDNA
C4654	13.8	0.5	20	1	AAA94533	Antisense oligonuc
4655	13.8	0.5	20	1	AAA38540	Jellyfish green fl
4656	13.8	0.5	20	1	AAZ29763	Human thymidylate
C4657	13.8	0.5	20	1	AAZ56191	Oligonucleotide A1
4658	13.8	0.5	20	1	ABK12263	Capra hircus aegag
4659	13.8	0.5	20	1	AAC62998	JNK antisense olig
C4660	13.8	0.5	20	1	AAC64800	Human plakophilin-
4661	13.8	0.5	20	1	AAZ74057	Forward PCR primer
C4662	13.8	0.5	20	1	AAF31794	Human RANK antisen
C4663	13.8	0.5	20	1	AAH75301	Mouse inducible NO
C4664	13.8	0.5	20	1	AAK95000	Human cdna clone-s
4665	13.8	0.5	20	1	AAF73065	Human daxx inhibit
C4666	13.8	0.5	20	1	AAZ5802	Mouse PARP-2 antis
4667	13.8	0.5	20	1	AAC92903	Human PI3 kinase p
4668	13.8	0.5	20	1	AAC92905	Human PI3 kinase p
C4669	13.8	0.5	20	1	AAH77763	PCR primer for hum
4670	13.8	0.5	20	1	AAH21418	C. lanceolata KASI
C4671	13.8	0.5	20	1	AAZ00481	Human FIRE cdna PC
4672	13.8	0.5	20	1	AAH56777	S. aureus groE ope
4673	13.8	0.5	20	1	AAF99014	Immunostimulatory
C4674	13.8	0.5	20	1	AAF99014	Immunostimulatory
C4675	13.8	0.5	20	1	AAZ43136	Human ERbeta Gene,
4676	13.8	0.5	20	1	AAH39349	SNP specific upper
C4677	13.8	0.5	20	1	AAH40269	SNP specific upper
C4678	13.8	0.5	20	1	AAZ54439	Primer for amplify
4679	13.8	0.5	20	1	AAD09639	Human PKA C-alpha
4680	13.8	0.5	20	1	AAD09640	Human HLA Class I
C4681	13.8	0.5	20	1	AAF54613	Human HLA Class I
C4682	13.8	0.5	20	1	AAF54596	Human HLA Class I
C4683	13.8	0.5	20	1	AAF54612	Human HLA Class I
C4684	13.8	0.5	20	1	AAF54615	Human HLA Class I
C4685	13.8	0.5	20	1	AAF54617	Human HLA Class I
4686	13.8	0.5	20	1	AAH40966	Primer SEQ ID 14 u
4687	13.8	0.5	20	1	AAZ12283	DNA encoding class
4688	13.8	0.5	20	1	AAD17451	Human TNF-alpha cD
4689	13.8	0.5	20	1	AAH49468	D. melanogaster pe
C4690	13.8	0.5	20	1	ABK53147	HIV-1 Gag gene spe
C4691	13.8	0.5	20	1	ABQ82398	Human NOV4 forward
4692	13.8	0.5	20	1	ABK13157	En8183 EN transpos
4693	13.8	0.5	20	1	ABK11174	PCR primer #1 for
4694	13.8	0.5	20	1	AAD46658	Human ABCC11 exon2
4695	13.8	0.5	20	1	ABN74918	Mouse caspase 2 an
4696	13.8	0.5	20	1	ABS52754	Ferrocene-type pol
C4697	13.8	0.5	20	1	ABS52755	Ferrocene-type pol
C4698	13.8	0.5	20	1	AAS97619	Murine SAC1 gene-s
4699	13.8	0.5	20	1	ABN89247	Human Talin antise
4700	13.8	0.5	20	1	ABS77655	Angiogenesis inhib
C4701	13.8	0.5	20	1	ABS77655	Angiogenesis inhib
C4702	13.8	0.5	20	1	ABT07491	Rat protein phosph
4703	13.8	0.5	20	1	ABL38801	Immunostimulatory
C4704	13.8	0.5	20	1	ABL38801	Immunostimulatory
4705	13.8	0.5	20	1	ABL59017	Nucleotide sequenc
1	13.8	0.5	20	1	ABQ92966	T. tauschii/wheat
1	13.8	0.5	20	1	ABN99676	Human clusterin in
1	13.8	0.5	20	1	ABA89809	Human oestrogen re
1	13.8	0.5	20	1	AAL40388	Mouse caspase 6 an
1	13.8	0.5	20	1	ABA02214	Human/mouse C/EBP
1	13.8	0.5	20	1	AAD29918	Mouse TID-1 cdna 5
1	13.8	0.5	20	1	ABK94486	Human BRCA1 gene r
1	13.8	0.5	20	1	ABS59782	Human damage speci
1	13.8	0.5	20	1	AAD30205	Human UGT1A6-1 gen
1	13.8	0.5	20	1	ABA97649	probe t. Unidenti
1	13.8	0.5	20	1	ABA97648	probe s. Unidenti
1	13.8	0.5	20	1	ABA97650	probe u. Unidenti
1	13.8	0.5	20	1	AAD39347	Human Von Willebra
1	13.8	0.5	20	1	ABL94407	Mouse C/EBP beta p
1	13.8	0.5	20	1	ABI95113	Capture oligonucle
1	13.8	0.5	20	1	ABI95444	Capture oligonucle
1	13.8	0.5	20	1	ABI94329	Capture oligonucle
1	13.8	0.5	20	1	AAL41524	Oligonucleotide in
1	13.8	0.5	20	1	AAL45509	HIV-1 gag amplific
1	13.8	0.5	20	1	ABS59590	Real-time forward
1	13.8	0.5	20	1	ABZ85453	Human oligonucleot
1	13.8	0.5	20	1	ABZ88060	Human oligonucleot
1	13.8	0.5	20	1	ABZ88985	Human oligonucleot
1	13.8	0.5	20	1	ABZ90674	Human oligonucleot
1	13.8	0.5	20	1	ABZ93123	Human oligonucleot
1	13.8	0.5	20	1	ABZ88828	Human oligonucleot
1	13.8	0.5	20	1	ABZ89594	Human oligonucleot
1	13.8	0.5	20	1	ABZ90507	Human oligonucleot
1	13.8	0.5	20	1	ABZ97297	Human nucleic acid
1	13.8	0.5	20	1	ABZ86168	Human oligonucleot
1	13.8	0.5	20	1	ABZ94127	Human oligonucleot
1	13.8	0.5	20	1	ABZ85671	Human oligonucleot
1	13.8	0.5	20	1	ABZ86919	Human oligonucleot
1	13.8	0.5	20	1	ABZ99084	Human PDE4C Oligon
1	13.8	0.5	20	1	ABZ93066	Human oligonucleot
1	13.8	0.5	20	1	ABZ85437	Human oligonucleot
1	13.8	0.5	20	1	ABZ91047	Human oligonucleot
1	13.8	0.5	20	1	ABZ91735	Human oligonucleot
1	13.8	0.5	20	1	ABZ85702	Human oligonucleot
1	13.8	0.5	20	1	ABZ85292	Human oligonucleot
1	13.8	0.5	20	1	ABZ85546	Human oligonucleot
1	13.8	0.5	20	1	ABZ89893	Human oligonucleot
1	13.8	0.5	20	1	ABZ98459	Human ICAM oligonu
1	13.8	0.5	20	1	ABZ88711	Human oligonucleot
1	13.8	0.5	20	1	ABZ87697	Human oligonucleot
1	13.8	0.5	20	1	ABZ88668	Human oligonucleot
1	13.8	0.5	20	1	ABZ92288	Human oligonucleot
1	13.8	0.5	20	1	ABZ98730	Human oligonucleot
1	13.8	0.5	20	1	ABX13312	Human oligonucleot
1	13.8	0.5	20	1	ACC62221	Human tryptase a o
1	13.8	0.5	20	1	ABT34071	Human alipoprotein
1	13.8	0.5	20	1	ACC55341	Human NSDHL gene,
1	13.8	0.5	20	1	ACC45351	Mouse alipoprotein
1	13.8	0.5	20	1	ADA26702	Human ADAMTS13 exo
1	13.8	0.5	20	1	ABZ58576	Escherichia coli s
1	13.8	0.5	20	1	AAD55426	Rat Jun N-terminal
1	13.8	0.5	20	1	ABX12687	Chitinase YM-3 for
1	13.8	0.5	20	1	ACA60924	Human IL-4/IL-13 r
1	13.8	0.5	20	1	ACF39518	Caenorhabditis ele
1	13.8	0.5	20	1	ACD99446	BARCODE-MAT HPV re
1	13.8	0.5	20	1	ACD99446	Immunostimulatory
1	13.8	0.5	20	1	ACD05095	Immunostimulatory
1	13.8	0.5	20	1	ADB36516	Tumour necrosis fa
1	13.8	0.5	20	1	ADB36516	Immunostimulatory
1	13.8	0.5	20	1	ADB74233	Immunostimulatory
1	13.8	0.5	20	1	ADC65850	Human GPR34 PCR pr
1	13.8	0.5	20	1	AAD61201	Mouse TGF-beta rec
1	13.8	0.5	20	1	ADE43707	Human Ship-1 antis
1	13.8	0.5	20	1	ADE14470	Human KNSL1 sequen
1	13.8	0.5	21	1	AAZ26714	HSD11B1 antisense
1	13.8	0.5	21	1	AAQ10724	Human polymorphic
1	13.8	0.5	21	1	AAQ22345	Mutagenising oligo
1	13.8	0.5	21	1	AAQ28771	Antisense oligonuc
1	13.8	0.5	21	1	AAQ28771	HLA Class II gene

c4779	13.8	0.5	21	1	AAQ24706	J-beta-1b primer.
4780	13.8	0.5	21	1	AAT14900	Primer 6 for 3' po
4781	13.8	0.5	21	1	AAQ55571	Sequence of synthe
4782	13.8	0.5	21	1	AAQ67230	Triple helix-formi
4783	13.8	0.5	21	1	AAQ44571	Antisense oligonuc
4784	13.8	0.5	21	1	AAQ79210	Guanosine rich oli
4785	13.8	0.5	21	1	AAQ56046	Primer 5 to isolat
4786	13.8	0.5	21	1	AAQ70078	CZP2(487-713) prim
4787	13.8	0.5	21	1	AAT01778	Peptide nucleic ac
4788	13.8	0.5	21	1	AAT36683	Antisense oligonuc
4789	13.8	0.5	21	1	AAT51628	Viral integrase in
4790	13.8	0.5	21	1	AAT59010	beta3-adrenergic r
4791	13.8	0.5	21	1	AAT84680	KSHV glycoprotein
4792	13.8	0.5	21	1	AAT76136	Human eosinophil p
4793	13.8	0.5	21	1	AAV05263	Antisense primer u
4794	13.8	0.5	21	1	AAV79217	Oligonucleotide #1
4795	13.8	0.5	21	1	AAV40572	Human TSC gene exo
c4796	13.8	0.5	21	1	AAV40572	Human polymorphic
4797	13.8	0.5	21	1	AAZ26192	Human AUR2 inhibit
4798	13.8	0.5	21	1	AAV99727	HIV-2 ENV region p
4799	13.8	0.5	21	1	AAV63682	Eosinophil peroxid
4800	13.8	0.5	21	1	AAV53935	Exemplary oligonuc
4801	13.8	0.5	21	1	AAZ21762	Low adenosine anti
4802	13.8	0.5	21	1	AAA33375	Human caspase-9 PC
c4803	13.8	0.5	21	1	AAZ55720	Human biallelic ma
c4804	13.8	0.5	21	1	AAZ73879	Human biallelic ma
4805	13.8	0.5	21	1	AAZ75815	Human eosinophil p
4806	13.8	0.5	21	1	AAF19497	Antisense oligonuc
c4807	13.8	0.5	21	1	AAA62937	Human ELAM-1 antis
4808	13.8	0.5	21	1	AAZ48932	Oligonucleotide pro
4809	13.8	0.5	21	1	AAA57738	Oligonucleotide pro
c4810	13.8	0.5	21	1	AAA57739	HIV primer 2ENV-R2
4811	13.8	0.5	21	1	AAA73988	Streptococcus pneu
c4812	13.8	0.5	21	1	ADE80908	SNP containing pro
c4813	13.8	0.5	21	1	AAV06843	Human gene single
4814	13.8	0.5	21	1	AAF97680	Human gene single
4815	13.8	0.5	21	1	AAF97544	Human gene single
c4816	13.8	0.5	21	1	AAF97617	Human gene single
4817	13.8	0.5	21	1	AAF97628	Human gene single
4818	13.8	0.5	21	1	AAF96104	Human gene single
4819	13.8	0.5	21	1	AAF96440	Human gene single
4820	13.8	0.5	21	1	AAF97321	Human gene single
c4821	13.8	0.5	21	1	AAH62300	GLI-kruppel family
4822	13.8	0.5	21	1	AAH28431	PCR primer for int
4823	13.8	0.5	21	1	AAH12205	Human inflammatory
c4824	13.8	0.5	21	1	AAH91420	PCR primer used to
4825	13.8	0.5	21	1	AAF85206	Human polymorphic
c4826	13.8	0.5	21	1	AAH89104	Bacterial 16s RNA
4827	13.8	0.5	21	1	AAS11076	Bacterial 16s RNA
4828	13.8	0.5	21	1	AAS11058	Bacterial 16s RNA
c4829	13.8	0.5	21	1	AAS11038	HIV-1 Gag gene spe
c4830	13.8	0.5	21	1	ABK53146	HIV-1 Gag gene spe
c4831	13.8	0.5	21	1	ABK53111	Human single nucle
4832	13.8	0.5	21	1	ABK65817	Human cholecystoki
c4833	13.8	0.5	21	1	ABK88537	RT-PCR primer used
4834	13.8	0.5	21	1	ABQ78573	Human NOV5 forward
4835	13.8	0.5	21	1	ABV99452	Human chromosome 1
c4836	13.8	0.5	21	1	ABL44206	Polyimmunoglobulin
4837	13.8	0.5	21	1	ABK81198	Human soluble LIGH
c4838	13.8	0.5	21	1	AAD22905	Human endogenous r
4839	13.8	0.5	21	1	ABX04726	HIV-1 gag amplific
c4840	13.8	0.5	21	1	AAL45508	HIV-1 gag amplific
c4841	13.8	0.5	21	1	AAL45473	FEN-1 related DNA
c4842	13.8	0.5	21	1	ADE53231	Human eosinophil p
4843	13.8	0.5	21	1	ABZ95191	Exemplary oligonuc
4844	13.8	0.5	21	1	ABQ83714	Human pigmentatio
c4845	13.8	0.5	21	1	ABT33998	Human G-protein co
4846	13.8	0.5	21	1	ACC70856	Cardiovascular dis
4847	13.8	0.5	21	1	ACA90032	Forward PCR primer
c4848	13.8	0.5	21	1	ABZ23347	Human REL-A short
4849	13.8	0.5	21	1	ADA26144	Human CD31 (PECAM)
c4850	13.8	0.5	21	1	ACC78817	Human ELAM-1 targe
4851	13.8	0.5	21	1	ADC39012	
c4852	13.8	0.5	21	1	C4852	Human src biomarke
c4853	13.8	0.5	21	1	C4853	Human CYP2E1 mutan
c4854	13.8	0.5	21	1	C4854	Human G-protein co
c4855	13.8	0.5	22	1	C4855	Human Huntington's
4856	13.8	0.5	25	1	4856	16s rRNA gene PCR
4857	13.8	0.5	25	1	4857	HLA DRB345 gene PC
c4858	13.8	0.5	25	1	C4858	16s rRNA gene PCR
c4859	13.8	0.5	25	1	C4859	HLA DPB1 gene PCR
c4860	13.8	0.5	25	1	C4860	16s rRNA gene PCR
c4861	13.8	0.5	28	1	C4861	ON-41 oligonucleot
c4862	13.6	0.5	15	1	C4862	Human GSR allele s
4863	13.6	0.5	15	1	4863	Human MPP3 gene po
4864	13.6	0.5	15	1	4864	Human APPBP1 gene,
c4865	13.6	0.5	15	1	C4865	Human APPBP1 gene,
c4866	13.6	0.5	20	1	C4866	Human beta-actin d
c4867	13.6	0.5	20	1	C4867	Human beta-actin d
4868	13.6	0.5	20	1	4868	Human oligonucleot
c4869	13.6	0.5	20	1	C4869	Human oligonucleot
c4870	13.6	0.5	20	1	C4870	Human oligonucleot
c4871	13.6	0.5	20	1	C4871	Probe to 35kd pulm
4872	13.6	0.5	20	1	4872	Probe AD03 to dete
c4873	13.6	0.5	20	1	C4873	EIV 5' fragment pr
4874	13.6	0.5	20	1	4874	Antisense oligomer
4875	13.6	0.5	20	1	4875	Sequence of PCR pr
c4876	13.6	0.5	20	1	C4876	Blocker oligonucle
c4877	13.6	0.5	20	1	C4877	C-myc gene antisen
4878	13.6	0.5	20	1	4878	Primer for the det
c4879	13.6	0.5	20	1	C4879	Phage lambda J gen
4880	13.6	0.5	20	1	4880	Human gene signatu
c4881	13.6	0.5	20	1	C4881	Human gene signatu
c4882	13.6	0.5	20	1	C4882	Antisense oligomer
c4883	13.6	0.5	20	1	C4883	Multi-tumour aberr
c4884	13.6	0.5	20	1	C4884	Antisense oligonuc
c4885	13.6	0.5	20	1	C4885	Antisense oligonuc
c4886	13.6	0.5	20	1	C4886	Complementary huma
c4887	13.6	0.5	20	1	C4887	Probe #17 for inte
c4888	13.6	0.5	20	1	C4888	Treatment of human
c4889	13.6	0.5	20	1	C4889	Mouse Apo E forwar
4890	13.6	0.5	20	1	4890	Primer #35 for cys
c4891	13.6	0.5	20	1	C4891	Human tumour necro
c4892	13.6	0.5	20	1	C4892	Third-strand oligo
4893	13.6	0.5	20	1	4893	Locl-specific prim
4894	13.6	0.5	20	1	4894	Rat insulin-like g
4895	13.6	0.5	20	1	4895	Human PRCC-TFE3 co
c4896	13.6	0.5	20	1	C4896	Human Notch-3 muta
4897	13.6	0.5	20	1	4897	PCR primer 1 used
c4898	13.6	0.5	20	1	C4898	Antisense MDR1 oli
c4899	13.6	0.5	20	1	C4899	ErbB-2 gene antisense
c4900	13.6	0.5	20	1	C4900	JunB gene antisense
4901	13.6	0.5	20	1	4901	Mouse c-Fos protei
c4902	13.6	0.5	20	1	C4902	Human Notch3 mutan
4903	13.6	0.5	20	1	4903	Mouse alpha 3 conn
4904	13.6	0.5	20	1	4904	BMP-1A DNA amplif
c4905	13.6	0.5	20	1	C4905	Human mdm2 phospho
c4906	13.6	0.5	20	1	C4906	Human N-ras specif
c4907	13.6	0.5	20	1	C4907	Ras gene modulatin
4908	13.6	0.5	20	1	4908	CCR5 gene inhibiti
4909	13.6	0.5	20	1	4909	CXCR4 gene inhibit
c4910	13.6	0.5	20	1	C4910	DNA tandem nucleot
c4911	13.6	0.5	20	1	C4911	Tumour necrosis fa
c4912	13.6	0.5	20	1	C4912	PEBP2 alpha A gene
4913	13.6	0.5	20	1	4913	PCR primer used to
4914	13.6	0.5	20	1	4914	PCR primer used to
4915	13.6	0.5	20	1	4915	PCR primer used to
4916	13.6	0.5	20	1	4916	PCR primer used to
4917	13.6	0.5	20	1	4917	PCR primer used to
4918	13.6	0.5	20	1	4918	PCR primer used to
4919	13.6	0.5	20	1	4919	Peritoneal macroph
c4920	13.6	0.5	20	1	C4920	PCR primer p38-S25
4921	13.6	0.5	20	1	4921	ASTH1 gene intron/
c4922	13.6	0.5	20	1	C4922	PCR primer used to
c4923	13.6	0.5	20	1	C4923	PCR primer used to
4924	13.6	0.5	20	1	4924	PCR primer used to

c4925 13.6 0.5 20 1 AAX95057 PCR primer used to
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4927 13.6 0.5 20 1 AAZ28022 Seq ID No: 8 of WO
c4928 13.6 0.5 20 1 AAZ47566 Antisense oligonuc
4929 13.6 0.5 20 1 AAZ48056 Human IGF-II antis
c4930 13.6 0.5 20 1 AAA60405 Human telomerase a
c4931 13.6 0.5 20 1 AAA33978 Low adenosine anti
4932 13.6 0.5 20 1 AAZ46619 Reverse primer spe
4933 13.6 0.5 20 1 AAA46764 Oligonucleotide se
4934 13.6 0.5 20 1 AAA40976 Human TNFalpha ant
c4935 13.6 0.5 20 1 AAA59816 Primer for RIP 140
c4936 13.6 0.5 20 1 AAA90438 Mouse GANP reverse
4937 13.6 0.5 20 1 AAA99058 Porcine virus acti
4938 13.6 0.5 20 1 AAA09616 Primer SEQ ID 8 us
4939 13.6 0.5 20 1 AAA13090 PCR primer used fo
4940 13.6 0.5 20 1 AAZ99922 PCR primer used to
c4941 13.6 0.5 20 1 AAA94525 Antisense oligonuc
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4944 13.6 0.5 20 1 AAC61860 Antisense oligonuc
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4946 13.6 0.5 20 1 AAA07907 Hs-UNC-53/2 specif
4947 13.6 0.5 20 1 AAZ74552 Human biallelic ma
4948 13.6 0.5 20 1 AAZ75568 Human biallelic ma
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4952 13.6 0.5 20 1 AAC55854 PCR primer used to
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c4957 13.6 0.5 20 1 AAF20100 Human tumour necro
c4958 13.6 0.5 20 1 AAA15603 Reverse PCR primer
c4959 13.6 0.5 20 1 AAA57980 Candida albicans T
4960 13.6 0.5 20 1 AAA86885 Probe for wild typ
c4961 13.6 0.5 20 1 AAC93192 Human STAT3 phosph
4962 13.6 0.5 20 1 AAA80584 Human ASTH1J gene
c4963 13.6 0.5 20 1 ABL57553 Synthetic deoxyrib
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4970 13.6 0.5 20 1 AAS01198 Human RAD51 antis
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4972 13.6 0.5 20 1 AAC67211 Human E2F transcri
c4973 13.6 0.5 20 1 AAF73008 Human daxx inhibi
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4975 13.6 0.5 20 1 AAC92738 Human hnrNP A1 pho
4976 13.6 0.5 20 1 AAH57065 Human oestrogen re
4977 13.6 0.5 20 1 AAH57065 Human oestrogen re
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4980 13.6 0.5 20 1 AAH25808 Adipogenesis inhib
4981 13.6 0.5 20 1 AAH25827 Streptococcus pyog
4982 13.6 0.5 20 1 AAH56682 S. pneumoniae groE
4983 13.6 0.5 20 1 AAH56570 Escherichia coli g
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4986 13.6 0.5 20 1 AAF29930 Human estrogen rec
4987 13.6 0.5 20 1 AAF99650 Immunostimulatory
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4994 13.6 0.5 20 1 AAC67698 Oligonucleotide #9
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4997 13.6 0.5 20 1 AAF24291 Complementary nucl

4998 13.6 0.5 20 1 AAH47246 Human C-PLACE10032
4999 13.6 0.5 20 1 AAC82915 Human beta-actin d
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5002 13.6 0.5 20 1 AAD09641 Human PKA C-alpha
5003 13.6 0.5 20 1 AAS08736 Human PD-ABC form
5004 13.6 0.5 20 1 AAS08736 Human PD-ABC form
5005 13.6 0.5 20 1 AAS08827 Genomic DNA methyl
5006 13.6 0.5 20 1 AAI98550 Primer #22. Homo
c5007 13.6 0.5 20 1 AAF75050 Human BCMP 11 cDNA
5008 13.6 0.5 20 1 AAS12922 PDGF B hairpin/ham
5009 13.6 0.5 20 1 AAH62087 Breast cancer-asso
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5017 13.6 0.5 20 1 ABA81742 PCR primer KP212.
5018 13.6 0.5 20 1 ABK90287 Bcl-2-targeting an
5019 13.6 0.5 20 1 AAD43244 Antisense oligonuc
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c5021 13.6 0.5 20 1 ABA91533 DNA oligonucleotid
5022 13.6 0.5 20 1 ABA91527 DNA-RNA-DNA oligon
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5024 13.6 0.5 20 1 ABQ65299 Human gene methyl
5025 13.6 0.5 20 1 ABK85429 Oligonucleotide #7
5026 13.6 0.5 20 1 AAD41025 Mouse PI3K p85 ant
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5029 13.6 0.5 20 1 AAS97811 Murine SAC1 gene-s
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5045 13.6 0.5 20 1 ABK34037 Human CSNK2B PCR p
5046 13.6 0.5 20 1 ABK67993 Mutant DNA library
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5052 13.6 0.5 20 1 ABN79650 Mouse Fas chimeric
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5054 13.6 0.5 20 1 ABL43506 Human chromosome 1
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5057 13.6 0.5 20 1 ABA98707 PCR primer RI. Sy
5058 13.6 0.5 20 1 ABV72239 Antisense oligonuc
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c5060 13.6 0.5 20 1 ABK37370 Rat PTP1B mRNA lev
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5062 13.6 0.5 20 1 AAD35748 Human hIbeta4BP an
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5064 13.6 0.5 20 1 ABA97633 Poly o nucleotide
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5069 13.6 0.5 20 1 ABK28025 Human CSNK2B methy
5070 13.6 0.5 20 1 ABK69224 Human phosphorylas

5071	13.6	0.5	20	1	ABK88956	Interleukin-10 (IL	c5144	13.6	0.5	20	1	ABX10791	Human dual specifi
5072	13.6	0.5	20	1	ABQ74646	Ki67 gene antisens	5145	13.6	0.5	20	1	AAD55805	Major ampullate sp
c5073	13.6	0.5	20	1	ABL94461	Mouse C/EBP beta p	5146	13.6	0.5	20	1	AAL53961	DNA mutation detec
5074	13.6	0.5	20	1	ABL94394	Mouse C/EBP beta p	5147	13.6	0.5	20	1	AAL53959	DNA mutation detec
c5075	13.6	0.5	20	1	ABL94252	Human C/EBP beta p	c5148	13.6	0.5	20	1	AAL53967	DNA mutation detec
5076	13.6	0.5	20	1	ABS70610	Dendritic cell sti	5149	13.6	0.5	20	1	AAL53958	DNA mutation detec
c5077	13.6	0.5	20	1	ABI94166	Capture oligonucle	c5150	13.6	0.5	20	1	AAL53962	DNA mutation detec
5078	13.6	0.5	20	1	ABI94468	Capture oligonucle	5151	13.6	0.5	20	1	AAL53960	DNA mutation detec
5079	13.6	0.5	20	1	ABL54171	Oligonucleotide.	c5152	13.6	0.5	20	1	AAL53964	DNA mutation detec
c5080	13.6	0.5	20	1	ABZ89486	Human oligonucleot	c5153	13.6	0.5	20	1	AAL53966	DNA mutation detec
5081	13.6	0.5	20	1	ABZ89718	Human oligonucleot	5154	13.6	0.5	20	1	ABT32534	Neuroblastoma-rela
5082	13.6	0.5	20	1	ABZ99083	Human PDE4C oligon	5155	13.6	0.5	20	1	ABT32356	Neuroblastoma-rela
5083	13.6	0.5	20	1	ABZ91619	Human oligonucleot	c5156	13.6	0.5	20	1	AAL61847	Human ETBR-LP-2 an
c5084	13.6	0.5	20	1	ABZ91619	Human oligonucleot	c5157	13.6	0.5	20	1	ACD99656	Immunostimulatory
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c5086	13.6	0.5	20	1	ABZ86522	Human oligonucleot	c5159	13.6	0.5	20	1	ACD99816	Immunostimulatory
5087	13.6	0.5	20	1	ABZ88944	Human oligonucleot	c5160	13.6	0.5	20	1	ACH03191	Immunostimulatory
c5088	13.6	0.5	20	1	ABZ89490	Human oligonucleot	5161	13.6	0.5	20	1	ACF06256	Human NOV4 probe s
c5090	13.6	0.5	20	1	ABZ89503	Human oligonucleot	c5162	13.6	0.5	20	1	ABT43815	Human PIP5K1a anti
5091	13.6	0.5	20	1	ABZ90826	Human oligonucleot	5163	13.6	0.5	20	1	ACF05559	Human secreted pro
5092	13.6	0.5	20	1	ABZ98749	Human tryptase a o	5164	13.6	0.5	20	1	ACD05204	Tumour necrosis fa
5093	13.6	0.5	20	1	ABZ98961	Human PDE4A oligon	c5165	13.6	0.5	20	1	AAL61587	Human inhibitor-ka
5094	13.6	0.5	20	1	ABZ90740	Human oligonucleot	5166	13.6	0.5	20	1	ADB93133	Human Type II coll
c5095	13.6	0.5	20	1	ABZ99023	Human oligonucleot	c5167	13.6	0.5	20	1	ADB37152	Immunostimulatory
c5096	13.6	0.5	20	1	ABZ90288	Human oligonucleot	c5168	13.6	0.5	20	1	ADB36727	Immunostimulatory
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c5100	13.6	0.5	20	1	ABZ97376	Human IL4-R oligon	5171	13.6	0.5	20	1	ADC23725	Human NOVX forward
5101	13.6	0.5	20	1	ABZ89225	Human oligonucleot	c5172	13.6	0.5	20	1	ADC13699	Pediococcus detect
c5102	13.6	0.5	20	1	ABZ95794	Human oligonucleot	c5173	13.6	0.5	20	1	ADC53902	Oligonucleotide 16
5103	13.6	0.5	20	1	ABZ89376	Human tumour necro	5174	13.6	0.5	20	1	AAD60260	Oreochromis niloti
c5104	13.6	0.5	20	1	ABZ92584	Human oligonucleot	5175	13.6	0.5	20	1	ADD20133	Human mdm2 antisen
c5105	13.6	0.5	20	1	ABZ98728	Human tryptase a o	c5176	13.6	0.5	20	1	ADD21650	SNP typing-related
c5106	13.6	0.5	20	1	ABZ98829	Human oligonucleot	c5177	13.6	0.5	20	1	ADD68563	SNP typing-related
c5107	13.6	0.5	20	1	ABZ87741	Human oligonucleot	5178	13.6	0.5	20	1	ADD68537	Human gene express
c5108	13.6	0.5	20	1	ABZ90974	Human oligonucleot	5180	13.6	0.5	20	1	ADD56647	Forward Ag5892 RT-
c5109	13.6	0.5	20	1	ABZ91436	Human oligonucleot	c5181	13.6	0.5	20	1	ADE28930	HRAS gene regulator
c5110	13.6	0.5	20	1	ABZ88937	Human oligonucleot	c5182	13.6	0.5	20	1	ADE86164	RET gene regulator
5111	13.6	0.5	20	1	ABZ98627	Human tryptase a o	c5183	13.6	0.5	20	1	ADE86160	HIV PRT antisense
5112	13.6	0.5	20	1	ABZ85307	Human oligonucleot	c5184	13.6	0.5	20	1	ADD81701	HIV PRT antisense
c5113	13.6	0.5	20	1	ABZ85307	Human oligonucleot	c5185	13.6	0.5	20	1	ADD81281	HIV PRT antisense
c5114	13.6	0.5	20	1	ABZ93877	Human oligonucleot	5186	13.6	0.5	20	1	ADD81478	HIV PRT antisense
c5115	13.6	0.5	20	1	ABZ99269	Human PDE4C oligon	c5187	13.6	0.5	20	1	ADD81703	HIV PRT antisense
c5116	13.6	0.5	20	1	ABZ88750	Human oligonucleot	c5188	13.6	0.5	20	1	ADE10334	Plasmid pKN108-der
5117	13.6	0.5	20	1	ABZ92509	Human oligonucleot	5189	13.6	0.5	20	1	ADE10335	Plasmid pKN108-der
c5118	13.6	0.5	20	1	ABZ92815	Human oligonucleot	5190	13.6	0.5	20	1	ADE84223	Human lymphoid cel
5119	13.6	0.5	20	1	ABZ98578	Human ICAM oligonu	c5191	13.6	0.5	21	1	AAZ26573	Human polymorphic
c5120	13.6	0.5	20	1	ABZ98645	Human tryptase a o	5192	13.6	0.5	21	1	ADD24723	Human CYP2E1 mutan
c5121	13.6	0.5	20	1	ABZ98645	Human oligonucleot	c5193	13.6	0.5	22	1	AAI14678	Triple helix formi
c5122	13.6	0.5	20	1	ABZ88388	Human oligonucleot	c5194	13.6	0.5	24	1	AAT03687	Homopyrimidine pro
c5123	13.6	0.5	20	1	ABZ80359	CD45 antisense PCR	c5195	13.6	0.5	24	1	AAL42406	Human ORC413-64 PC
5124	13.6	0.5	20	1	ABQ84589	DPPI0 related PSQ	c5196	13.6	0.5	25	1	AAC96455	HLA DOB1 gene PCR
5125	13.6	0.5	20	1	AAD50403	Mouse HPRT DNA amp	5197	13.6	0.5	25	1	AAC96092	16S rRNA gene PCR
5126	13.6	0.5	20	1	ABZ77107	Human stearyl-CoA	5198	13.6	0.5	25	1	AAC96353	HLA DPB1 gene PCR
5127	13.6	0.5	20	1	ADA26838	Human ZD52F10 reve	5199	13.6	0.5	25	1	AAC95751	HLA DOB1 gene PCR
5128	13.6	0.5	20	1	ACC68889	Human TGR23 phosph	5200	13.4	0.5	15	1	AAT52142	Human ICAM hammerh
c5129	13.6	0.5	20	1	ACA92598	Human N ras antis	5201	13.4	0.5	15	1	AAAI1718	Human MIF gene D5k
5130	13.6	0.5	20	1	ABZ79328	Acetyl-Coenzyme A-	5202	13.4	0.5	15	1	AAF60455	Oligonucleotide cl
c5131	13.6	0.5	20	1	ADA00265	RIP 140 gene PCR p	c5203	13.4	0.5	16	1	ABL57076	Molecular beacon t
c5132	13.6	0.5	20	1	ABQ77167	Human ABC12 exon	c5204	13.4	0.5	16	1	AAD57846	Target oligonucleo
5133	13.6	0.5	20	1	ABZ10372	Haematopoietic cel	c5205	13.4	0.5	17	1	AAF03225	Hammerhead ribozym
5134	13.6	0.5	20	1	ABZ10249	Haematopoietic cel	c5206	13.4	0.5	17	1	AAF03224	Hammerhead ribozym
5135	13.6	0.5	20	1	ADA20472	Prostate tumour re	c5207	13.4	0.5	17	1	AAF03226	Hammerhead ribozym
5136	13.6	0.5	20	1	ADA20493	Prostate tumour re	c5208	13.4	0.5	17	1	ADB40890	Tumour suppression
5137	13.6	0.5	20	1	ADA84290	Human CSNK2B PCR p	c5209	13.4	0.5	20	1	AAC82922	Human S-9 derived
5138	13.6	0.5	20	1	ADA84294	Human DBCCR1 PCR p	c5210	13.4	0.5	20	1	AAF87713	Human glutathione
5139	13.6	0.5	20	1	ACA10235	Human NOVX DNA PCR	c5211	13.4	0.5	20	1	AAQ52305	FKBP12C PCR primer
5140	13.6	0.5	20	1	ABT43367	Neuroblastoma-rela	5212	13.4	0.5	20	1	ABZ94127	Human oligonucleot
5141	13.6	0.5	20	1	ABT43222	Antisense oligonuc	c5213	13.4	0.5	21	1	AAF87033	Anchored 3' oligo
c5142	13.6	0.5	20	1	ABX34233	Human dual specifi	5214	13.4	0.5	21	1	AAF80105	Nucleotide sequenc
c5143	13.6	0.5	20	1	ABX10779	Human dual specifi	c5215	13.4	0.5	21	1	ABL57072	Molecular beacon t
							5216	13.4	0.5	21	1	ABS58234	Sequence surroundi

5217	13.4	1	AAAT42561	3' primer #1087-11	5290	13	0.5	14	1	ABQ83271	EGT CDNA tag relat
5218	13.4	1	AAZ26403	Human polymorphic	5291	13	0.5	14	1	ABX79769	EST polymorphic DN
C5219	13.4	1	ABA04964	Human FD14 PCR pri	5292	13	0.5	15	1	AAAX18361	RT-PCR primer of t
C5220	13.4	1	AAAC96197	16s rRNA gene PCR	C5293	13	0.5	17	1	AAAX69797	Human flt1 VEGF re
5221	13.4	1	AAAC96197	Human PAPP-Ea asso	C5294	13	0.5	18	1	AAAC64943	Camellia sinensis
C5222	13.2	1	AAAX87332	Reverse transcript	C5295	13	0.5	18	1	AAAC64941	Camellia sinensis
C5223	13.2	1	AAAX15198	Triple helix formi	C5296	13	0.5	19	1	AAAC83562	DNA synthesis meth
5224	13.2	1	AAAX15196	Triple helix formi	5297	13	0.5	20	1	AAABZ92288	Human oligonucleot
5225	13.2	1	AAAS52682	mRNA display splin	C5298	13	0.5	20	1	AAAZ74552	Human biallelic ma
5226	13.2	1	AAAK98126	Triple helix formi	C5299	13	0.5	21	1	AAAH88904	Human polymorphic
C5227	13.2	1	AAQ20030	Cross-linking olig	C5300	13	0.5	21	1	AAQ61989	HIV replication in
C5228	13.2	1	AAQ30373	Oligomer HUM beta	C5301	13	0.5	21	1	AAAT35001	HIV inhibitor #4.
C5229	13.2	1	AAQ30376	Oligomer HUM beta	C5302	13	0.5	21	1	AAAZ26572	Human polymorphic
5230	13.2	1	ABA97625	Probe d. Unidenti	C5303	13	0.5	22	1	AAAV58375	Biotinylated prime
C5231	13.2	1	ADE27307	Stearoyl-CoA desat	C5304	13	0.5	22	1	AAV99617	(T)-primer for fir
5232	13.2	1	ADE27597	Stearoyl-CoA desat	C5305	13	0.5	22	1	AAAL56810	T(13) bio-primer o
C5233	13.2	1	AAQ20028	Cross-linking olig	C5306	13	0.5	24	1	AAAC96274	HLA DPB1 gene PCR
C5234	13.2	1	AAQ20029	Cross-linking olig	5307	13	0.5	25	1	AAAC96374	HLA DPB1 gene PCR
C5235	13.2	1	AAQ30375	Oligomer HUM beta	C5308	13	0.5	25	1	AAAC96070	16s rRNA gene PCR
C5236	13.2	1	AAQ30374	Oligomer HUM beta	5309	12.8	0.5	17	1	AAAX69805	Human flt1 VEGF re
C5237	13.2	1	AAAT49298	5' end fragment of	5310	12.8	0.5	17	1	AAQ20006	Oligonucleotide #2
C5238	13.2	1	AAAT74905	5' end fragment of	C5311	12.8	0.5	17	1	AAQ20005	Oligonucleotide #1
C5239	13.2	1	AAAT47271	Capped RNA influen	5312	12.8	0.5	17	1	AAA22975	Integrin subunit b
C5240	13.2	1	AAAT47276	Capped RNA influen	C5313	12.8	0.5	17	1	AAA25444	Oestrogen receptor
C5241	13.2	1	AAAT47269	Capped RNA influen	5315	12.8	0.5	17	1	AAAF02388	Oestrogen receptor
C5242	13.2	1	AAAT47279	Capped RNA influen	C5316	12.8	0.5	17	1	ABSF74957	Hammerhead ribozym
C5243	13.2	1	AAAT47277	Capped RNA influen	C5317	12.8	0.5	17	1	ABZF65528	Human PAPP-Ea asso
C5244	13.2	1	AAAT47273	Capped RNA influen	C5318	12.8	0.5	17	1	ABZF65527	Human HER2 DNzyme
C5245	13.2	1	AAAT47264	5' fragment of alf	C5319	12.8	0.5	17	1	AAZ59379	Human HER2 DNzyme
C5246	13.2	1	AAAT47272	Capped RNA influen	5320	12.8	0.5	19	1	AAZ59379	Forward PCR primer
C5247	13.2	1	AAAT47278	Capped RNA influen	C5321	12.8	0.5	20	1	ABZ92287	Human oligonucleot
C5248	13.2	1	AAAT47267	Capped RNA influen	C5322	12.8	0.5	20	1	ABX12581	Human cytochrome p
C5249	13.2	1	AAAT47270	Capped RNA influen	C5323	12.8	0.5	20	1	AAAS03670	PCR primer re012,
5250	13.2	1	ABA91534	DNA oligonucleotid	C5324	12.8	0.5	20	1	AAAZ94533	Antisense oligonuc
C5251	13.2	1	ABZ85667	Human oligonucleot	5325	12.8	0.5	20	1	ABZ99084	Human PDE4C oligon
5252	13.2	1	ABZ90371	Human oligonucleot	C5326	12.8	0.5	20	1	ABZ87697	Human oligonucleot
5253	13.2	1	AAQ30371	Oligomer HUM beta	C5327	12.8	0.5	20	1	AAV42066	Mouse alpha 3 conn
5254	13.2	1	AAQ68869	Self paired oligon	C5328	12.8	0.5	20	1	AAF99576	Immunostimulatory
C5255	13.2	1	AAAT47265	5' fragment #2 of	C5329	12.8	0.5	20	1	ABSF78292	Angiogenesis inhib
C5256	13.2	1	ABL57554	Synthetic deoxyrib	C5330	12.8	0.5	20	1	ABL38654	Immunostimulatory
C5257	13.2	1	ABA97633	Poly o nucleotide	C5331	12.8	0.5	20	1	ABS70610	Immunostimulatory
C5258	13.2	1	ABA97639	Poly u nucleotide	C5332	12.8	0.5	20	1	ACH03114	Dendritic cell sti
C5259	13.2	1	ABZ88937	Human oligonucleot	C5333	12.8	0.5	20	1	ADB37078	Immunostimulatory
5260	13.2	1	ABZ87698	Human oligonucleot	C5334	12.8	0.5	20	1	AAD60260	Oligonucleotide 16
C5261	13.2	1	AAH91825	Human oligonucleot	C5335	12.8	0.5	21	1	AAH91826	Human inflammatory
C5262	13.2	1	ABK70498	Human inflammatory	C5336	12.8	0.5	21	1	AAZ75372	Human biallelic ma
C5263	13.2	1	ABQ78573	In-situ analysis s	5337	12.8	0.5	23	1	AAAC83568	Human FMR1 gene 5'
C5264	13.2	1	AAQ78573	RT-PCR primer used	C5338	12.8	0.5	23	1	AAH28300	3' untranslated re
C5265	13.2	1	AAAT28045	3'-primer B for hu	C5339	12.8	0.5	23	1	ABT05505	NOVX related probe
C5266	13.2	1	AAAT28046	3'-primer C for hu	C5340	12.8	0.5	25	1	AAAS20313	Human Cgamma gene
C5267	13.2	1	AAAT28044	3'-primer A for hu	C5341	12.8	0.5	25	1	ACI27529	PCR primer, 25657,
C5268	13.2	1	AAAT58485	First primer #1 fo	5342	12.6	0.4	20	1	ABA91535	Human microarray D
C5269	13.2	1	AAAT58486	First primer #2 fo	C5343	12.6	0.4	20	1	AAH80594	DNA oligonucleotid
C5270	13.2	1	AAV03675	First primer #3 fo	5344	12.6	0.4	20	1	AAH80594	Oligonucleotide hy
C5271	13.2	1	AAZ47342	Oligo dt primer.	C5345	12.6	0.4	20	1	ABA91532	DNA oligonucleotid
C5272	13.2	1	AAZ47344	PCR primer A used	5346	12.6	0.4	20	1	ADD81485	HIV PRT antisense
C5273	13.2	1	AAZ47343	PCR primer B used	5347	12.6	0.4	20	1	AAAL53965	DNA mutation detec
C5274	13.2	1	AAH22185	Human hepatocyte a	C5348	12.6	0.4	20	1	AAH80593	Oligonucleotide hy
C5275	13.2	1	AAH22187	Human hepatocyte a	5349	12.6	0.4	20	1	AAAL53963	DNA mutation detec
C5276	13.2	1	AAH22186	Human hepatocyte a	C5350	12.6	0.4	20	1	ADD81484	HIV PRT antisense
C5277	13.2	1	AAAT93818	Antitumoural phosp	5351	12.6	0.4	20	1	AAV69993	Mouse c-jun protei
C5278	13.2	1	AAF60331	Human liver RNA re	5352	12.6	0.4	20	1	AAAC65597	Human uteroglobin
C5279	13.2	1	ABQ81205	Human endostatin c	5353	12.6	0.4	20	1	ABZ85536	Human oligonucleot
5280	13.2	1	AAAS3817	Primer BTU1-75 hyb	5354	12.6	0.4	20	1	ABQ92966	T. tauschii/wheat
C5281	13.2	1	ABZ25620	Human zinc finger	C5355	12.6	0.4	20	1	AAV48864	ErbB-2 gene antise
C5282	13.2	1	ABN86391	Basophilic nucleop	5356	12.6	0.4	20	1	AAA40976	Human TNFalpha ant
C5283	13.2	1	ABQ94378	Tumour suppression	C5357	12.6	0.4	20	1	ABL57553	Synthetic deoxyrib
C5284	13.2	1	ABQ94374	Tumour suppression	5358	12.6	0.4	20	1	AAF24291	Complementary nucl
C5285	13.2	1	ABQ94375	Tumour suppression	C5359	12.6	0.4	20	1	ABA91531	DNA oligonucleotid
C5286	13.2	1	AAAT90275	Pyrimidine ring mo	5360	12.6	0.4	20	1	ABA91533	DNA oligonucleotid
C5287	13.2	1	AAH91554	Human inflammatory	5361	12.6	0.4	20	1	ABA91527	DNA-RNA-DNA oligon
5288	13	1	ABQ83276	EGT CDNA tag relat	C5362	12.6	0.4	20	1	ABA91536	DNA oligonucleotid
C5289	13	1	ABQ83275	EGT CDNA tag relat						ABK85429	Oligonucleotide #7

EGT CDNA tag relat
EST polymorphic DN
RT-PCR primer of t
Human flt1 VEGF re
Camellia sinensis
Camellia sinensis
DNA synthesis meth
Human oligonucleot
Human biallelic ma
Human polymorphic
HIV replication in
HIV inhibitor #4.
Human polymorphic
Biotinylated prime
(T)-primer for fir
T(13) bio-primer o
HLA DPB1 gene PCR
HLA DPB1 gene PCR
16s rRNA gene PCR
Human flt1 VEGF re
Oligonucleotide #2
Oligonucleotide #1
Integrin subunit b
Oestrogen receptor
Oestrogen receptor
Hammerhead ribozym
Human PAPP-Ea asso
Human HER2 DNzyme
Human HER2 DNzyme
Forward PCR primer
Human oligonucleot
Human cytochrome p
PCR primer re012,
Antisense oligonuc
Human PDE4C oligon
Human oligonucleot
Mouse alpha 3 conn
Immunostimulatory
Angiogenesis inhib
Immunostimulatory
Dendritic cell sti
Immunostimulatory
Immunostimulatory
Oligonucleotide 16
Human inflammatory
Human biallelic ma
Human FMR1 gene 5'
3' untranslated re
NOVX related probe
Human Cgamma gene
PCR primer, 25657,
Human microarray D
DNA oligonucleotid
Oligonucleotide hy
DNA oligonucleotid
HIV PRT antisense
DNA mutation detec
Oligonucleotide hy
DNA mutation detec
HIV PRT antisense
Mouse c-jun protei
Human uteroglobin
Human oligonucleot
T. tauschii/wheat
ErbB-2 gene antise
Human TNFalpha ant
Synthetic deoxyrib
Complementary nucl
DNA oligonucleotid
DNA oligonucleotid
DNA-RNA-DNA oligon
DNA oligonucleotid

5363	12.6	0.4	20	1	ABA97638	Poly t nucleotide	c5436	12.4	0.4	22	1	AAH22188	Human hepatocyte a
5364	12.6	0.4	20	1	ABL94461	Mouse C/EBP beta p	c5437	12.4	0.4	22	1	ABZ96312	Human C/EBP antise
5365	12.6	0.4	20	1	ABZ89486	Human oligonucleot	c5438	12.4	0.4	23	1	AAX55048	C/EBP-beta antise
c5366	12.6	0.4	20	1	ABZ89718	Human oligonucleot	c5439	12.4	0.4	23	1	AAA34495	Human adenosine re
c5367	12.6	0.4	20	1	AAL53961	DNA mutation detec	5440	12.4	0.4	23	1	AAZ47417	Probe 1 used to co
c5368	12.6	0.4	20	1	AAL53959	DNA mutation detec	c5441	12.4	0.4	23	1	AAF20617	Human C/EBP polynu
5369	12.6	0.4	20	1	AAL53967	DNA mutation detec	c5442	12.4	0.4	23	1	ABZ96311	Human C/EBP antise
c5370	12.6	0.4	20	1	AAL53958	DNA mutation detec	c5443	12.4	0.4	24	1	AZ224999	Sense probe to Fra
5371	12.6	0.4	20	1	AAL53962	DNA mutation detec	c5444	12.4	0.4	25	1	AAC96355	HLA DPB1 gene PCR
c5372	12.6	0.4	20	1	AAL53960	DNA mutation detec	c5445	12.4	0.4	25	1	AZ49618	PCR primer-2 for s
5373	12.6	0.4	20	1	AAL53964	DNA mutation detec	c5446	12.2	0.4	17	1	AAF06381	Hammerhead ribozym
5374	12.6	0.4	20	1	AAL53966	DNA mutation detec	5447	12.2	0.4	17	1	AAX69806	Human flt1 VEGF re
c5375	12.6	0.4	20	1	ACD05204	Tumour necrosis fa	c5448	12.2	0.4	17	1	AAA22593	Integrin subunit b
c5376	12.6	0.4	21	1	AAAL4463	AUUUA RNA target s	5449	12.2	0.4	17	1	ABK00237	Human NOGO Hammerh
c5377	12.6	0.4	21	1	AAL50228	Human ARE-mRNA seq	5450	12.2	0.4	17	1	ABK02172	Human NOGO DNazyme
c5378	12.6	0.4	21	1	AAL53707	Adenylate Uridylat	c5451	12.2	0.4	17	1	ABZ61926	Human H-Ras DNazym
c5379	12.6	0.4	21	1	AAD49639	Human adenylate ur	c5452	12.2	0.4	18	1	ABL57566	Synthetic deoxyrib
c5380	12.6	0.4	21	1	ACC83520	AU rich element (A	c5453	12.2	0.4	18	1	ABA97651	Poly w nucleotide
c5381	12.6	0.4	21	1	ADE86000	AU-rich element mo	c5454	12.2	0.4	18	1	ABL95913	Probe poly w for a
5382	12.6	0.4	21	1	AAH91420	Human inflammatory	c5455	12.2	0.4	18	1	ABL44451	Human chromosome 1
c5383	12.6	0.4	22	1	AAT28053	3'-primer K for hu	c5456	12.2	0.4	19	1	AAV44620	Human uncoupling p
c5384	12.6	0.4	22	1	AAT58493	First primer #10 f	5457	12.2	0.4	19	1	AAH84722	Cyclin E ribozyme
c5385	12.6	0.4	22	1	AAZ47351	PCR primer K used	5458	12.2	0.4	19	1	AAH59884	Cyclin E ribozyme
c5386	12.6	0.4	22	1	AAH22194	Human hepatocyte a	5459	12.2	0.4	20	1	AAH59884	Human transcriptio
c5387	12.6	0.4	22	1	AAS01584	Human fibrillin-1	c5460	12.2	0.4	20	1	AAH59884	Human transcriptio
5388	12.6	0.4	22	1	AAS01637	Human fibrillin-1	5461	12.2	0.4	20	1	ABZ90451	Bovine lysosomal a
c5389	12.6	0.4	22	1	AAT28049	3'-primer F for hu	5462	12.2	0.4	20	1	AAZ270845	Human oligonucleot
c5390	12.6	0.4	22	1	AAT58489	First primer #6 fo	5463	12.2	0.4	20	1	AAZ270845	Human biallelic ma
c5391	12.6	0.4	22	1	AAZ47347	PCR primer F used	c5464	12.2	0.4	20	1	ABQ84614	DPP10 related PSQ
c5392	12.6	0.4	22	1	AAH22190	Human hepatocyte a	c5465	12.2	0.4	20	1	AAH56777	S. aureus groE ope
c5393	12.6	0.4	22	1	AAV47448	Antisense oligonuc	c5466	12.2	0.4	20	1	ABZ89895	Human oligonucleot
c5394	12.6	0.4	22	1	ADC66134	Human CFTR exon 21	5467	12.2	0.4	20	1	AAH56777	Candida albicans T
c5395	12.6	0.4	23	1	ABL56411	PCR primer F used	c5468	12.2	0.4	20	1	AAH56777	Escherichia coli g
5397	12.4	0.4	14	1	AAV09230	3' poly(T) primer	c5469	12.2	0.4	21	1	AAZ22193	Human oligonucleot
c5398	12.4	0.4	14	1	AAV09234	3' poly(T) primer	5470	12.2	0.4	21	1	AAZ22193	Nucleotide sequenc
5399	12.4	0.4	14	1	AAV12222	Poly(T) oligonucle	c5471	12.2	0.4	21	1	AAZ22193	Mismatched target
c5400	12.4	0.4	14	1	AAV12226	Poly(T) oligonucle	5472	12.2	0.4	21	1	AAZ22193	Human polymorphic
5401	12.4	0.4	14	1	AAT99552	Oligo-dT primer us	c5473	12.2	0.4	22	1	AAZ22193	FEN-1 related DNA
c5402	12.4	0.4	14	1	AAX02696	Barley HPPD primer	c5474	12.2	0.4	22	1	AAZ22193	3'-primer J for hu
5403	12.4	0.4	14	1	AAX19465	Human senescence f	c5475	12.2	0.4	22	1	AAZ22193	First primer #9 fo
c5404	12.4	0.4	14	1	ABL88471	Human senescence f	c5476	12.2	0.4	22	1	AAZ22193	PCR primer I used
5405	12.4	0.4	14	1	AAD24496	Oligo dT 3Pi prime	c5477	12.2	0.4	22	1	AAH22193	Human hepatocyte a
c5406	12.4	0.4	14	1	AAD24492	Retinoid-regulated	c5478	12.2	0.4	22	1	AAZ22193	3'-primer E for hu
5407	12.4	0.4	15	1	AAT52144	Retinoid-regulated	c5479	12.2	0.4	22	1	AAZ22193	First primer #5 fo
c5408	12.4	0.4	15	1	AAX69796	Human ICAM hammerh	c5480	12.2	0.4	22	1	AAZ22193	GC6 gene 3' primer
c5409	12.4	0.4	17	1	AAF03223	Human flt1 VEGF re	c5481	12.2	0.4	22	1	AAZ22193	PCR primer E used
5410	12.4	0.4	17	1	ABQ99687	Hammerhead ribozym	5482	12.2	0.4	22	1	AAH22193	Human hepatocyte a
5411	12.4	0.4	17	1	ABQ99687	Murine Ikbkap exon	5483	12.2	0.4	22	1	AAH22193	PCR primer Gelo-19
5412	12.4	0.4	18	1	AAF56305	Human mGluR1alpha	5484	12.2	0.4	22	1	AAH22193	5' PCR primer for
5413	12.4	0.4	20	1	ABA02214	Human oligonucleot	c5485	12.2	0.4	22	1	AAH22193	Forward primer #15
c5414	12.4	0.4	20	1	ABQ84589	DPP10 related PSQ	5486	12.2	0.4	22	1	AAH22193	HIV-1 LTR region a
c5415	12.4	0.4	21	1	AAZ226823	Human polymorphic	5487	12.2	0.4	22	1	AAH22193	Oligonucleotide #3
c5416	12.4	0.4	21	1	AAQ70078	Primer 6 for 3' po	c5488	12.2	0.4	22	1	AAH22193	Human zinc finger
c5417	12.4	0.4	21	1	AAQ70078	Primer 5 to isolat	c5489	12.2	0.4	22	1	AAH22193	Dye-labeled molecu
c5418	12.4	0.4	21	1	AAQ70078	CZP2(487-713) prim	c5490	12.2	0.4	22	1	AAH22193	Dye-labeled dideox
c5419	12.4	0.4	22	1	AAT28050	3'-primer G for hu	c5491	12.2	0.4	22	1	AAH22193	Oligonucleotide us
c5420	12.4	0.4	22	1	AAT28051	3'-primer H for hu	c5492	12.2	0.4	22	1	AAH22193	Arbitrary anchor p
c5421	12.4	0.4	22	1	AAT28051	First primer #7 fo	c5493	12.2	0.4	22	1	AAH22193	Human senescence f
c5422	12.4	0.4	22	1	AAT58490	First primer #8 fo	c5494	12.2	0.4	22	1	AAH22193	Rapid analysis of
c5423	12.4	0.4	22	1	AAZ47348	PCR primer G used	c5495	12.2	0.4	22	1	AAH22193	Fruit-associated b
c5424	12.4	0.4	22	1	AAZ47349	PCR primer H used	c5496	12.2	0.4	22	1	AAH22193	B. gymnorhiza sal
c5425	12.4	0.4	22	1	AAH22191	Human hepatocyte a	c5497	12.2	0.4	22	1	AAH22193	Human cDNA synthe
c5426	12.4	0.4	22	1	AAH22192	Human hepatocyte a	c5498	12.2	0.4	22	1	AAH22193	Scarlet runner bea
c5427	12.4	0.4	22	1	AAT28055	3'-primer M for hu	c5499	12.2	0.4	22	1	AAH22193	Mouse E2 cDNA ampl
c5428	12.4	0.4	22	1	AAT28047	3'-primer D for hu	c5500	12.2	0.4	22	1	AAH22193	H-T11-C PCR primer
c5429	12.4	0.4	22	1	AAT58487	First primer #4 fo	c5501	12.2	0.4	22	1	AAH22193	Mouse E4 protein,
c5430	12.4	0.4	22	1	AAT58495	First primer #12 f	c5502	12.2	0.4	22	1	AAH22193	Anchored oligo-dT
c5431	12.4	0.4	22	1	AAX55049	C/EBP-beta antise	c5503	12.2	0.4	22	1	AAH22193	Anti-cancer drug r
c5432	12.4	0.4	22	1	AAA34496	Human adenosine re	c5504	12.2	0.4	22	1	AAH22193	Human cervical can
c5433	12.4	0.4	22	1	AAZ47353	PCR primer M used	c5505	12.2	0.4	22	1	AAH22193	Primer relating to
c5434	12.4	0.4	22	1	AAZ47345	PCR primer D used	c5506	12.2	0.4	22	1	AAH22193	Anchored oligo-dT
c5435	12.4	0.4	22	1	AAF20618	Human C/EBP polynu	c5508	12.2	0.4	22	1	AAH22193	Human cDNA synthe

c5509	12	0.4	17	1	ACC64290	Murine oligonucleo
c5510	12	0.4	20	1	AAH00614	Staphylococcus det
5511	12	0.4	20	1	ABI94721	Capture oligonucle
c5512	12	0.4	20	1	ABZ88600	Human oligonucleot
c5513	12	0.4	20	1	AAD09639	Human PKA C-alpha
5514	12	0.4	20	1	AAF54617	Human HLA Class I
5515	12	0.4	20	1	ABT07491	Rat protein phosph
5516	12	0.4	20	1	ABA97649	probe t. Unidenti
5517	12	0.4	20	1	ABA97650	probe u. Unidenti
c5518	12	0.4	20	1	ABZ90674	Human oligonucleot
5519	12	0.4	20	1	ABZ89594	Human oligonucleot
c5520	12	0.4	20	1	AAX92277	PCR primer used to
5521	12	0.4	20	1	AAA94525	Antisense oligonuc
5522	12	0.4	20	1	AAA94526	Antisense oligonuc
5523	12	0.4	20	1	AAA80059	Hepatitis B virus
c5524	12	0.4	20	1	AAA37705	Human Rad51 antise
c5525	12	0.4	20	1	AAS01198	Human RAD51 antise
5526	12	0.4	20	1	AAH80810	Oligonucleotide hy
5527	12	0.4	20	1	AAH80811	Oligonucleotide hy
c5528	12	0.4	20	1	AAD43244	Antisense oligonuc
5529	12	0.4	20	1	ADD81701	HIV PRT antisense
5530	12	0.4	20	1	ADD81702	HIV PRT antisense
5531	12	0.4	21	1	AAA80353	Human ASTH1I 5' re
5532	12	0.4	21	1	AAT76513	Endothelial nitric
5533	12	0.4	21	1	AAX54304	Endothelial nitric
5534	12	0.4	21	1	AAA33748	Low adenosine anti
5535	12	0.4	21	1	AAF19870	Human endothelial
5536	12	0.4	21	1	ABZ95564	Human endothelial
c5537	12	0.4	21	1	AAQ55571	Sequence of synthe
c5538	12	0.4	21	1	AAQ67230	Triple helix-formi
c5539	12	0.4	21	1	AAQ79210	Guanosine rich oli
c5540	12	0.4	21	1	AAT51628	Viral integrase in
c5541	12	0.4	21	1	AAX79217	Oligonucleotide #1
c5542	12	0.4	21	1	ADA26144	Human REL-A short
5543	12	0.4	22	1	AAV26091	Mandarin mb2chl ge
c5544	12	0.4	22	1	AAQ90036	Human SMP30 gene P
c5545	12	0.4	22	1	AAT62686	Primer for human s
5546	12	0.4	22	1	ABS52173	Human forward prim
c5547	12	0.4	23	1	ABL51554	Human NSAID regula
5548	12	0.4	24	1	AAZ24998	Antisense probe to
c5549	12	0.4	24	1	AAC91733	Human pollinosis-a
5550	12	0.4	25	1	ADE64628	Recombinant blood
c5551	11.8	0.4	17	1	AAX69437	Human fltl VEGF re
c5552	11.8	0.4	17	1	AAF06380	Hammerhead ribozym
c5553	11.8	0.4	17	1	AAX69438	Human fltl VEGF re
5554	11.8	0.4	17	1	ABK02792	Human CD20 Hammerh
5555	11.8	0.4	17	1	ABK02791	Human CD20 Hammerh
c5556	11.8	0.4	17	1	AAF03320	Hammerhead ribozym
5557	11.8	0.4	17	1	ABK00932	Human NOGO Inozyme
5558	11.8	0.4	17	1	ABK00933	Human NOGO Inozyme
5559	11.8	0.4	17	1	ABK00049	Human NOGO Hammerh
c5560	11.8	0.4	19	1	ADE55656	Human c-fos transcr
5561	11.8	0.4	19	1	ADE55772	Human c-fos siNA 1
5562	11.8	0.4	20	1	AAH50702	Sense strand encod
c5563	11.8	0.4	20	1	AAH80592	Oligonucleotide hy
c5564	11.8	0.4	20	1	AAH80591	Oligonucleotide hy
c5565	11.8	0.4	20	1	AAH80590	Oligonucleotide hy
c5566	11.8	0.4	20	1	ABZ88121	Human oligonucleot
c5567	11.8	0.4	20	1	ADD81483	HIV PRT antisense
c5568	11.8	0.4	20	1	ADD81482	HIV PRT antisense
c5569	11.8	0.4	20	1	ADD81481	HIV PRT antisense
5570	11.8	0.4	20	1	ADE43612	Human KNSL1 sequen
5571	11.8	0.4	20	1	AAQ70719	C-myc gene antisen
5572	11.8	0.4	20	1	AAQ87813	Antisense oligomer
5573	11.8	0.4	20	1	AAT60649	Antisense oligonuc
5574	11.8	0.4	20	1	AAT60650	Antisense oligonuc
5575	11.8	0.4	20	1	AAT95343	Treatment of human
5576	11.8	0.4	20	1	ABZ89225	Human oligonucleot
c5577	11.8	0.4	21	1	AAI56640	S36 primer to ampl
c5578	11.8	0.4	21	1	AAF96326	Human gene single
5579	11.8	0.4	21	1	AAF96504	Human gene single
5580	11.8	0.4	22	1	ADD21875	Protein translatio
5581	11.8	0.4	23	1	ABK90968	PCR primer, 22164,

N-acetylgalactosam
PCR primer #2 for
Human secretory pr
Human microarray D
Human microarray D
Human microarray 1
Human chromosome re
Human apoptosis re
Reverse transcript

c5582	11.8	0.4	24	1	ADD06134
c5583	11.8	0.4	24	1	ABL56688
5584	11.8	0.4	25	1	AAC90736
c5585	11.8	0.4	25	1	ACI62001
5586	11.8	0.4	25	1	ACK11064
5587	11.8	0.4	25	1	ABL43221
c5588	11.6	0.4	16	1	AAA99205
c5589	11.6	0.4	16	1	AAA99206
c5590	11.6	0.4	16	1	AAA97561

ALIGNMENTS

RESULT 1

AAAL07489/c

ID AAL07489 standard; DNA; 47 BP.

XX

AC AAL07489;

DT 21-NOV-2001 (first entry)

XX

DE Human reproductive system related antigen DNA SEQ ID NO: 10177.

XX Human; reproductive system related antigen; reproductive system disorder;

KW cancer; gene therapy; ds.

XX Homo sapiens.

XX WO200155320-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001339.

XX 31-JAN-2000; 2000US-0179065P.

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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465570/50.

Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.

Disclosure; SEQ ID NO 10176; 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention

Sequence 38 BP; 35 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

The invention relates to determining an analyte in a sample comprising (a) providing a target nucleic acid comprising a region A, a nucleobase sequence B, and a sequence I linked to the 5' terminus of the nucleobase sequence B, where the nucleobase sequence B is not specific for the analyte, and the region A specifically binds to the analyte, (b) binding the target nucleic acid to the analyte, separating the analyte bound to the target nucleic acid from the remaining part of the sample, (d) hybridising a primer to the target nucleic acid, where the primer comprises a nucleobase sequence B', and the nucleobase sequence B, hybridises to the nucleobase sequence B, (e) elongating the hybridised primer to produce an elongation product E using the target nucleic acid as a template and using nucleotides, where at least 30 % of the nucleotides contain at least one promiscuous base which is capable of base pairing with each of adenine, guanine, cytosine, and thymine, (f) separating the target nucleic acid from the elongation product E, (g) hybridising a further primer which comprises the nucleobase sequence B' to the elongation product E, where the elongation product E is capable of acting as a template for the elongation of the further primer, (h) elongating the hybridised further primer of step (g) to produce an elongation product E' using the elongation product E as a template and using nucleotides, where at least 30 % of the nucleotides contain at least one promiscuous base, (i) separating the elongation product E from the elongation product E', (j) hybridising a further primer comprising a nucleobase sequence B' to the target nucleic acid or the elongation product E, (k) elongating the further primer of step (j) to produce another elongation product E using the target nucleic acid or elongation product E as a template and using nucleotides, where at least 30 % of the nucleotides contain at least one promiscuous base, (l) separating product E of step (k) from the target nucleic acid or elongation product E, (m) optionally repeating steps (g) - (l) a sufficient number of times to generate a desired amount of double stranded nucleic acids and (n) determining the elongation product E and/or elongation product E' as a measure of the presence or amount of the analyte, where the lengths of the sequence I and the nucleobase sequence B are chosen such that, when the further primer hybridises to the elongation product E in step (g), the further primer spans a sequence formed by elongation of the

CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAACUAUACUAGUUUACAGAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules;
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 29 BP; 22 A; 1 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.9%; Score 24.4; DB 1; Length 29;
Best Local Similarity 88.5%; Pred. No. 1.7e+02;
Matches 23; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2778 TAGAATTGAAAAAATAAAAAAAAAA 2803
Db 4 UAGAACUGAAAAAATAAAAAAAAAA 29

RESULT 57
AA711173
ID AAA71173 standard; DNA; 29 BP.
XX
AC AAA71173;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #154.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Canis familiaris.
XX PN WO9958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX Example 8; Fig 134; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-

CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAACUAUACUAGUUUACAGAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 29 BP; 22 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 24.4; DB 1; Length 29;
Best Local Similarity 96.2%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2778 TAGAATTGAAAAAATAAAAAAAAAA 2803
Db 4 TAGAACTGAAAAAATAAAAAAAAAA 29

RESULT 58
AAD27121/c
ID AAD27121 standard; RNA; 36 BP.
XX
AC AAD27121;
XX
DT 09-APR-2002 (first entry)
XX
DE RNA template, (AU)4 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW lead compound; RNA polymerase; ss.
XX
OS Unidentified.
XX
PN US6322966-B1.
XX PD 27-NOV-2001.
XX
XX 11-MAY-1999; 99US-00309670.
XX PF 11-MAY-1999; 99US-00309670.
XX PR (ZHON/) ZHONG W.
XX (HONG/) HONG Z.
XX (LAUJ/) LAU J Y N.
PI Zhong W, Hong Z, Lau JYN;
XX WPI; 2002-096587/13.
XX
XX Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.
XX
PS Example 1; Fig 1C; 10pp; English.
XX
XX The present invention relates to an assay system for hepatitis C virus


```
CC invention. Rice sd-1 is located on chromosome 1.
XX
SQ Sequence 30 BP; 0 A; 3 C; 0 G; 27 T; 0 U; 0 Other;

Query Match
Best Local Similarity 0.9%; Score 24.2; DB 1; Length 30;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2156 TTTTTCCTCCTTTTTTTTTTTTTTTTTTTTTTTT 2184
Db ||||| ||||| ||||| ||||| |||||
2 TTTTTCCTCCTTTTTTTCTTTTTTTTTTTT 30

RESULT 61
AAF85682
ID AAF85682 standard; DNA; 37 BP.
XX
AC AAF85682;
XX
DT 25-JUN-2001 (first entry)
XX
DE Pea blight resistance protein related oligonucleotide #1.
XX
KW Pea; blight resistance; nucleotide triphosphate decomposition; ds.
XX
OS Unidentified.
XX
PN JP2001017176-A.
XX
PD 23-JAN-2001.
XX
PF 02-JUL-1999; 99JP-00189129.
XX
PR 02-JUL-1999; 99JP-00189129.
XX
PA (KYOU ) UNIV KYOTO.
XX
DR WPI; 2001-320697/34.
XX
PT New blight-resistant polypeptide useful for giving blight resistance to a
PT plant.
XX
PS Example; Page 6; 20pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a pea
CC protein with nucleotide triphosphate decomposing activity. The gene can
CC be used for conferring blight resistance on a plant
XX
SQ Sequence 37 BP; 2 A; 3 C; 3 G; 29 T; 0 U; 0 Other;

Query Match
Best Local Similarity 0.9%; Score 24.2; DB 1; Length 37;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2151 TTGATTTTCTCCTTTTTTTTTTTTTTTTTTTT 2179
Db ||||| ||||| | ||||| |||||
9 TTGATTTTCTTTTTTTTTTTTTTTTTTTTTTTT 37

RESULT 62
AAF26222
ID AAF26222 standard; DNA; 30 BP.
XX
AC AAF26222;
XX
DT 26-APR-2001 (first entry)
XX
DE APC binding protein associated primer ON-AT- SEQ ID 7.
XX
KW APC binding protein; cell proliferation; adenomatous polyposis coli;
XX tumor cell detection; primer; ss.
XX
OS Unidentified.
```

```

XX The present PCR primer was used to amplify DNA encoding a fragment of
CC zeocin selective marker. The amplified fragment was used to construct a
CC vector for expression of zalphall ligand polypeptide. Zalphall ligand is
CC a cytokine. The zalphall ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
CC for cloning the zalphall gene. The zalphall ligand is useful for treating
CC tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for
CC treating leukaemias and lymphomas. Antagonists against zalphall ligand
CC are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect
XX Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;
SQ
Query Match          0.9%; Score 24; DB 1; Length 34;
Best Local Similarity 84.4%; Pred. No. 3.le+02;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2155 TTTTCTCCTTTTTTTTTTTTTTTTTTTTTTTT 2186
DB      1 TTTTCTCGAGACTTTTTTTTTTTTTTTTTTTT 32

RESULT 65
AAD09727
ID      AAD09727 standard; DNA; 34 BP.
XX
AC      AAD09727;
XX
DT      10-SEP-2001 (first entry)
XX
DE      ZC18698 primer, to synthesise human activated CD3+ selected cell cDNA.
XX
KW      Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW      cancer; inflammation; gene therapy; primer; ss.
XX
OS      Homo sapiens.
XX
PN      WO200146422-A1.
XX
PD      28-JUN-2001.
XX
PF      22-DEC-2000; 2000WO-US035308.
XX
PR      23-DEC-1999; 99US-00471767.
PR      01-DEC-2000; 2000US-0250841P.
XX
PA      (ZYMO ) ZYMOGENETICS INC.
XX
PI      Presnell SR, Kindsvogel W;
XX
DR      WPI; 2001-408648/43.
XX
PT      Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.
XX
PS      Example 4B; Page 145; 167pp; English.
XX
CC      The patent discloses novel human cytokine, ZCYTO18 protein and its
CC      corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC      expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in
CC      K5626 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in
CC      a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer
CC      and inflammation. ZCYTO18 protein is useful for killing cancer cells. It
CC      is useful for increasing platelets in a patient or injured tissue. It is
CC      also used in genetherapy. The present sequence is a PCR primer, ZC18698

```

used to synthesise a cDNA strand from human activated CD3+ selected cells. This primer is used for the identification of human ZCYTO18 message in activated T-cell library

Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match
Best Local Similarity 0.9%; Score 24; DB 1; Length 34;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2155 TTTTTCCTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2186
|||||
Db 1 TTTTTCCTCGAGACTTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 66
AAS20662
ID AAS20662 standard; DNA; 34 BP.
XX
AC AAS20662;
XX
DT 09-APR-2002 (first entry)
XX
DE Primer ZC18698 used to create XhoI site into human zalphall Ligand cDNA.
XX
KW Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytostatic; human; primer; ss.
XX
OS Synthetic.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
PR 09-MAR-1999; 99US-01233547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI; 2002-040208/05.
XX
PT New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
PS Example 6; Col 135; 105pp; English.
XX
CC The present invention relates to the isolation of a novel cytokine,
CC zalphall Ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall Ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC zalphall Ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall Ligand gene,
CC and in gene therapy. Zalphall Ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC a primer used in the methods of the present invention
XX

SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;
 Query Match 0.9%; Score 24; DB 1; Length 34;
 Best Local Similarity 84.4%; Pred. No. 3.1e+02;
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      2155 TTTTTCCTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2186
           |||||
Db       1 TTTTTCCTCGAGACTTTTTTTTTTTTTTTTTTTT 32
  
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RESULT 67
 ADD68172
 ID ADD68172 standard; DNA; 34 BP.
 XX
 AC ADD68172;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE PCR primer relating to the invention ZC18698 SEQ ID NO:30.
 XX
 KW ss; PCR; primer; zcytor17; antiinflammatory; dermatological;
 KW immunosuppressive; antimicrobial; vaccine; inflammatory disease;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW atopic dermatitis; eczema; psoriasis; endotoxaemia; septicæmia;
 KW toxic shock syndrome; infectious disease.
 XX
 OS Synthetic.
 XX
 PN WO2003060090-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 21-JAN-2003; 2003WO-US001984.
 XX
 PR 18-JAN-2002; 2002US-0350325P.
 PR 25-APR-2002; 2002US-0375323P.
 PR 19-DEC-2002; 2002US-0435315P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;
 PI Novak JE, Gross JA, Dillon SR;
 XX
 DR WPI; 2003-618179/58.
 XX
 PT New zcytor17 ligand polypeptides, useful for treating inflammatory
 PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
 PT disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia.
 XX
 PS Example 6; SEQ ID NO 30; 372pp; English.
 XX
 CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
 CC polypeptide of the invention has antiinflammatory, dermatological,
 CC immunosuppressive, and antimicrobial activity, and may have a use in a
 CC vaccine. The polypeptide is useful for treating inflammatory diseases,
 CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicæmia, toxic
 CC shock syndrome or infectious diseases. The present sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.9%; Score 24; DB 1; Length 34;
 Best Local Similarity 84.4%; Pred. No. 3.1e+02;
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2155 TTTTTCCTCCTTTTTTTTTTTTTTTTTTTT 2186
 |||||
 Db 1 TTTTTCGAGACTTTTTTTTTTTTTTTTTTTT 32

RESULT 68

XX	15-AUG-2002	(first entry)
DT	Mononucleotide repeat locus BAT26 probe #2.	
XX	Mononucleotide repeat locus; human; BAT26; probe; microsatellite; tumour;	
DE	ss.	
XX	Homo sapiens.	
KW	Key	
KW	Location/Qualifiers	
OS	modified_base 1	
XX	/*tag= a	
FH	/mod_base= OTHER	
FT	/note= "Labelled with LightCycler fluorescent dye LC-Red-	
FT	640"	
FT		
FT		
XX	EP1207210-A1.	
PN	22-MAY-2002.	
XX	13-NOV-2001; 2001EP-00126930.	
PD	15-NOV-2000; 2000EP-00124897.	
XX	(HOFF) ROCHE DIAGNOSTICS GMBH.	
PF	(HOFF) HOFFMANN LA ROCHE & CO AG F.	
XX	Dietmaier W;	
PI	WPI; 2002-437469/47.	
XX	Analyzing repeat sequences in DNA using a probe which hybridizes to	
DR	adjacent repetitive and non-repetitive regions and determining hybrid	
XX	melting point is useful to detect microsatellite instability such as in	
PT	hereditary cancer.	
PT	Claim 16; Page 7; 19pp; English.	
XX	The present invention relates to a method for analysing a target nucleic	
PS	acid consisting of repetitive and non-repetitive sequences. The method	
XX	comprises hybridising a polynucleotide probe comprising a segment	
CC	complementary to a non-repetitive region and a segment complementary to	
CC	an adjacent repetitive region, where the second segment consists of a	
CC	defined number of repeats, and determining the melting point temperature	
CC	of the hybrid. The method is used to analyse microsatellites, especially	
CC	microsatellite instability, particularly as a means for detecting an	
CC	hereditary tumours. Alternatively, the method is used to identify an	
CC	individual in a population. The present sequence is a probe for	
CC	Mononucleotide repeat locus BAT26, and was used to illustrate the	
CC	invention	
XX	Sequence 32 BP; 27 A; 1 C; 2 G; 2 T; 0 U; 0 Other;	
SQ	Query Match 0.8%; Score 23.6; DB 1; Length 32;	
	Best Local Similarity 86.7%; Pred. No. 3.1e+02;	
	Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	2161 TCCTCTTTTTCCTTTTTTTTTTTTTTTTAACT 2190	
Db	32 TTTTTCCTTTTTTTTACCT 3	
RESULT 70		
AAD46356		
ID	AAD46356 standard; DNA; 35 BP.	
XX	AAD46356;	
AC	AAD46356;	
XX	29-AUG-2003 (revised)	
DT	07-AUG-2003 (revised)	
DT	27-JAN-2003 (first entry)	
XX	XX	

PD 19-JUL-2001.
XX
XX
PF 12-JAN-2001; 2001WO-US001190.
XX
XX 13-JAN-2000; 2000US-0176409P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 12-JAN-2001; 2001US-00760500.
XX
XX (NANO-) NANOSPHERE INC.
PA
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Li Z;
PI
XX WPI; 2001-451868/48.
XX
XX Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
PT viral diseases, by contacting the nucleic acid with oligonucleotides
PT attached to nanoparticles and having sequences complementary a portion of
PT the nucleic acid.
XX
XX Example 24; Fig 44; 323pp; English.
PS
XX The sequence represents a cyclic disulphide linked oligonucleotide which
CC may be coupled with colloidal gold particles (nanoparticles) and used to
CC demonstrate the method of the invention. The invention relates to
CC isolating or detecting a nucleic acid of interest, in a mixture of
CC nucleic acids, by binding it to 2 or more complementary nucleotides which
CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
CC colloidal gold) are used to both isolate and detect (e.g. by linking the
CC particle to a fluorescent probe) the resultant complex. The methods are
CC useful for detecting nucleic acids, natural or synthetic, and modified or
CC unmodified. The methods may also be applied in the diagnosis of genetic,
CC bacterial and viral diseases, in forensics, in DNA sequencing, for
CC paternity testing, for cell line authentication, and for monitoring gene
CC therapy. The methods are further useful in research and analytical
CC laboratories in DNA sequencing, in the field to detect the presence of
CC specific pathogens, for quick identification of an infection to assist in
CC drug prescription, and in homes and health centres for inexpensive first-
CC line screening. The methods, which are based on observing colour change
CC with the naked eye, are cheap, fast, simple, robust (reagents are
CC stable), do not require specialised or expensive equipment, and little or
CC no instrumentation is required
XX
XX Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 23.4; DB 1; Length 30;
Best Local Similarity 96.0%; Pred. No. 2.9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2161 TCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 25 TCTGCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
RESULT 73
ABK65048/c
ID ABK65048 standard; DNA; 30 BP.
XX
XX AC ABK65048;
XX
XX 02-JUL-2002 (first entry)
DT
XX Nanoparticle-oligonucleotide #68.
DE
XX Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW ss.
KW Synthetic.
XX WO200218643-A2.
XX PN
XX 07-MAR-2002.
PD

XX 10-AUG-2001; 2001WO-US025237.
XX
XX 11-AUG-2000; 2000US-0224631P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
XX
XX (NANO-) NANOSPHERE INC.
PA
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
PI
XX WPI; 2002-258024/30.
XX
XX Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX
XX Example 24; Fig 44; 412pp; English.
PS
XX The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA; and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroid residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX
XX Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 23.4; DB 1; Length 30;
Best Local Similarity 96.0%; Pred. No. 2.9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2161 TCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 25 TCTGCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
RESULT 74
ABS64686/c
ID ABS64686 standard; DNA; 30 BP.
XX
XX AC ABS64686;
XX
XX 15-NOV-2002 (first entry)
DT
XX Nucleic acid detection method associated polynucleotide #68.
DE
XX Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
XX Synthetic.
XX WO200246472-A2.
XX PN

```
XX 13-JUN-2002.
XX
XX
XX PF 07-DEC-2001; 2001WO-US046418.
XX
XX PR 08-DEC-2000; 2000US-0254392P.
XX PR 08-DEC-2000; 2000US-0254418P.
XX PR 11-DEC-2000; 2000US-0255235P.
XX PR 11-DEC-2000; 2000US-0255236P.
XX PR 12-JAN-2001; 2001US-00760500.
XX PR 28-MAR-2001; 2001US-00820279.
XX PR 09-APR-2001; 2001US-0282640P.
XX PR 10-AUG-2001; 2001US-00927777.
XX
XX PA (NANO-) NANOSPHERE INC.
XX
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX
XX DR WPI; 2002-608256/65.
XX
XX PT Detecting nucleic acid having two portions, by providing nanoparticles
XX PT having oligonucleotides attached to it, contacting nucleic acid and
XX PT nanoparticles to allow hybridization, and observing detectable change.
XX
XX PS Example 24; Fig 44; 442pp; English.
XX
XX CC The invention describes a method of detecting (M1) a nucleic acid having
XX CC two portions, involving providing nanoparticles having oligonucleotides
XX CC attached to it, which has a sequence complementary to sequence of two
XX CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX CC allow hybridisation of oligonucleotides with two or more portions of
XX CC nucleic acid, and observing a detectable change brought about by
XX CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX CC conjugates (II) and the aggregate probe are useful for detecting two or
XX CC more nucleic acids (from a biological source) having at least two
XX CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX CC with a disease, synthetic, or structurally-modified natural or synthetic
XX CC RNA or DNA, or a product of a polymerase chain reaction amplification.
XX CC (II) is useful for preparing a nanoprobe conjugate for detecting an
XX CC analyte, and for detecting a nucleic acid bound to an electrode surface.
XX CC (I) and (II) are useful for fabrication, and for separating a selected
XX CC nucleic acid having two portions from other nucleic acids. (I), (II) and
XX CC the aggregate probe are useful for detecting an analyte (especially
XX CC polyvalent analyte) in a sample. This sequence represents a
XX CC polynucleotide used to demonstrate the method of the invention
XX
XX SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 23.4; DB 1; Length 30;
XX Best Local Similarity 96.0%; Pred. No. 2.9e+02;
XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2161 TCTCCTTTT TTTT TTTT TTTT TTTT TTTT 2185
XX Db ||| ||||| ||||| ||||| ||||| |||||
XX 25 TCTGCTTTT TTTT TTTT TTTT TTTT TTTT 1
XX
XX RESULT 75
XX AAL61658/c
XX ID AAL61658 standard; DNA; 30 BP.
XX
XX AC AAL61658;
XX
XX DT 22-SEP-2003 (first entry)
XX
XX DE Oligonucleotide #19 used in the nucleic acid detection method.
XX
XX KW Nucleic acid detection; fabrication; ss.
XX
XX OS Unidentified.
XX
XX PN WO2003035829-A2.
```

```
XX 01-MAY-2003.
XX
XX PF 08-OCT-2002; 2002WO-US032088.
XX
XX PR 09-OCT-2001; 2001US-0327864P.
XX PR 07-DEC-2001; 2001US-00008978.
XX
XX PA (NANO-) NANOSPHERE INC.
XX
XX PI Park S, Taton TA, Mirkin CA;
XX
XX DR WPI; 2003-430409/40.
XX
XX PT Detecting nucleic acid having two portions, by providing nanoparticles
XX PT having oligonucleotides attached to it, contacting nucleic acid and
XX PT nanoparticles to allow hybridization, and observing detectable change.
XX
XX PS Example 24; Fig 44; 467pp; English.
XX
XX CC The invention relates to a method of detecting a nucleic acid having two
XX CC portions. The method involves providing nanoparticles having
XX CC oligonucleotides attached to it which has a sequence complementary to
XX CC sequence of two portions of nucleic acid, contacting nucleic acid and
XX CC nanoparticles to allow hybridisation of oligonucleotides with two or more
XX CC portions of nucleic acid and observing a detectable change brought about
XX CC by hybridisation. The method and aggregate probes are useful for
XX CC detecting two or more nucleic acids (from a biological source) having at
XX CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
XX CC associated with a disease, synthetic or structurally modified natural or
XX CC synthetic RNA or DNA, or a product of a polymerase chain reaction
XX CC amplification. The invention is useful for preparing a nanoprobe
XX CC conjugate for detecting an analyte and for detecting a nucleic acid bound
XX CC to an electrode surface. It is also useful for fabrication and for
XX CC separating a selected nucleic acid having two portions from other nucleic
XX CC acids. The present sequence is an oligo used to illustrate the method of
XX CC the invention
XX
XX SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 23.4; DB 1; Length 30;
XX Best Local Similarity 96.0%; Pred. No. 2.9e+02;
XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2161 TCTCCTTTT TTTT TTTT TTTT TTTT TTTT 2185
XX Db ||| ||||| ||||| ||||| ||||| |||||
XX 25 TCTGCTTTT TTTT TTTT TTTT TTTT TTTT 1
XX
XX RESULT 76
XX AAA94321
XX ID AAA94321 standard; DNA; 36 BP.
XX
XX AC AAA94321;
XX
XX DT 11-JAN-2001 (first entry)
XX
XX DE RNA-protein fusion oligonucleotide 37-P.
XX
XX KW RNA-protein fusion; protein library; protein isolation; DNA-RNA hybrid;
XX KW gene cloning; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_RNA 1..13
XX FT /*tag= a
XX FT /label= RNA
XX FT modified_base 36
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "attached to puromycin, a peptide acceptor"
XX
```

PN WO2000047775-A1.
XX
PD 17-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US002589.
XX
PR 09-FEB-1999; 99US-00247190.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Szostak JW, Roberts RW, Liu R;
XX
DR WPI; 2000-533022/48.
XX
PT Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
XX
PS Disclosure; Page 44; 121pp; English.
XX
CC The present sequence is one of a number of oligonucleotides which were
CC used for the generation of RNA-protein fusions, including fusions having
CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC and in vitro or in situ translation of an mRNA molecule with a peptide
CC acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC under high salt conditions to produce a protein library. This method is
CC useful for improving or altering existing proteins, as well as for
CC isolating new proteins and nucleic acid or small molecule targets. It may
CC also be used to improve human or humanised single-chain antibodies for
CC the treatment of a number of diseases. The method is useful for the
CC isolation of proteins with specific binding properties, for screening
CC cDNA libraries and cloning new genes on the basis of protein-protein
CC interactions. Unlike prior art, the new method does not rely on
CC maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC complex, which is very fragile and is therefore of limited use. The
CC method does not rely on topological links between the protein and the
CC nucleic acid so that the information of the protein is retained and can
CC be recovered in readable, nucleic acid form
XX
SQ Sequence 36 BP; 25 A; 4 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 0.8%; Score 23.4; DB 1; Length 36;
Best Local Similarity 92.0%; Pred. No. 4.6e+02;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAAATAAAAAAAAAAAAAA 2804
Db 8 GAACUGAAAAAATAAAAAAAAAAAAAA 32

RESULT 77
ABK99274/c
ID ABK99274 standard; RNA; 36 BP.
XX
AC ABK99274;
XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #4.
XX
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS Synthetic.
XX
PN US2002064771-A1.
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-00828034.
XX
PR 07-APR-2000; 2000US-0195852P.

(ZHON/) ZHONG W.
(HONG/) HONG Z.
(FERR/) FERRARI E.

Zhong W, Hong Z, Ferrari E;
MPI; 2002-582330/62.

Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed, and template and primer which do not form a stable duplex in the absence of HCV NS5B.

Example; Page 6; 17pp; English.

The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NS5B replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of the template, where the template is at least three nucleotides and the primer is two or three nucleotides, and the template and primer do not form a stable duplex in solution in the absence of the HCV NS5B protein. The complex is useful for detecting HCV replicase activity and permits establishment of sensitive RNA-dependent RNA polymerase assays to screen and evaluate antiviral inhibitors and to improve the specificity and efficacy of the inhibitors. The complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of HCV NS5B-catalysed nucleotide incorporation and investigation of mechanistic inhibitors for mis-incorporation or chain termination. Specifically, the short RNA template and primer pairs are useful in screening assays which are used for determining kinetic, thermodynamic and mechanistic properties of NS5B replication and ultimately in the development of inhibitors of NS5B. Newly identified inhibitors of replicase activity may be used for developing anti-HCV pharmaceuticals. Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis templates

Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 23.4; DB 1; Length 36;
Best Local Similarity 81.8%; Pred. No. 4.6e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2154 ATTTTTCCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2186
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36 ATATATATATTTTTTTTTTTTTTTTTTTTTTTTTTTT 4

RESULT 78
AAD271118/c
ID AAD27118 standard; RNA; 36 BP.

XX AAD27118;
AC
XX
DT 09-APR-2002 (first entry)
XX RNA template, (AU)5 used to direct RNA synthesis by HCV RNA polymerase.
DE Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
XX lead compound; RNA polymerase; ss.
OS Unidentified.
XX US6322966-B1.
PN
XX
PD 27-NOV-2001.
XX
PF 11-MAY-1999; 99US-00309670.
XX
PR 11-MAY-1999; 99US-00309670.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.


```
Best Local Similarity 79.4%; Pred. No. 5.4e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2767 AGTATTCTTGTGTAGATTGAAAAA 2800
Db 2 AATATCCTTCTTATATAAAAAA 35

RESULT 93
AAL61669
ID AAL61669 standard; DNA; 35 BP.
XX
AC AAL61669;
XX
XX 22-SEP-2003 (first entry)
XX
DE Oligonucleotide #28 used in the nucleic acid detection method.
XX
KW Nucleic acid detection; fabrication; ss.
XX
OS Unidentified.
XX
PN WO2003035829-A2.
XX
PD 01-MAY-2003.
XX
PF 08-OCT-2002; 2002WO-US032088.
XX
PR 09-OCT-2001; 2001US-0327864P.
PR 07-DEC-2001; 2001US-00008978.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Park S, Taton TA, Mirkin CA;
XX
XX WPI; 2003-430409/40.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Disclosure; Page 58-59; 467pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid having two
CC portions. The method involves providing nanoparticles having
CC oligonucleotides attached to it which has a sequence complementary to
CC sequence of two portions of nucleic acid, contacting nucleic acid and
CC nanoparticles to allow hybridisation of oligonucleotides with two or more
CC portions of nucleic acid and observing a detectable change brought about
CC by hybridisation. The method and aggregate probes are useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic or structurally modified natural or
CC synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. The invention is useful for preparing a nanoprobe.
CC conjugate for detecting an analyte and for detecting a nucleic acid bound
CC to an electrode surface. It is also useful for fabrication and for
CC separating a selected nucleic acid having two portions from other nucleic
CC acids. The present sequence is an oligo used to illustrate the method of
CC the invention
XX
SQ Sequence 35 BP; 24 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
Query Match 0.8%; Score 22.8; DB 1; Length 35;
Best Local Similarity 79.4%; Pred. No. 5.4e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2767 AGTATTCTTGTGTAGATTGAAAAA 2800
Db 2 AATATCCTTCTTATATAAAAAA 35

RESULT 94
```

```
ABQ80396/c
ID ABQ80396 standard; DNA; 35 BP.
XX
AC ABQ80396;
XX
DT 06-NOV-2003 (first entry)
XX
DE Probe APC 2.
XX
XX Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW infection; screening; colour change; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "Gold-S'-A"
XX
PN WO2003048769-A1.
XX
PD 12-JUN-2003.
XX
PF 27-NOV-2002; 2002WO-US038069.
XX
PR 30-NOV-2001; 2001US-0334644P.
XX
PA (NANO-) NANOSPHERE INC.
XX
XX Storhoff JJ, Fritz BM, Herrmann M;
XX WPI; 2003-617993/58.
XX
PT Detecting target polynucleotide in a sample, by amplifying target,
PT hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
PT detection system, and determining amount of signal generated due to
PT binding.
XX
PS Example 1; Page 35; 74pp; English.
XX
CC The sequences given in ABQ80394-99 represent probes and targets which
CC were used in the method of the invention for detecting a target
CC polynucleotide in a sample. The method comprises amplifying the target,
CC hybridizing the target to oligonucleotides bound to nanoparticles in a
CC nanoparticle detection system, determining the amount of signal generated
CC as a result of binding, optionally repeating the above steps, and
CC detecting the presence of the target oligonucleotide by analysing for the
CC amount of signal produced after at least one amplification cycle. The
CC method is useful for detecting target polynucleotide in a sample, and for
CC determining the quantity of target polynucleotide in a sample. The method
CC is useful in research and analytical laboratories in DNA sequencing, in
CC the field to detect the presence of specific pathogens, in the doctor's
CC office for quick identification of an infection to assist in prescribing
CC a drug for treatment, and in homes and health centres for inexpensive
CC first-line screening. The method is based on observing colour change with
CC the naked eye, hence the method is cheap, fast, simple, robust, do not
CC require specialized or expensive equipment, and little or no
CC instrumentation is required
XX
SQ Sequence 35 BP; 28 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 22.8; DB 1; Length 35;
Best Local Similarity 92.3%; Pred. No. 5.4e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2161 TCTCCTTTTTTTTTTTTTTTTTTTT 2186
Db 26 TCTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 95
AAQ79096
ID AAQ79096 standard; DNA; 29 BP.
```


CC that bind specifically to almost any compound or catalyse almost any
CC reaction
XX
SQ Sequence 34 BP; 22 A; 4 C; 6 G; 0 T; 1 U; 1 Other;
Query Match 0.8%; Score 22.4; DB 1; Length 34;
Best Local Similarity 91.7%; Pred. No. 6e+02;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2780 GAATTGAAAAA 2803
Db 8 GAACUGAAAAA 31
RESULT 110
AAC90605
ID AAC90605 standard; RNA; 34 BP.
XX
AC AAC90605;
XX
DT 20-MAR-2001 (first entry)
XX
DE Tomato spotted wilt virus S RNA partial sequence #9.
XX
KW Tospovirus resistance; transgenic plant; tomato spotted wilt virus;
KW Impatiens necrotic spot virus; TSWV; ss.
XX
OS Tomato spotted wilt virus.
XX
FH Key Location/Qualifiers
FT misc_binding 1
FT /*tag= a
FT /bound_moiety= "binds nucleotide 32 of AAC89654"
FT 2. .10
FT /*tag= b
FT /bound_moiety= "binds nucleotides 30-22 of AAC89654"
FT 17. .32
FT /*tag= c
FT /bound_moiety= "binds nucleotides 30-5 of AAC89564"
FT 33. .34
FT /*tag= d
FT /bound_moiety= "binds nucleotides 1-2 of AAC89654"
XX
PN US6150585-A.
XX
PD 21-NOV-2000.
XX
PF 26-NOV-1996; 96US-00757011.
XX
PR 03-NOV-1989; 89US-00431259.
PR 05-DEC-1989; 89US-00446024.
PR 02-MAY-1991; 91US-00694734.
PR 14-APR-1993; 93US-00047346.
PR 26-OCT-1993; 93US-00143397.
PR 27-JUL-1994; 94US-00280903.
XX
PA (NOVS) NOVARTIS FINANCE CORP.
XX
PI Peters D, Gielen J, De Haan PT, Van Grinsven MQJM, Kool AJ;
PI Goldbach RW;
XX
XX WPI; 2001-060031/07.
XX
DR Recombinant DNA construct comprising a DNA sequence encoding an RNA
PT sequence that codes for a tospovirus protein, useful for producing plants
PT with reduced susceptibility to tospovirus infection.
XX
PS Example 9; Fig 16B; 49pp; English.
XX
CC The present invention provides DNA constructs encoding RNA sequences from
CC a tospovirus which can be used to produce transgenic plants with immunity
CC to tospoviruses. Examples of tospoviruses include the tomato spotted wilt
CC virus and the Impatiens necrotic spot virus

XX
SQ Sequence 34 BP; 4 A; 0 C; 2 G; 0 T; 28 U; 0 Other;
Query Match 0.8%; Score 22.4; DB 1; Length 34;
Best Local Similarity 3.1%; Pred. No. 6e+02;
Matches 1; Conservative 25; Mismatches 6; Indels 0; Gaps 0;
Qy 2156 TTTTCTCTCTTTT 2187
Db 2 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 33
RESULT 111
AAD46356/c
ID AAD46356 standard; DNA; 35 BP.
XX
AC AAD46356;
XX
DT 29-AUG-2003 (revised)
DT 07-AUG-2003 (revised)
DT 27-JAN-2003 (first entry)
XX
DE Vp3 oligonucleotide used to generate pox virus late promoter.
XX
KW Recombinant leporipox virus; vector vaccine; treatment; prophylaxis;
KW infectious disease; promoter; ss.
XX
OS Viruses.
XX
PN WO200272852-A2.
XX
PD 19-SEP-2002.
XX
PF 07-MAR-2002; 2002WO-EP002858.
XX
PR 08-MAR-2001; 2001EP-00200869.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Spibey N;
XX
DR WPI; 2002-723365/78.
XX
PT Use of a live, recombinant leporipox virus in the manufacture of a vector
PT vaccine for the treatment and/or prophylaxis of infectious disease in non
PT -lepori species.
XX
PS Example 1; Page 9; 28pp; English.
XX
CC The invention relates to the use of a live, recombinant leporipox virus
CC (which comprises exogenous DNA that is operably linked to at least one
CC expression control element and is incorporated in a non-essential region
CC of the virus genome) in the manufacture of a vector vaccine for the
CC treatment and/or prophylaxis of infectious disease in non-lepori species
CC such as felines or canines. The present sequence is an oligonucleotide
CC used to generate pox virus late promoter. This sequence is used in the
CC exemplification of the invention. (Updated on 07-AUG-2003 to correct OS
CC field.) (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 35 BP; 5 A; 4 C; 2 G; 24 T; 0 U; 0 Other;
Query Match 0.8%; Score 22.4; DB 1; Length 35;
Best Local Similarity 81.2%; Pred. No. 6.4e+02;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2773 CTGTTAGAAATTGAAAAA 2804
Db 33 CATTAGATCTAAAAA 2
RESULT 112
AAN70281
ID AAN70281 standard; DNA; 27 BP.

AC AAQ30432;
XX 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX
DE Oligomer IL6805 for forming triplex with HUMIL6 target duplex.
XX
KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW malignancy; hepatitis; inflammation; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT
FT misc_feature 11. .12
FT /*tag= d
FT /note= "o-xyloso dimer synthon linkage"
FT 12. .23
FT /*tag= c
FT /label= inverted_polarity_region
FT /note= "see comments"
FT 23
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
XX
PN WO9209705-A1.
XX
PD 11-JUN-1992.
XX
PF 25-NOV-1991; 91WO-US008811.
XX
PR 23-NOV-1990; 90US-00617907.
PR 18-JAN-1991; 91US-00643382.
PR 08-APR-1991; 91US-00683420.
PR 17-APR-1991; 91US-00686544.
PR 17-APR-1991; 91US-00686546.
PR 17-APR-1991; 91US-00686547.
PR 27-SEP-1991; 91US-00766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX
XX WPI; 1992-217083/26.
DR
XX New oligomers contg. modified bases - which form a triplex with G-C
FT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.
XX
PS Claim 12; Page 71; 77pp; English.
XX
CC The synthetic oligomer is capable of forming a triplex at physiological
CC pH with a purine rich target sequence by coupling into the major groove
CC of the duplex. The specific target sequence of this oligomer is the human
CC interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC concd. on one strand of the duplex. The oligomer, and others like it are
CC useful in diagnosis and therapy of diseases characterised by specific DNA
CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC tumours and inflammation. The triple helices form under mild conditions
CC thus assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer contains an inverted polarity region
CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC (nucleotides have the 3'positions of xylose sugars linked via the o-
CC xylene ring). Two nucleotides are coupled through a xylene residue to
CC form the dimer synthon. This additional modifications may render the
CC oligomer stable to nuclease activity. The oligomer is able to inhibit
CC gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;
Query Match 0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred.No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2165 CTTTTTTTTTTTTTTTTTTT 2186
DB 1 CTTTTTTTTTTTTTTTTTTT 22
RESULT 125
AAQ30430
ID AAQ30430 standard; DNA; 23 BP.
XX
AC AAQ30430;
XX 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX
DE Oligomer IL6803 for forming triplex with HUMIL6 target duplex.
XX
KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW malignancy; hepatitis; inflammation; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 11. .12
FT /*tag= d
FT /note= "o-xyloso dimer synthon linkage"
FT 12. .23
FT /*tag= c
FT /label= inverted_polarity_region
FT /note= "see comments"
FT 23
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN WO9209705-A1.
XX
XX 11-JUN-1992.
PD
XX 25-NOV-1991; 91WO-US008811.
XX
PR 23-NOV-1990; 90US-00617907.
PR 18-JAN-1991; 91US-00643382.
PR 08-APR-1991; 91US-00683420.
PR 17-APR-1991; 91US-00686544.
PR 17-APR-1991; 91US-00686546.
PR 17-APR-1991; 91US-00686547.
PR 27-SEP-1991; 91US-00766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
PI
XX WPI; 1992-217083/26.
DR
XX New oligomers contg. modified bases - which form a triplex with G-C
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.
XX
PS Claim 12; Page 71; 77pp; English.
XX
CC The synthetic oligomer is capable of forming a triplex at physiological
CC pH with a purine rich target sequence by coupling into the major groove
CC of the duplex. The specific target sequence of this oligomer is the human
CC interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC concd. on one strand of the duplex. The oligomer, and others like it are
CC useful in diagnosis and therapy of diseases characterised by specific DNA
CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC tumours and inflammation. The triple helices form under mild conditions
CC thus assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer contains an inverted polarity region
CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC (nucleotides have the 3'positions of xylose sugars linked via the o-
CC xylene ring). Two nucleotides are coupled through a xylene residue to
CC form the dimer synthon. This additional modifications may render the
CC oligomer stable to nuclease activity. The oligomer is able to inhibit
CC gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
CC

XX (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX WPI; 2002-134193/18.
DR
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2150 ATTGATTTTTTCTCCTTTTTTTTTTTT 2179
Db 1 ATATATATTTTTTCTTTTTTTTTTTTTTT 30

RESULT 141
ABL95890
ID ABL95890 standard; DNA; 30 BP.
XX
AC ABL95890;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly f for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
XX WPI; 2002-195876/25.
DR
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
XX their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
PT
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of

CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2150 ATTGATTTTTTCTCCTTTTTTTTTTTT 2179
Db 1 ATATATATTTTTTCTTTTTTTTTTTTTTT 30

RESULT 142
ABS55182
ID ABS55182 standard; DNA; 31 BP.
XX
AC ABS55182;
XX
DT 12-DEC-2002 (first entry)
XX
DE Tumour-suppressor gene associated oligonucleotide.
XX
KW Tumour-suppressor; cancer; ss.
XX
OS Unidentified.
XX
PN KR2001061173-A.
XX
PD 07-JUL-2001.
XX
PF 28-DEC-1999; 99KR-00063661.
XX
PR 28-DEC-1999; 99KR-00063661.
XX
PA (CHAE/) CHAE J H.
PA (CHOI/) CHOI W H.
PA (CHUN/) CHUNG T J.
PA (JUNG/) JUNG H J.
PA (KIMC/) KIM C G.
PA (KIMH/) KIM H G.
PA (PARK/) PARK C I.
PA (PARK/) PARK J H.
XX
PI Chae JH, Choi WH, Chung TJ, Jung HJ, Kim CG, Kim HG, Park CI;
PI Park JH;
XX
DR WPI; 2002-016333/02.
XX
PT Vector containing polymerase chain reaction primers of tumor-suppressor
PT gene, useful for diagnosis of cancer.
XX
PS Disclosure; Page 11; 19pp; Korean.
XX
CC The present invention relates to a new vector comprising polymerase chain
CC reaction (PCR) primers of tumour-suppressor gene. The invention can be
CC useful for the diagnosis of cancer. The present nucleic acid sequence
CC represents an oligonucleotide as described in the invention
XX
SQ Sequence 31 BP; 22 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2774 TTGTTAGAATTGAAAAAATAAAAAA 2803
Db 2 TGGTTGAATATGAAAAAATAAAAAA 31

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PD XX 30-NOV-2000.
PF XX 24-MAY-2000; 2000WO-AU0000498.
PR XX 24-MAY-1999; 99AU-000000510.
PA XX (TACH/) TACHAS G.
PI XX Tachas G;
XX DR WPI; 2001-025093/03.
XX PT Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion.
XX CC Example 3; Page 150; 164pp; English.
XX CC The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori
XX SQ Sequence 26 BP; 23 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2162 CTCCTTTTTCCTTTTTTTTTTTTTTTT 2186
DB 26 CTCCTTTTTCCTTTTTTTTTTTTTTTT 2
RESULT 145
AAZ43904
ID AAZ43904 standard; DNA; 27 BP.
AC AAZ43904;
XX 10-MAR-2000 (first entry)
DT M. tuberculosis rpo-beta primer 17.
DE RNA polymerase; rpo-beta; detection; diagnostic; trap probe; primer; ss.
XX Mycobacterium tuberculosis.
OS EP962536-A1.
PN 08-DEC-1999.
XX 29-MAY-1999; 99EP-00110458.
XX 04-JUN-1998; 98DE-01024900.
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX Weindel K, Brand J;
PI WPI; 2000-055287/05.
XX Selective detection of nucleic acids by amplification with labeled
XX primers and detection with a trap probe.
PS Example 1c; Page 19; 27pp; German.
XX This invention describes a novel method for the selective detection of
CC nucleic acids which comprises amplification of the nucleic acid with the

```


CC (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC under a first nucleic acid concentration, melting hybridized cohesive
CC circularization ends, and reannealing the ends at a second concentration.
CC The methods are useful for the cloning small amounts of nucleic acids and
CC forming genomic libraries of complex populations of DNA or cDNA. The
CC methods allow the cloning of minute amounts of nucleic acids efficiently
CC and avoids the size selection problems of prior art systems. Larger
CC nucleic acid fragments are just as easily cloned, allowing highly
CC representative libraries to be made. Vector to vector ligation is avoided
CC using the methods. AAA40351-A40366 represents primers used to illustrate
CC the method of the invention
XX
SQ Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 4.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2162 CTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 1 CTAGTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 148
AAQ43410
ID AAQ43410 standard; DNA; 31 BP.
AC AAQ43410;
XX
DT 25-MAR-2003 (revised)
DT 29-OCT-1993 (first entry)
XX
DE Structural production oligonucleotide S-Strand-1.
XX
KW Molecular scaffolding; molecule orientation; orient; juxtaposition;
KW functional artificial components; one; two; three; dimensional;
KW structure formation; therapeutic; analytical; industrial; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .15
FT /*tag= a
FT /note= "exposed/exposable sticky end"
FT misc_feature 1
FT /*tag= b
FT /note= "P04-Cytosine"
FT misc_feature 31
FT /*tag= c
FT /note= "Thymine - Teflon based solid support"
XX
PN WO9312244-A1.
XX
XX 24-JUN-1993.
XX
PF 03-DEC-1992; 92WO-US010431.
XX
PR 12-DEC-1991; 91US-00805564.
XX
PA (UJNY) UNIV NEW YORK STATE.
XX
PI Seeman NC, Zhang Y;
XX
DR WPI; 1993-214185/26.
XX
XX Prodn. of structure including double stranded polynucleotide - comprises
PT cleavage of loop in core structure of 1st polynucleotide with restriction
PT enzyme and ligation to 2nd polynucleotide, used to orient mols., etc.
XX
PS Example; Page 34; 58pp; English.
XX
CC The sequence is that of the oligonucleotide S-Strand-1 which can be used
CC in the formation or modification of one-, two- and three- dimensional

CC structures. It may be used as molecular scaffolding to orient and
CC juxtapose other molecules. It has analytical, industrial or therapeutic
CC potential. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 31 BP; 2 A; 4 C; 2 G; 23 T; 0 U; 0 Other;

Query Match 0.8%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 6e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2162 CTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 6 CGCGTTT TTTT TTTT TTTT TTTT TTTT TTTT 30

RESULT 149
ABS64697/c
ID ABS64697 standard; DNA; 35 BP.
AC ABS64697;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polynucleotide #79.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046418.
XX
PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-608256/65.
XX
XX Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Disclosure; Page 57; 442pp; English.
XX
CC The invention describes a method of detecting (M1) a nucleic acid having
CC two portions, involving providing nanoparticles having oligonucleotides
CC attached to it, which has a sequence complementary to sequence of two
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC allow hybridisation of oligonucleotides with two or more portions of
CC nucleic acid, and observing a detectable change brought about by
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC conjugates (II) and the aggregate probe are useful for detecting two or
CC more nucleic acids (from a biological source) having at least two
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC with a disease, synthetic, or structurally-modified natural or synthetic
CC RNA or DNA, or a product of a polymerase chain reaction amplification.
CC (II) is useful for preparing a nanoprobe conjugate for detecting an
CC analyte, and for detecting a nucleic acid bound to an electrode surface.

PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2150 ATTGATTTTTTCTCCTTTTTTTTTTTT 2177
Db || ||||| || ||||| ||||| |||||
3 ATATATTTTTTTTCTTTTTTTTTTTT 30
RESULT 162
ABL95892
ID ABL95892 standard; DNA; 30 BP.
XX
AC ABL95892;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly h for assaying nucleic acids.
XX
DE Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
KW
XX Unidentified.
OS
XX WO200208414-A1.
PN
XX 31-JAN-2002.
PD
XX 27-JUN-2001; 2001WO-IB001147.
PF
XX 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX

PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2150 ATTGATTTTTTCTCCTTTTTTTTTTTT 2177
Db || ||||| || ||||| ||||| |||||
3 ATATATTTTTTTTCTTTTTTTTTTTT 30
RESULT 163
AAV06769
ID AAV06769 standard; DNA; 33 BP.
XX
AC AAV06769;
XX
DT 02-JUN-1998 (first entry)
XX
DE Oligonucleotide containing a pentanucleotide loop.
XX
KW Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
KW circular; bridged; hairpin; detection; pentanucleotide loop; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT repeat_region 1..14 /*tag= a
FT misc_structure 15..19 /*tag= b
FT /*note= "pentanucleotide loop"
FT
XX WO9714708-A1.
PN
XX 24-APR-1997.
PD
XX 29-MAR-1996; 96WO-US004525.
PF
XX 04-OCT-1995; 95US-0004778P.
PR
XX (RESE) RESEARCH CORP TECHNOLOGIES INC.
PA
XX KOOL ET;
PI
XX WPI; 1997-245044/22.
DR
XX New C-5 thiol-substituted nucleoside derivatives - whose presence in
PT oligo:nucleotide(s) allows formation of covalent cross-links between non-
PT complementary DNA domains.
PT
XX Example 7; Page 89; 122pp; English.
PS
XX This sequence represents an oligonucleotide containing a pentanucleotide
CC loop. The invention relates to C-5 thiol-substituted nucleoside

XX Example; Page 10; 13pp; Japanese.

CC The invention relates to performing a thermal cycle of PCR by using a substrate on which a deoxyribonucleic acid (DNA) is immobilized. The method is useful in the medical, biochemical, molecular biological and genetic engineering fields. Sequences ABQ79871-881 represent PCR primers used in the method of the invention

XX Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 21.4; DB 1; Length 27;

Best Local Similarity 95.7%; Pred. No. 5e+02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA AAAAAAAAAA 2803

Db 1 AATTCAAAAAA AAAAAAAAAA 23

RESULT 169

ABX12469

ID ABX12469 standard; DNA; 27 BP.

AC ABX12469;

XX 10-MAY-2003 (first entry)

DT Cocksackie B virus 4 (CBV-4) strain VD2921, PCR primer dT26V.

DE Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4; strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; PCR; primer; ss.

XX Cocksackievirus.

OS WO2002103060-A2.

XX 27-DEC-2002.

PD 19-JUN-2002; 2002WO-IB003278.

XX 20-JUN-2001; 2001SE-00002198.

PR (INNO-) INNOVENTUS PROJECT AB.

PA Tuvemo HT, Frisk GE, Yin H;

XX WPI; 2003-278229/27.

DR Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.

XX Example 5; Page 44; 79pp; English.

XX The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. detection of diabetogenic enteroviral RNA in peripheral mononuclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a primer used to determine the genomic structure of diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921

XX Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;

SQ Query Match 0.8%; Score 21.4; DB 1; Length 27;

Best Local Similarity 85.2%; Pred. No. 5e+02;

Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2161 TCTCCTTTTTTTTTTTTTTTTTTTTTTTA 2187

Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTIV 27

RESULT 170

ADC75074

ID ADC75074 standard; DNA; 27 BP.

XX ADC75074;

AC 01-JAN-2004 (first entry)

DT Biosensor related oligonucleotide of the invention SEQ ID NO:2.

XX ss; biosensor; hybridisation.

OS Synthetic.

XX JP2003172737-A.

PN 20-JUN-2003.

XX 07-DEC-2001; 2001JP-00374764.

PF 07-DEC-2001; 2001JP-00374764.

XX (TOJO) TOYO KOHAN CO LTD.

PA WPI; 2003-819164/77.

XX Solid support body comprising crystal resonator on which a surface treatment layer is formed, and a substrate whose surface treatment layer is chemically modified, useful as biosensor.

PT Disclosure; SEQ ID NO 2; 7pp; Japanese.

PS The invention relates to a novel solid support body comprising a crystal resonator on which a surface treatment layer is formed. The biosensor is useful for analysing biological samples e.g., gene, a protein, and a peptide, and for analysing bioactive substances. Preferably, the biosensor is useful for analysing base sequences by carrying out hybridisation. The present sequence is used in the exemplification of the invention.

XX Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

SQ Query Match 0.8%; Score 21.4; DB 1; Length 27;

Best Local Similarity 95.7%; Pred. No. 5e+02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA AAAAAAAAAA 2803

Db 1 AATTCAAAAAA AAAAAAAAAA 23

RESULT 171

AAA57855/c

ID AAA57855 standard; DNA; 28 BP.

XX AAA57855;

AC 11-OCT-2000 (first entry)

XX Deoxy-A22-tagged substrate oligonucleotide.

DE Ribozyme; catalytic RNA; analyte detection; effector molecule; nucleic acid substrate; in vitro selection; ribozyme ligase; conformation dependent activity; allosteric activation; ss.

XX

23-JUN-1994.

Method for synthesising covalently linked complementary DNA - uses primers which can bind reverse transcriptase and anneal to a distinct template, allowing synthesis to occur.

probe MRCO59 is bound by a hydrolysable linkage to a solid support at its 3' end. It is used by reacting excess probe with a target nucleic acid; nicking hybridised probe at least once within a predetermined sequence to form 2 or more probe fragments hybridised to the target sequence, which results in the probe fragments becoming hybridised to another probe; and identifying probe fragments, so detecting the target sequence. The probe can react with target sequence to complete a cycling sequence. Using this system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)

Sequence 26 BP: 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other; XX

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 76.9%; Pred. No. 5e+02;
Matches 20; Conservative 3; Mismatches 3; Indels

```
QY      2155 TTTTCTCCCTTTTTTTTTTTT 2180
          ||||| | ::|||||
pb      1 TTTTTTTTTUUUUTTTTTTTTTT 26
```

RESULT 183
AAN92242
ID AAN92242 standard: DNA: 26 BP.

AC	AAN92242;	(revised)
XX		(revised)
DT	25-MAR-2003	(first en
DT	31-OCT-2002	
DT	25-APR-1990	

DE SS probe MRC060.

xx probe MRC060: solid support: ribonuclease.

OS Synthetic.

XX	Key	Location/Qualifiers
----	-----	---------------------

```

FT misc_feature 1. .12 /*tag= a /note= "deoxyribonucleotides."
FT
FT
FT misc_feature 13. .16 /*tag= b /note= "ribonucleotides."
FT
FT
FT misc_feature 17. .26 /*tag= c /note= "deoxyribonucleotides."
FT
FT

```

XX PN WO8910415-A.

02-NOV-1989.

29-APR-1988: 88US-00187814.

PR 29-APR-1988: 88US-00187814.

PA (MEIO-) MEIOGENICS INC.

PI Duck P, Bender R;

WPI: 1989-339977/46.

Detecting target nucleic acid molecules - using excess complementary nucleic acid probes and nicking to complete a cycling sequence.

PS Disclosure: Page 24: 34pp; English.

Probe MRCO60 is bound by a hydrolysable linkage to a solid support at its 3' end. It is used by reacting excess probe with a target nucleic acid; nicking hybridised probe at least once within a predetermined sequence to form 2 or more probe fragments hybridised to the target sequence, which

results in the probe fragments becoming hybridised to another probe; and identifying probe fragments, so detecting the target sequence. The probe can react with target sequence to complete a cycling sequence. Using this system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)

Sequence 26 BP: 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other; XX

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 5e+02;
Matches 19; Conservative 4; Mismatches 3; Indels

Qy 2155 TTTTTTCTCCCTTTTTTTTTTTTTT 2180
 ||||| | |:::| | | | |
 db 1 TTTTTTTTTTTTTUUUUUUUUUUUUUUUU 26

RESULT 184
AAX07466
ID AAX07466 standard; cdNA; 26 BP.

AC AAX07466:

08-JUN-1999 (first entry)

xx DE Human BS124 specific EST clone oligonucleotide.

BS124; breast; cancer; detection; diagnosis; prevention; treatment; EST;
KW
SS.

OS Synthetic.

PN WO9859049-A1.

30-DEC-1998.

19-JUN-1998; 98WO-US012862.

XX	20-JUN-1997:	97US-00879354.
PR		

PA (ABBO) ABBOTT LAB.

AA
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC;
PI Scheffel CP, Stroupe SD, Yu H;

WPI: 1999-105623/09.

AA New isolated BSI24 polynucleotides and polypeptides - used for detecting,
PT diagnosing, preventing or treating diseases or conditions of the breast,
PT such as breast cancer.
PT

xx PS Disclosure: page 97: 125pp: English.

AA The sequence is that of an oligonucleotide used in the isolation of a
CC
CC BS124-specific EST clone. It is useful for detecting, diagnosing,
CC
CC staging, preventing or treating, or determining predisposition to
CC diseases or conditions of the breast, such as breast cancer

sequence 26 BP: 0 A: 0 C: 1 G: 25 T: 0 U: 0 Other:

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels

Qy 2168 TTTTCTTTTTTTTTTTTTTAAGTTTG 2193
|||||
Nb 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 26
|||||

RESULT 185

The invention relates to human secreted salivary polypeptide designated as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63 can be used in detecting agonists and antagonists of its activity, and is also useful as a host defense polypeptide, immune modulating factor, antipathogenic polypeptide, cell-cell signalling molecule, growth factor, cytokine, or as secreted extracellular matrix associated proteins with growth factor hormone activity. It is useful for treating conditions associated with pathological microbes, including bacterial, fungal and

XX
PT
Nicot
aides
NC
Sacc
PM
Curre
I
vato
4
1
vi
1
1

Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG 26

RESULT 200
ABQ76254
ID ABQ76254 standard; DNA; 27 BP.
XX
AC ABQ76254;
XX
DT 08-NOV-2002 (first entry)
XX
DE Murine SCCE 5'-RACE oligonucleotide SEQ ID 42.
XX
KW SCCE; murine; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; ss.
XX
OS Mus musculus.
XX
PN WO200262135-A2.
XX
PD 15-AUG-2002.
XX
PF 08-FEB-2002; 2002WO-IB001300.
XX
PR 09-FEB-2001; 2001CA-02332655.
PR 09-FEB-2001; 2001DK-00000218.
XX
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
PI Egelrud T, Hansson L;
XX
DR WPI; 2002-643380/69.
XX
PT Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
PS Example 6; Page 36; 74pp; English.
XX
CC This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a
CC compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of
CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents a 5' RACE cDNA
CC synthesis primer used in a method of detecting homologues to human
CC stratum corneum chymotryptic enzyme, SCCE, gene. SCCE is a serine
CC protease synonymous with human kallikrein 7 (KLK7) and is used in the
CC development of the transgenic mammals described in the invention
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

Query Match 0.8%; Score 21.2; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 5.5e+02;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTTTTTAA 2187
Db 5 TTTTTTTTTTTTTTTTTTTTTTTT 26

RESULT 201
ABX89953
ID ABX89953 standard; DNA; 30 BP.
XX
AC ABX89953;
XX
DT 30-APR-2003 (first entry)
XX
DE PolyA adapter DNA.
KW Probe; detection; genotyping; cell status; chromosomal resistance gene;
KW array; ss.
XX
OS Synthetic.
XX
PN DE10117857-A1.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2001; 2001DE-01017857.
XX
PR 10-APR-2001; 2001DE-01017857.
XX
PA (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX
PI Ellinger T, Ehricht R, Wagenhaus A, Ermantraut E;
XX
DR WPI; 2003-068801/07.
XX
PT Detecting specific interactions between molecular targets and probes,
PT useful for determining genotypic and physiological status of cells, by
PT attaching an markable adapter to the target.
XX
PS Example 1; Page 8; 25pp; German.
XX
CC This invention describes a novel method for detecting the specific
CC interaction between a target sequence, especially a nucleic acid, and a
CC probe on an array, in which adapter molecules are fixed to the target,
CC forming a continuous sequence. Labelling of the target is independently
CC mediated by interaction of the adapter molecule with a label. The method
CC is used to investigate the genotypic and physiological status of cells,
CC e.g. to detect chromosomal resistance genes in Staphylococcus aureus. The
CC method provides a modular, specific and sensitive system for quantitative
CC or qualitative detection of a specific target. It provides efficient,
CC homogeneous and parallel labeling of a target, before, during or after
CC interaction with the probe array, and both DNA and RNA can be labeled.
CC The detection signal may be amplified and only low concentrations of
CC label (particularly 0.1-1 micro M) are used, so non-specific signals are
CC minimised. This sequence represents a polyA adapter used in the method
CC described in the invention
XX
SQ Sequence 30 BP; 5 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 21.2; DB 1; Length 30;
Best Local Similarity 88.5%; Pred. No. 7.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2167 TTTTTTTTTTTTTTTTTTTTAACTTT 2192
Db 1 TTTTTTTTTTTTTTTTATATAT 26

RESULT 202
AAQ75733
ID AAQ75733 standard; DNA; 21 BP.
XX


```

AC AAQ75733;
XX
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
XX JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 8; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.le+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2170 TTTTTTTTTTTTTTTTAACT 2190
Db 1 TTTTTTTTTTTTTTTTAACT 21

RESULT 203
AAQ75757/c
ID AAQ75757 standard; DNA; 21 BP.
XX
XX AC AAQ75757;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX PA
XX

```

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX

PS Disclosure; Page 8; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX

SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2782 ATTGAAAAA AAAAAAAAAA 2802

Db |||||||

21 ATTGAAAAA AAAAAAAAAA 1

RESULT 204

AAX26973

ID AAX26973 standard; cDNA; 21 BP.

XX

AC AAX26973;

XX

DT 25-JUN-1999 (first entry)

XX

DE Primer used to reverse transcribe mamaglobin RNA.

XX

KW Human; mammary-specific protein; mamaglobin; antigen; vaccine;

KW mamaglobin-expressing cancer; breast cancer;

KW autologous tumor lymphocyte; diagnosis; marker; primer; ss.

XX

OS Synthetic.

XX

PN WO9914230-A1.

XX

PD 25-MAR-1999.

XX

PF 18-SEP-1998; 98WO-US017991.

XX

PR 18-SEP-1997; 97US-00933149.

XX

PA (UNIW) UNIV WASHINGTON.

XX

PI Watson MA, Fleming TP;

XX

DR WPI; 1999-244021/20.

XX

PT Mamaglobin, secreted protein overexpressed in breast cancer.

XX

PS Example 2; Page 55; 60pp; English.

XX

CC The present primer was used to reverse transcribe RNA encoding a human

CC mammary-specific protein, designated mamaglobin. The specification

CC describes a protein comprising a mamaglobin antigen that is recognized

CC by B and/or Tc cells specific for the natural, secreted and glycosylated

CC form of mamaglobin polypeptide. This protein, or recombinant vectors

CC that express it, are used in vaccines for treating mamaglobin-

CC expressing cancers, specifically of the breast. Such cancers can also be

CC treated using autologous tumor lymphocytes activated ex vivo with an

CC mamaglobin antigen, then returned to the patient. Expression of

CC mamaglobin is elevated in 27% of stage I primary breast cancers, so it

CC represents a marker useful for diagnosis of this disease

XX

•

XX
KW Branched chain compound; nucleic acid synthesis; primer extension;
KW reverse transcription; nucleic acid hybridization;
KW nucleic acid amplification; ss.

CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is a PCR primer specific for
CC human TFAP2C DNA. This sequence is used to illustrate the method of the
CC invention
XX
SQ Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match. 0.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1123 TGTCTGTGAAGCCGAATTTC 1143
Db 21 TGTCTGTGAAGCCGAATTTC 1

RESULT 212
ACH03246
ID ACH03246 standard; DNA; 21 BP.

AC ACH03246;

XX 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #881.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX Synthetic.

XX US2003050268-A1.

XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.

XX (BERG/) BERG D J.

XX Krieg AM, Berg DJ;

XX WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.

XX Disclosure; Page 33; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid

XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
Db 1 TTTTTTTTTTTTTTTTTTTT 21

RESULT 213

ADB37209

ID ADB37209 standard; DNA; 21 BP.

XX ADB37209;

XX 04-DEC-2003 (first entry)

DE Immunostimulatory nucleic acid #823.

XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.

XX Synthetic.

XX US2003087848-A1.

XX 08-MAY-2003.

XX 02-FEB-2001; 2001US-00776479.

XX 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.

XX (PETE/) PETERSEN D M.

XX (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2003-657977/62.

XX Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure; Page 17; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.

XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
Db 1 TTTTTTTTTTTTTTTTTTTT 21

RESULT 214

AAQ64724/c

ID AAQ64724 standard; cDNA to mRNA; 22 BP.

XX AAQ64724;

XX 25-MAR-2003 (revised)

XX 04-JAN-1995 (first entry)

DE 2',5'-linked tetraadenylate-anti(dT)18 oligonucleotide chimeric mol.

XX antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW RNA cleavage; antiviral therapy; chimeric molecule; PKR;
KW protein synthesis regulation; phosphorylation; eIF-2alpha;
KW eukaryotic translation initiation factor; ss.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT misc_feature 1. .4
FT /*tag= a
FT /label= 2',5'-linked tetraadenylate
FT /note= "nucleotides linked through phosphodiester bonds
FT at hydroxyl groups of 2' and 5' carbons"
FT 4. .5
FT /*tag= b
FT /note= "the 2-5A moiety (*tag = a) and the antisense DNA
FT sequence (*tag = c) are linked by two 1,4-butanediol
FT molecules linked through phosphodiester bonds"
FT 5. .22
FT /*tag= c
FT /note= "antisense region, complementary to oligo dT"
FT
XX WO9409129-A2.
XX
XX 28-APR-1994.
XX
XX 20-OCT-1993; 93WO-US010103.
XX
XX 21-OCT-1992; 92US-00965666.
PR 17-SEP-1993; 93US-00123449.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CLEV-) CLEVELAND CLINIC RES INST.
XX
XX Torrence P, Silverman R, Maitra R, Lesiak K;
XX WPI; 1994-151315/18.
DR
XX Specific cleavage of RNA, useful partic. for treating viral infection,
PT cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
PT of 2-5A dependent RNase.
XX
XX Example 9; Page 66; 86pp; English.
PS
XX This sequence was used to determine whether 2-5A-antisense chimeric
CC molecules are inhibitory to cell growth. The molecules AAQ64709, AAQ64711
CC and AAQ64724 all lacked cytotoxicity. In the novel 2-5A-antisense
CC oligonucleotide chimeric molecules, the antisense region targets the
CC chimeric molecule to a particular region of RNA to be specifically
CC cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A
CC RNase. Typical applications are treatment of viral infections (esp. for
CC cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular
CC disorders (e.g. restenosis after angioplasty), genetic disorders,
CC osteoarthritis or rheumatoid arthritis. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTTTTTTTTTTTTTTTTTT 2186
Db 22 TTTTTTTTTTTTTTTTTTTT 2
RESULT 215
AAAF17413/C
ID AAF17413 standard; DNA; 22 BP.
XX
AC AAF17413;

XX 09-MAR-2001 (first entry)
DT L1 cleavage site related sequence #3.
XX
DE
XX Retrotransposon; genetic defect; cystic fibrosis; ds.
KW
XX Unidentified.
OS
XX US6150160-A.
PN
XX 21-NOV-2000.
PD
XX 28-APR-1997; 97US-00847844.
PF
XX 16-NOV-1995; 95US-0006831P.
PR 15-NOV-1996; 96US-00749805.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA (UYPE-) UNIV PENNSYLVANIA.
XX
XX Moran JV, Dombroski BA, Kazazian HH, Boeke JD;
PI WPI; 2001-060015/07.
XX
XX DNAC comprising a promoter P and an L1 cassette sequence having a core
PT retrotransposon element, useful for random insertion of a heterologous or
PT homologous DNA sequence into a cell genome and for correcting genetic
PT defects.
XX
PS Disclosure; Fig 14; 87pp; English.
XX
XX The present invention relates to DNA for a promoter and an L1 cassette
CC sequence having a core retrotransposon element. The invention is useful
CC for random insertion of a heterologous or homologous DNA sequence into a
CC cell genome, and for correction of a genetic defect in the cell into
CC which the insertion is made. Genetic defects which may be corrected
CC includes cystic fibrosis, mutations in the dystrophin gene, genetic
CC defects associated with blood clotting and other genetic defects
XX
SQ Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTTTTTTTTTTTTTTTTTT 2186
Db 22 TTTTTTTTTTTTTTTTTTTT 2
RESULT 216
AAC62450
ID AAC62450 standard; DNA; 23 BP.
XX
AC AAC62450;
XX
XX 07-FEB-2001 (first entry)
DT
XX Cleavage of nucleic acids from solid supports assay oligonucleotide #1.
DE
XX Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW nucleic acid purification; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT misc_RNA 23
FT /*tag= a
XX
XX WO200058329-A1.
PN
XX

PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB001190.
XX
PR 29-MAR-1999; 99GB-00007245.
XX
PA (GOLD/) GOLDSBOROUGH A.
XX
DR WPI; 2000-664908/64.
XX
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves cleaving
PT the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS Disclosure; Page 16; 47pp; English.
XX
CC The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is
CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention
XX
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 217
AAC62451
ID AAC62451 standard; RNA; 23 BP.
XX
AC AAC62451;
XX
DT 07-FEB-2001 (first entry)
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #2.
XX
KW Nucleic acid cleavage; solid support; affinity chromatography;
KW sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.
XX
OS Synthetic.
XX
PN WO200058329-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB001190.
XX
PR 29-MAR-1999; 99GB-00007245.
XX
PA (GOLD/) GOLDSBOROUGH A.
XX
DR WPI; 2000-664908/64.
XX
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves cleaving
PT the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS Example 1; Page 32; 47pp; English.
XX
CC The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is

CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention
XX
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 0 T; 23 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 23;
Best Local Similarity 0.0%; Pred. No. 3.9e+02;
Matches 0; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 1 UUUUUUUUUUUUUUUUUUUUUUUUUUU 21

RESULT 218
AAFI6627
ID AAF16627 standard; DNA; 23 BP.
XX
AC AAF16627;
XX
DT 13-MAR-2001 (first entry)
XX
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.
XX
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
XX
PN WO200071164-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-AU0000498.
XX
PR 24-MAY-1999; 99AU-00000510.
XX
PA (TACH/) TACHAS G.
XX
PI Tachas G;
XX
DR WPI; 2001-025093/03.
XX
PT Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion.
XX
PS Example 3; Page 152; 164pp; English.
XX
XX
CC The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori
XX
SQ Sequence 23 BP; 1 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 3 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 23

```

XX 06-JUN-1995; 95US-00470911.
PF
XX
XX 28-AUG-1992; 92US-00938189.
PR
XX 02-FEB-1993; 93US-00014943.
PR
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
PA
XX Bergemann AD, Johnson EM;
PI
XX
XX WPI; 1998-321632/28.
DR
XX
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR
PT element or other proteins.
PT
XX
XX Example 7.1.1; Col 33; 63pp; English.
PS
XX
XX This is the nucleotide sequence of an oligonucleotide used as a
CC competitor with the PUR element in the method of the invention, involving
CC the use of the PUR protein and its fragments, which inhibit PUR protein
CC binding to PUR element or other proteins. Inhibitors of PUR activity may
CC be useful for treating viral infections and hyperproliferative diseases
CC such as cancer
CC
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
    Query Match          0.7%; Score 21; DB 1; Length 24;
    Best Local Similarity 100.0%; Pred. No. 4.4e+02;
    Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2186
DB 24 TTTTTTTTTTTTTTTTTTTT 4

RESULT 221
AAX04086/c
ID AAX04086 standard; DNA; 24 BP.
XX
AC AAX04086;
XX
DT 12-APR-1999 (first entry)
XX
DE Oligonucleotide POLYA used in PUR cloning and sequencing.
XX
XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW monoclonal antibody; identification; characterisation; ss.
KW
XX Synthetic.
OS Homo sapiens.
OS
XX US5869622-A.
XX
XX 09-FEB-1999.
PD
XX
XX 07-JUN-1995; 95US-00486809.
PF
XX
XX 28-AUG-1992; 92US-00938189.
PR
XX 02-FEB-1993; 93US-00014943.
PR
XX 06-JUN-1995; 95US-00470911.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
PA
XX
XX Bergemann AD, Johnson EM;
PI
XX
XX WPI; 1999-152881/13.
XX
XX Monoclonal antibody specific for PUR protein - useful for treating
PT cancer.
PT
XX
XX Example; Col 33; 64pp; English.
PS
XX
XX The present invention describes a monoclonal antibody that specifically

```


PR 23-AUG-2000; 2000US-0227436P.
XX (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMEH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
DR
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
PT
XX
PS Claim 101; Page 57; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 24 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4

RESULT 227
ABV14842
ID ABV14842 standard; cDNA; 24 BP.
XX
AC ABV14842;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 14833.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
DR

XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 2483; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 228
ABS78477
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #961.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophilic joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX Bratzler RL;
PI
XX WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 229
ABS77949
ID ABS77949 standard; DNA; 24 BP.
XX
AC ABS77949;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #433.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 27; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, and
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 230
ABS78478/c
ID ABS78478 standard; DNA; 24 BP.
XX
AC ABS78478;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #962.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, and
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

RESULT 233
AAS17869/C
ID AAS17869 standard; DNA; 24 BP.
XX AC AAS17869;
XX AC AAS17869;
DT 08-MAY-2002 (first entry)
XX A24 oligonucleotide used to create doPTAR chemiluminescer particles.
DE XX Polymorphism detection; sequence detection; mutation detection; A24;
KW probe; non-dissociative termolecular complex; doPTAR sensitizer particle;
KW single nucleotide polymorphism; SNP; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 24
FT /*tag= a
FT /note= "A is covalently linked to a
FT PO2OCH2CH2CH2SSCH2CH2CH2OH moiety"
XX WO200190399-A2.
XX 29-NOV-2001.
XX 17-MAY-2001; 2001WO-US016089.
XX 19-MAY-2000; 2000US-00574596.
XX (DADE-) DADE BEHRING INC.
XX Patel RD;
XX WPI; 2002-097664/13.
XX Detecting presence of polynucleotide; differences between polynucleotide
PT sequences, useful for detecting single nucleotide polymorphism and
PT alleles of polynucleotide sequence involves use of three competitive
PT probes.
XX Example; Page 47; 75pp; English.
XX This invention represents a method for detecting the presence of a
CC polynucleotide sequence, differences in polynucleotide sequences or
CC mutations in genomic DNA. The method involves contacting 3
CC oligonucleotide probes with a sample containing a polynucleotide. The
CC first probe hybridises to a region of the polynucleotide sequence and the
CC second and third probes can bind a second region of the polynucleotide
CC sequence. The second and third probes are identical except for the
CC presence or difference of one or more nucleotides. The reaction medium is
CC then subjected to conditions for forming substantially non-dissociative
CC termolecular complexes, which can be at least one of, the polynucleotide
CC sequence with the first and second probes or the polynucleotide sequence
CC with the first and third probes. The oligonucleotide probes have labels
CC non-covalently bound to allow for their detection upon binding. The
CC method of the invention is useful for detecting the presence of a single
CC nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method
CC can be used for the direct detection of nucleic acid in very small
CC quantities without amplification. In addition, the method may be carried
CC out with amplification of the target and reference sequences. This
CC sequence represents an oligonucleotide probe A24 used to create doPTAR
CC chemiluminescer sensitizer particles in the method of the invention.
CC Binding the nucleic acid to a suspendable particle acts as a support and
CC provides a means of segregating the bound polynucleotide target from the
CC bulk solution
XX SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 24 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4
RESULT 234
ABK15639
ID ABK15639 standard; DNA; 24 BP.
XX AC ABK15639;
XX 08-MAY-2002 (first entry)
XX RNA-PCR procedure primer poly(dT)24.
XX RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy;
KW mRNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense;
KW high throughput screening; D-RNAi; DNA-RNA interference; RdRp;
KW RNA dependent RNA polymerase; posttranscriptional gene silencing.
XX OS Synthetic.
XX WO200210374-A2.
XX 07-FEB-2002.
XX 02-AUG-2001; 2001WO-US024412.
XX 02-AUG-2000; 2000US-0222479P.
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX Lin S, Chuong C, Widelitz RB;
XX WPI; 2002-188740/24.
XX Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or
PT treating or preventing microbe related genes, comprises thermocycling
PT steps of promoter-linked double-stranded cDNA or RNA synthesis.
XX Example 5; Page 26; 53pp; English.
XX The invention relates to generating mRNA-cDNA hybrids, comprising (a)
CC providing a solution containing a nucleic acid template, one or more
CC primers complementary to the sense conformation of the nucleic acid
CC template, and one or more promoter-linked primers complementary to the
CC antisense conformation of the nucleic acid template, and with an RNA
CC promoter, (b) treating the nucleic acid template with the one of more
CC primers to synthesise a first cDNA strand, (c) treating the first cDNA
CC strand with one or more promoter-linked primers to synthesise a promoter-
CC linked double-stranded nucleic acid, (d) treating the promoter-linked
CC double-stranded nucleic acid to synthesise amplified mRNA fragments and
CC (e) treating the mRNA fragments with one or more primers to synthesise
CC mRNA-cDNA hybrids by reverse transcription of the amplified mRNA
CC fragments. The method is useful for preparing high amounts of pure and
CC specific mRNA-cDNA hybrids for transducing biological effects of interest
CC in vitro as well as in vivo, for inhibiting gene function in prokaryotes
CC and eukaryotes in vivo and in vitro, for suppressing cancer-related
CC genes, in treating or preventing microbe related genes, in studying
CC candidate molecular pathways with systematic knock out of involved
CC molecules, in high throughput screening of gene functions based on
CC microarray analysis, and as a tool in studying gene function in
CC physiological conditions. The mRNA-cDNA hybrids may be used to screen for
CC special gene functions, for manipulating gene expression in vitro, and
CC for designing therapy for genetic diseases in vivo. The cDNA part of a D-
CC RNAi (DNA-RNA interference) can be modified by nucleotide analogue
CC incorporation to increase the stability and effectiveness of transfected
CC probe activities. The RdRp (RNA dependent RNA polymerase) enzyme may
CC provide higher affinity of the mRNA template of a D-RNAi compared to ds-
CC RNA due to lower binding interaction between DNA-RNA duplexes than RNA-
CC RNA duplexes. The cDNA part of a D-RNAi provides further antisense gene
CC knockout activity in addition to the posttranscriptional gene silencing

CC (PTGS) mechanisms of the sense-RNA template, resulting in multiple
CC specific gene interference effects with one probe. The present sequence
CC is a poly(dT) PCR primer used in conjunction with oligo(dC)10N primers to
CC reverse transcribe mRNA into first strand cDNA in the method of the
CC invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2186
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 235
ACA58802
ID ACA58802 standard; DNA; 24 BP.
XX
AC ACA58802;
XX
DT 10-JUN-2003 (first entry)
XX
DE Gastric ulcer treatment immunostimulatory nucleic acid #148.
XX
KW Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;
KW Helicobacter pylori.
XX
OS Synthetic.
XX
PN US2002198165-A1.
XX
PD 26-DEC-2002.
XX
PF 01-AUG-2001; 2001US-00920313.
XX
PR 01-AUG-2000; 2000US-0222248P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
XX
PI Bratzler RL, Petersen DM;
XX
DR WPI; 2003-370798/35.
XX
PT Prevention or treatment of gastric ulcer involves administering nucleic
PT acid.
XX
PS Disclosure; Page 14; 45pp; English.
XX
CC The invention relates to a method of prevention or treatment of gastric
CC ulcer comprising administering a nucleic acid to a subject in need for
CC treatment of gastric ulcer. A nucleic acid sample comprising
CC oligonucleotide 2006 was administered to a mouse model by an oral route
CC or a vehicle control. Colonisation of mice by Helicobacter pylori was
CC assessed at time points from 1 day to 1 month after treatment. The
CC ability of the nucleic acid to reduce H. pylori colonisation was
CC assessed. The method is useful for preventing or treating a gastric ulcer
CC on a subject e.g. human or non-human vertebrate animal including dog,
CC cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,
CC rabbit, turkey, chicken, primate, rat and mouse. The method effectively
CC treats or prevents gastric ulcers. The present sequence represents an
CC immunostimulatory nucleic acid for the treatment of gastric ulcers
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2186

DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 236
ABX79809
ID ABX79809 standard; cDNA; 24 BP.
XX
AC ABX79809;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #134.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
PN US6472154-B1.
XX
PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX
PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
PS Example; Col 579; 588pp; English.
XX
CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79809 are
CC the polymorphic repeats identified for a search of human ESTs
XX
SQ Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2186
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 237
ABZ80181

the effect of proposed drug on the aberrant protein. M1 is also useful for differential screening of tissue-specific gene expression at a cellular level, and for preparing labeled RNA/DNA probes for a gene chip technology, and for determining the efficacy of a drug regiment against a gene or its cDNAs. The present sequence is an Oligo (dT)24 RT-(reverse transcriptase) PCR primer used to produce first strand cDNA in the method of the invention

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Query Match          0.7%;   Score 21;   DB 1;   Length 24;
Best Local Similarity 100.0%;   Pred. No. 4.4e+02;
Matches 21;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```

QY 2166 TTTTTTTTTTTTTTTTTT 2186
Db 1 TTTTTTTTTTTTTTTTTT 21

RESULT 239
ACD99729
ID ACD99729 standard; DNA: 24 BP.

2 Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels

QY 2166 TTTTTTTTTTTTTTTT 2186

Db 1 TTTTTTTTTTTTTTTTTT 21

RESULT 240
ACH03285/C
ID ACH03285 standard; DNA; 24 BP.
XX
AC ACH03285;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #920.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

Query Match	0.7%;	Score 21;	DB 1;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 4.4e+02;		
Matches 21; Conservative	0;	Mismatches	0;	Indels

Qy	2166	TTTTTTTTTTTTTTTTTTTT	2186
Db	24	TTTTTTTTTTTTTTTTTTTT	4

RESULT 241
ACH03284
ID ACH03284 standard; DNA; 24 BP.

Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;

99Tz 99Tz 98Tz 98Tz

antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss. XX

Synthetic. OS

US2003050268-A1. XX

13-MAR-2003. XX

29-MAR-2002; 2002US-00112653. XX

29-MAR-2001; 2001US-0279642P. XX

(KRIE/) KRIEG A M. XX

(BERG/) BERG D J. XX

Krieg AM, Berg DJ; XX

WPI; 2003-521815/49. XX

Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid. XX

Disclosure; Page 34; 229pp; English. XX

The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. XX

This sequence represents an immunostimulatory nucleic acid XX

Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other; XX

Query Match 0.7%; Score 21; DB 1; Length 24; XX

Best Local Similarity 100.0%; Pred. No. 4.4e+02; XX

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186 XX

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21 XX

RESULT 242 XX

ADA66379/c XX

ID ADA66379 standard; mRNA; 24 BP. XX

AC ADA66379; XX

DT 20-NOV-2003 (first entry) XX

DE mRNA poly A. XX

ss; nucleic acid amplification; multiple step elimination; varying reaction condition elimination; poly A tract. XX

Unidentified. OS

Key Location/Qualifiers XX

primer_bind 1. .24 XX

/*tag= a XX

/note= "Binds to nucleotides 42-19 of the 1st strand cDNA synthesis primer" XX

US6582938-B1. XX

24-JUN-2003. XX

11-MAY-2001; 2001US-00854317. XX

XX 11-MAY-2001; 2001US-00854317.
PR (AFFY-) AFFYMETRIX INC.
XX
XX Su X, Dong H, Ryder TB;
PI WPI; 2003-656427/62.
XX
XX Amplification of nucleic acids, where the promoter is blocked from
PT extension at the 3' end, useful for eliminating multiple step reactions.
PT
XX Disclosure; Fig 2; 9pp; English.
XX
XX The invention relates to a method of amplification of nucleic acid which
CC comprises primer extension by reverse transcriptase and hybridising an
CC oligonucleotide to the single stranded DNA, where the oligonucleotide is
CC blocked from extension at the 3' end. The method is useful for
CC amplification of nucleic acids. In the new method, a promoter is
CC protected from degradation throughout the method. The promoter is
CC constructed so that it does not serve as a primer for extension of a
CC sequence that is complementary to the target sequence, i.e. it is
CC blocked. The method can be combined with other processes to eliminate the
CC need for multiple steps and varying reaction conditions and their
CC associated problems. At least three otherwise separate enzymatic
CC reactions can occur consecutively in one phase (i.e., without organic
CC extraction and precipitation), more preferably in the same reaction
CC vessel. Preferably, cDNA synthesis according to the new method may occur
CC in a modified low salt buffer. The present sequence represents the poly A
CC tract of a mRNA used to illustrate the method of the invention.
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 24 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4

RESULT 243
ADB37258
ID ADB37258 standard; DNA; 24 BP.
XX
AC ADB37258;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #872.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX

OS Rattus sp.
XX US5422262-A.
PN
XX 06-JUN-1995.
PD
XX 18-NOV-1991; 91US-00795859.
PF
XX 30-APR-1990; 90US-00517661.
PR
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX Andersson S, Russell DW;
PI
XX WPI; 1995-214658/28.
DR
XX Steroid 5 alpha-reductase nucleic acid segments and recombinant vectors -
PT where the sequences are useful in e.g. analysis of normal and abnormal
PT sexual differentiation.
XX
PS Example 1; Col 21; 72pp; English.
XX
XX 5-alpha reductase enzymes catalyse the conversion of testosterone to
CC dihydroxytestosterone. The rat steroid 5-alpha reductase I (SRD5A-I) cDNA
CC sequence has been isolated and purified using the PCR primer AAQ97396.
CC The rat enzyme cDNA can be used in the prepn. of genetic constructs for
CC the large scale production of SRD5A or as probes for enzyme-encoding
CC sequences from alternative sources. The sequences are also useful in the
CC analysis of normal and abnormal sexual differentiation, benign prostatic
CC hyperplasia, male pattern baldness; acne; hirsutism and endometriosis.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 29 BP; 1 A; 4 C; 4 G; 20 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 2165 CTTTTTTTTTTTTTTTTTTT 2185
Db 9 CTTTTTTTTTTTTTTTTTTT 29
XX
RESULT 264
AAT99803
ID AAT99803 standard; DNA; 29 BP.
XX
AC AAT99803;
XX
DT 20-MAR-1998 (first entry)
XX
DE Primer for rat steroid 5alpha-reductase coding sequence.
XX
KW Steroid 5alpha-reductase; enzyme; testosterone conversion; inhibitor;
KW rat; PCR primer; amplify; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN US5679521-A.
XX
PD 21-OCT-1997.
XX
PF 01-JUN-1995; 95US-00457616.
XX
PR 30-APR-1990; 90US-00517661.
PR 18-NOV-1991; 91US-00795859.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Russell DW, Andersson S;
XX
DR WPI; 1997-525718/48.

XX
PT Production of recombinant steroid 5alpha-reductase enzyme - by culturing
PT cell containing DNA encoding the enzyme.
XX
PS Example 1; Col 20; 70pp; English.
XX
CC This sequence is a primer for the DNA encoding rat steroid 5alpha-
CC reductase. The encoded enzyme can be produced by the method of the
CC invention. The method is for producing a steroid 5alpha-reductase, and
CC comprises preparing a recombinant host cell containing a DNA segment
CC encoding a steroid 5alpha-reductase and culturing the cell under
CC conditions such that the steroid 5alpha-reductase is produced by the
CC cell. The steroid 5alpha-reductase produced by the method is used for
CC identifying substances that affect the enzymatic activity of steroid
CC 5alpha-reductase. Substances identified as inhibiting steroid 5alpha-
CC reductase activity can be used for inhibiting the conversion of
CC testosterone
XX
SQ Sequence 29 BP; 1 A; 4 C; 4 G; 20 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 2165 CTTTTTTTTTTTTTTTTTTT 2185
Db 9 CTTTTTTTTTTTTTTTTTTT 29
XX
RESULT 265
AAT69677/c
ID AAT69677 standard; DNA; 30 BP.
XX
AC AAT69677;
XX
DT 25-MAR-2003 (revised)
DT 19-FEB-1998 (first entry)
XX
DE Downstream primer for synthetic full length CAT sense RNA.
XX
KW PCR primer; CAT RNA; detection; quantification; determination; ss.
XX
OS Synthetic.
XX
PN EP780479-A2.
XX
PD 25-JUN-1997.
XX
PF 19-DEC-1996; 96EP-00120480.
XX
PR 23-DEC-1995; 95DE-01048680.
XX
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Leying H, Hinzpeter M, Wittor H, Fritton H;
XX
DR WPI; 1997-322152/30.
XX
PT Detection and quantitation of nucleic acid using probe with label and
PT binding group - and after hybridisation treatment with RNase and capture
PT on solid phase, particularly for RNA.
XX
PS Example 2; Page 7; 13pp; German.
XX
CC The present sequence is a PCR primer for synthetic full length CAT sense
CC RNA, which was used in a novel method for the detection and quantitative
CC determination of specific oligonucleotides (ON) or polynucleotides (PN).
CC The method comprises combining a sample containing RNA or single stranded
CC DNA with a lysis/hybridisation buffer, treating the homogenised solution
CC with 1 or more probes, which are essentially complementary to the ON or
CC PN and contain at least 2 different labels, one a specific binding group
CC and the other a detectable chemical group, hybridising under stringent

Query Match 0.7%; Score 21; DB 1; Length 32;
Best Local Similarity 82.8%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2776 GTTGAATTTGAAAAAATAAAAAAAAAA 2804
Db 4 GGTAAAAAATAAAAAAAAAAATAAAAAA 32

RESULT 272
AAV03988
ID AAV03988 standard; DNA; 32 BP.
XX
AC AAV03988;
XX
DT 13-MAY-1998 (first entry)
XX
DE Primer B for Non-A non-B hepatitis viral peptide coding sequence.
XX
KW Non-A non-B hepatitis virus; antibody production; infection diagnosis;
KW PCR primer; amplify; ss.
XX
OS Synthetic.
OS Hepatitis virus.
XX
PN JP04084887-A.
XX
PD 18-MAR-1992.
XX
PF 25-JUL-1990; 90JP-00198588.
XX
PR 25-JUL-1990; 90JP-00198588.
XX
PA (KAGA) KAGAKU OYOBI KESSEI RYOHU.
XX
DR WPI; 1992-145501/18.
XX
PT Nucleic acid fragment coding peptide of non-A non-B hepatitis virus - for
PT the early diagnosis of non-A non-B hepatitis by ELISA or agglutination
PT methods.
XX
PS Example 2; Page 7; 12pp; Japanese.
XX

This sequence represents a primer for the coding sequence for a non-A non-B hepatitis virus peptide. The protein encoded by the amplified sequence can be used to prepare an antibody specific for non-A non-B hepatitis virus. The peptide and antibody can be used in both ELISA and agglutination methods and is useful in the early diagnosis of non-A non-B hepatitis

Sequence 32 BP; 1 A; 5 C; 5 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTTTTTTTT 2185
Db 12 CTTTTTTTTTTTTTTTTTTTTT 32

RESULT 273
AAQ43973
ID AAQ43973 standard; DNA; 32 BP.
XX
AC AAQ43973;
XX
DT 25-MAR-2003 (revised)
DT 28-OCT-1993 (first entry)
XX
DE Triple helix forming oligonucleotide I.
XX
KW Purine; pyrimidine; tracts; intramolecular triplex; therapeutic;

diagnostic; control; gene expression; mRNA synthesis suppression; ss.
Synthetic.
XX WO9312230-A1.
PN
XX
PD 24-JUN-1993.
XX
PF 11-DEC-1992; 92WO-US010792.
XX
PR 13-DEC-1991; 91US-00808452.
PR 21-JAN-1992; 92US-00826934.
XX
PA (STRI) SRI INT.
XX
PI Jayasena SD, Johnston BH;
XX
DR WPI; 1993-214172/26.
XX

New oligo:nucleotide(s) forming triple helix with target nucleic acid - contain purine and pyrimidine tracts in specific orientations, useful therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.

Disclosure; Page 47; 101pp; English.

The sequence is that of an oligonucleotide, I, which is able to form a triple helix with a duplex nucleic acid (dsNA) contg. a target sequence which comprises at least one pyrimidine tract, and at least one adjacent purine tract. It is useful for therapeutic or diagnostic control of gene expression, e.g. suppression of mRNA synthesis from a target gene. A specified application is targetting of RNA in the HIV-1 genome. A appropriately labelled it may also be used as a probe. Attachment of cleavage agents caused permanent inactivation of the target by site-specific cleavage. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 32 BP; 8 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2186
Db 9 TTTTTTTTTTTTTTTTTTTT 29

RESULT 274
AAT77235
ID AAT77235 standard; DNA; 32 BP.
XX
AC AAT77235;
XX
DT 12-FEB-1998 (first entry)
XX
DE Rat fibroblast growth factor FGF-10 RACE primer X.
XX
KW Fibroblast growth factor; rat; human; recombinant DNA; bone disease;
KW wound healing; cartilage; RACE primer; ss.
XX
OS Synthetic.
OS Rattus rattus.
XX
PN WO9720929-A1.
XX
PD 12-JUN-1997.
XX
PF 06-DEC-1996; 96WO-JP003579.
XX
PR 07-DEC-1995; 95JP-00345689.
PR 28-MAR-1996; 96JP-00103240.
PR 24-JUL-1996; 96JP-00214378.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.

CC infestans), Plasmopara (e.g. Plasmopara viticola), Podosphaera (e.g.
CC Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi , Puccinia
CC striiformis , Puccinia graminis f.sp. tritici, Puccinia asparagi ,
CC Puccinia recondita , Puccinia arachidis), Puthium (e.g. Puthium
CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
CC Rhizoctonia (e.g. Rhizoctonia solani , Rhizoctonia cerealis), Sclerotium
CC (e.g. Sclerotium rolfii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
CC Septoria (e.g. Septoria lycopersici , Septoria tritici), Thielaviopsis (e.g.
CC nodorum / Phaeosphaeria nodorum , Septoria tritici), Venturia
CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae ,
CC Verticillium albo-atrum). Mutations in the proteolytic consensus
CC sequences contained within FCWP1 provides improved stability of its
CC antifungal activity. Also disclosed are ribosomal proteins with similar
CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
CC antifungal proteins. The present sequence is a PCR primer used to isolate
CC cDNA for FCWP1. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6573361B1.
XX
SQ Sequence 32 BP; 3 A; 3 C; 5 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2163 TCCTTTTTTTTTTTTTTTT 2183
Db |||||
12 TCCTTTTTTTTTTTTTTTT 32

RESULT 277
AAS95728/c
ID AAS95728 standard; DNA; 45 BP.

XX AAS95728;

XX 14-FEB-2002 (first entry)

DE Allele discrimination P1 primer #12.

XX Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.

XX Homo sapiens.

XX WO200177390-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US011151.

XX 05-APR-2000; 2000US-0194843P.

XX (MOLE-) MOLECULAR STAGING INC.

XX Abarzua P;

XX WPI; 2002-049157/06.

XX Detecting single nucleotide polymorphism involves amplifying target
PT sequences using small primer probe that matches or mismatches to target
PT sequence and extending primer probe which is then detected.

XX Claim 15; Page 41; 67pp; English.

XX The invention relates to detecting single nucleotide polymorphisms by

CC contacting an allele-specific oligonucleotide primer (P1) with a target
CC polynucleotide to form a hybridisation complex, where the target sequence
CC is complementary to P1 at one end but the terminal nucleotide and the
CC third nucleotide from the terminal at the other end of P1 may not be
CC complementary. The complex is then contacted with an exonuclease
CC deficient DNA polymerase enzyme under conditions that promote extension
CC of P1 with the target DNA as the template, thereby forming an extended
CC segment of P1. Oligonucleotide probes hybridising to one or more target
CC polynucleotides distinguish between matched and mismatched 3' ends, hence
CC the absence of sequence amplification indicates the presence of a single
CC nucleotide mismatch. Primer sequences complementary to a sequence on an
CC amplification target circle can be used in rolling circle amplification
CC (RCA). The method is useful for diagnosing a disease caused by, induced
CC by or related to a mutation in at least one gene, such as Parkinson's
CC disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC fluorescence decorators used in the detection of RCA products
XX
SQ Sequence 45 BP; 2 A; 5 C; 0 G; 38 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2784 TGAAAAAATAAAAAAAAAA 2804
Db |||||
37 TGAAAAAATAAAAAAAAAA 17

RESULT 278
AAS95724/c

ID AAS95724 standard; DNA; 45 BP.

XX AAS95724;

XX 14-FEB-2002 (first entry)

DE Allele discrimination P1 primer #8.

XX Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.

XX Homo sapiens.

XX WO200177390-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US011151.

XX 05-APR-2000; 2000US-0194843P.

XX (MOLE-) MOLECULAR STAGING INC.

XX Abarzua P;

XX WPI; 2002-049157/06.

XX Detecting single nucleotide polymorphism involves amplifying target
PT sequences using small primer probe that matches or mismatches to target
PT sequence and extending primer probe which is then detected.

XX Claim 15; Page 41; 67pp; English.

XX The invention relates to detecting single nucleotide polymorphisms by


```
XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 4.8e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db 24 ATTCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 281
ABX79828/c
ID ABX79828 standard; cDNA; 27 BP.
XX
AC ABX79828;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #153.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
PN US6472154-B1.
XX
PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX
PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
PS Example; Col 717; 588pp; English.
XX
CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESRs
XX
SQ Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 6.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 4.8e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
Db 24 ATTCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 281
ABX79828/c
ID ABX79828 standard; cDNA; 27 BP.
XX
AC ABX79828;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #153.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
PN US6472154-B1.
XX
PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX
PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
PS Example; Col 717; 588pp; English.
XX
CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESRs
XX
SQ Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 6.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;
Query Match 0.7%; Score 20.8; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 6.4e+02;
Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAAAAAAAAA 2804
Db 27 ARAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 283
AAS63424/c
ID AAS63424 standard; DNA; 32 BP.
XX
AC AAS63424;
XX
DT 29-JAN-2002 (first entry)
XX
DE Oligonucleotide-nanoparticle probe #48.
```


RESULT 289
AAL61641/C
ID AAL61641 standard; DNA; 32 BP.
XX
AC AAL61641;
XX
DT 22-SEP-2003 (first entry)
XX
DE Thiol-modified oligo #2 used in the nucleic acid detection method.
XX
KW Nucleic acid detection; fabrication; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 1 /*tag= a
FT /*note= "Linked to HS(CH2)6 group"
FT misc_feature 32 /*tag= b
FT /*note= "Linked to (CH2)6-F (fluorescein)"
XX
PN WO2003035829-A2.
XX
PD 01-MAY-2003.
XX
PF 08-OCT-2002; 2002WO-US032088.
XX
PR 09-OCT-2001; 2001US-0327864P.
PR 07-DEC-2001; 2001US-00008978.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Park S, Taton TA, Mirkin CA;
XX WPI; 2003-430409/40.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 18; Page 167; 467pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid having two
CC portions. The method involves providing nanoparticles having
CC oligonucleotides attached to it which has a sequence complementary to
CC sequence of two portions of nucleic acid, contacting nucleic acid and
CC nanoparticles to allow hybridisation of oligonucleotides with two or more
CC portions of nucleic acid and observing a detectable change brought about
CC by hybridisation. The method and aggregate probes are useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic or structurally modified natural or
CC synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. The invention is useful for preparing a nanoprobe
CC conjugate for detecting an analyte and for detecting a nucleic acid bound
CC to an electrode surface. It is also useful for fabrication and for
CC separating a selected nucleic acid having two portions from other nucleic
CC acids. The present sequence is an oligo used to illustrate the method of
CC the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
Db 24 TCGTTTTTTTTTTTTTTTTTTT 1

RESULT 290
ABX79177/C
ID ABX79177 standard; DNA; 32 BP.
XX
AC ABX79177;
XX
DT 15-APR-2003 (first entry)
XX
DE Fluorescein-labelled alkanethiol-modified oligonucleotide #2.
XX
KW Nanoparticle; ss; nucleic acid detection; viral disease;
KW human immunodeficiency virus infection; hepatitis virus infection;
KW herpes virus infection; cytomegalovirus infection; forensic science;
KW Epstein-Barr virus infection; bacterial disease; gene therapy;
KW sexually transmitted disease; inherited disorder; DNA sequencing;
KW paternity testing; cell line authentication.
XX
OS Synthetic.
XX
PN US2002155462-A1.
XX
PD 24-OCT-2002.
XX
PF 12-OCT-2001; 2001US-00976577.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
WPI; 2003-198491/19.
XX
PT Detecting nucleic acids having at least 2 portions comprises use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the nucleic acid sequence.
XX
PS Example 18; Page 40; 130pp; English.
XX
CC The invention relates to detecting a nucleic acid (NA) having at least 2
CC portions, comprises providing a type of nanoparticles (NP) having
CC attached to oligonucleotides (O) (O) on each NP has a sequence
CC complementary to sequence of at least 2 portions of NA), contacting NA
CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
CC on NP with NA. The nanoparticle is useful for separating a selected
CC nucleic acid having at least 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having at least 2 portions. The method of
CC using NP is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication and for monitoring gene therapy. The method is
CC useful in research and analytical laboratories in DNA sequencing and in
CC the field to detect the presence of specific pathogens. Detecting nucleic
CC acids based on observing a colour change with the naked eye is cheap,
CC fast, simple and robust, and do not require specialised expensive
CC equipment. The present sequence is a fluorescein labelled oligonucleotide
CC used to demonstrate the method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.8; DB 1; Length 32;

CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication, for monitoring gene therapy, etc. This method
CC involves detecting nucleic acids based on observing a colour change with
CC the naked eye so is cheap, fast, simple and robust, and does not require
CC specialised expensive equipment. The present sequence represents an
CC oligonucleotide used to demonstrate the method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2163 TCCTTTTTTTTTTTTTTTTTTTTTTTT 2186
Db 24 TCGGTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 293
ACD27121/c
ID ACD27121 standard; DNA; 32 BP.
XX
AC ACD27121;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
KW DNA sequencing; paternity testing; cell line authentication.
XX
OS Synthetic.
XX
PN US2002164605-A1.
XX
PD 07-NOV-2002.
XX
PF 28-SEP-2001; 2001US-00966312.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-247253/24.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change,
PT useful in forensics.
XX
PS Example 18; Page 40; 130pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acid
CC sequences having two portions. The method involves providing
CC nanoparticles having oligonucleotides attached to them, which has a
CC sequence complementary to sequence of two portions of nucleic acid,
CC contacting nucleic acid and nanoparticles, to allow hybridisation of
CC oligonucleotides with two or more portions of nucleic acid, and observing
CC a detectable change brought about by hybridisation. The method of the
CC invention and the aggregate probes are useful for detecting two or more
CC nucleic acids (from a biological source) having at least two portions,
CC such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with

CC a disease, synthetic, or structurally- modified natural or synthetic RNA
CC or DNA, or a product of a polymerase chain reaction amplification.
CC Nanoparticles and nanoparticle- oligonucleotide conjugates of the
CC invention are useful for nanofabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. The method of
CC the invention is useful in forensics, DNA sequencing, for paternity
CC testing, cell line authentication, and monitoring gene therapy.
CC Diagnostic assays employing the nanoparticle-oligonucleotide conjugates
CC of the invention improve the sensitivity of the nucleic acid detection
CC assay. The present sequence represents an oligonucleotide used to
CC demonstrate the method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2163 TCCTTTTTTTTTTTTTTTTTTTTTTTT 2186
Db 24 TCGGTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 294
ACD27381/c
ID ACD27381 standard; DNA; 32 BP.
XX
AC ACD27381;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #50.
XX
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KW pathogen detection.
XX
OS Synthetic.
XX
PN US2002182611-A1.
XX
PD 05-DEC-2002.
XX
PF 28-SEP-2001; 2001US-00966491.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-596264/56.
XX
PT Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.
XX
PS Example 18; Page 40; 109pp; English.
XX
CC This invention relates to a novel method for detecting a nucleic acid by
CC contacting a nucleic acid with at least two types of nanoparticles having
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides
CC on the nanoparticles, and observing a detectable change. The
CC oligonucleotides on each nanoparticle have a sequence complementary to
CC its respective portion of the sequence of the nucleic acid to be
CC detected. The method of the invention may be used for the detection of a
CC nucleic acid used in, e.g. research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens, in

CC the doctor's office for quick identification of an infection to assist in
CC prescribing a drug for treatment, and in homes and health centres for
CC inexpensive first-line screening. The method of the invention detects
CC nucleic acids based on observing a colour change with the naked eye. This
CC method is cheap, fast, simple, robust and does not require specialised or
CC expensive equipment. The present sequence represents an oligonucleotide
CC used to demonstrate the method of the invention

XX SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2163 TCCTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2186
| | | | | | | | | | | | | | | | | | | | | |
Db 24 TCGGTTTTTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 295
ACD27186/c
ID ACD27186 standard; DNA; 32 BP.

XX AC ACD27186;

XX DT 15-OCT-2003 (first entry)

XX DE Nanotechnology nucleic acid detection method associated #50.

XX KW Nanoparticle; ss; nucleic acid detection; DNA sequencing.

XX OS Synthetic.

XX PN US2002182613-A1.

XX PD 05-DEC-2002.

XX PF 12-OCT-2001; 2001US-00976971.

XX PR 29-JUL-1996; 96US-0031809P.

XX PR 21-JUL-1997; 97WO-US012783.

XX PR 29-JAN-1999; 99US-00240755.

XX PR 25-JUN-1999; 99US-00344667.

XX PR 26-APR-2000; 2000US-0200161P.

XX PR 26-JUN-2000; 2000US-00603830.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;

XX DR WPI; 2003-596265/56.

XX PT Detection of nucleic acid for, e.g. research and analytical laboratories
in deoxyribonucleic acid sequencing, involves contacting nucleic acid
with nanoparticles having oligonucleotides.

XX PS Example 18; Page 40; 107pp; English.

XX CC This invention relates to a novel method for detecting a nucleic acid by
contacting nucleic acid with at least two types of nanoparticles having
oligonucleotides, allowing hybridisation of the oligonucleotides on the
nanoparticles, and observing a detectable change. The oligonucleotides on
each nanoparticle have a sequence complementary to its respective portion
of the sequence of the nucleic acid. The method of the invention may be
used for the detection of a nucleic acid used in, e.g. research and
analytical laboratories in DNA sequencing, in the field to detect the
presence of specific pathogens, in the doctor's office for quick
identification of an infection to assist in prescribing a drug for
treatment, and in homes and health centres for inexpensive first-line
screening. The inventive method of detecting nucleic acids based on
observing a colour change with the naked eye are cheap, fast, simple,
robust (the reagents are stable), do not require specialised or expensive

CC equipment, and little or no instrumentation is required. The present
CC sequence represents an oligonucleotide used to demonstrate the method of
CC the invention

XX SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2163 TCCTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2186
| | | | | | | | | | | | | | | | | | | | | |
Db 24 TCGGTTTTTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 296
ACD27056/c
ID ACD27056 standard; DNA; 32 BP.

XX AC ACD27056;

XX DT 15-OCT-2003 (first entry)

XX DE Nanotechnology nucleic acid detection method oligonucleotide #50.

XX KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.

XX OS Synthetic.

XX PN US2003044805-A1.

XX PD 06-MAR-2003.

XX PF 15-OCT-2001; 2001US-00981344.

XX PR 29-JUL-1996; 96US-0031809P.

XX PR 21-JUL-1997; 97WO-US012783.

XX PR 29-JAN-1999; 99US-00240755.

XX PR 25-JUN-1999; 99US-00344667.

XX PR 26-APR-2000; 2000US-0200161P.

XX PR 26-JUN-2000; 2000US-00603830.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;

XX DR WPI; 2003-521746/49.

XX PT Detection of nucleic acid having -2 portions used to prepare biomaterials
and in nanofabrication methods, comprises providing nanoparticles,
contacting nucleic acid and nanoparticles, and observing change.

XX PS Example 18; Page 40; 130pp; English.

XX CC This invention relates to a novel method for detecting nucleic acids. The
method comprises providing nanoparticles with oligonucleotides attached
to them, which have a sequence complementary to a sequence of two
portions of nucleic acid, contacting the nucleic acid and nanoparticles
to allow hybridisation of the oligonucleotides with two or more portions
of the nucleic acid, and observing a detectable change brought about by
the hybridisation. The nucleic acid to be detected must have at least two
portions and the distances between these are chosen so that when the
nanoparticle-oligonucleotide conjugate binds the target sequence a
detectable change occurs. The method of the invention is useful for
detecting two or more nucleic acids (from a biological source) having at
least two portions, such as viral RNA, bacterial or fungal DNA, a gene
associated with a disease, synthetic, or structurally-modified natural
or synthetic RNA or DNA, or a product of a polymerase chain reaction
amplification. Nanoparticle-oligonucleotide conjugates of the invention
are useful for preparing a nanoprobe conjugate for detecting an analyte,
and for detecting a nucleic acid bound to an electrode surface.
XX CC Nanoparticles and nanoparticle conjugates of the invention are useful for

XX
CC This invention relates to a novel method for detecting nucleic acids. The
CC method comprises providing nanoparticles with oligonucleotides attached
CC to them, which have a sequence complementary to a sequence of two
CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC to allow hybridisation of the oligonucleotides with two or more portions
CC of the nucleic acid, and observing a detectable change brought about by
CC the hybridisation. The nucleic acid to be detected must have at least two
CC portions and the distances between these are chosen so that when the
CC nanoparticle-oligonucleotide conjugate binds the target sequence a
CC detectable change occurs. The method of the invention is useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic, or structurally-modified natural
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC and for detecting a nucleic acid bound to an electrode surface.
CC Nanoparticles and nanoparticle conjugates of the invention are useful for
CC nanofabrication and for separating a selected nucleic acid having two
CC portions from other nucleic acids. Diagnostic assays employing
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC nucleic acid detection methods and can be used to detect nucleic acids
CC that are present in only small amounts in a sample. The present sequence
CC represents an oligonucleotide used to demonstrate the method of the
CC invention

XX

PA (JINR/) JIN R.

XX Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having a oligo-dt primer of a specific sequence and a
PT detectable marker at its 5' end.
XX
PS Disclosure; Page 11; 45pp; English.
XX
CC The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dt primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence in formation. The present
CC sequence represents an oligo dt primer used in the method of the
CC invention
XX
SQ Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 5.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2783 TTGAAAAA 2804
Db 23 TTTAAAAA 2
RESULT 308
AAI66361/c
ID AAI66361 standard; DNA; 24 BP.
XX
AC AAI66361;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX
KW Human; phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer;
KW haemopathy; development disorder; HIV infection; immunological disease;
KW inflammation; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200175014-A2.
XX
PD 11-OCT-2001.
XX
PF 16-MAR-2001; 2001WO-CN000328.
XX
PR 17-MAR-2000; 2000CN-00114973.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-025836/03.

XX New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and
PT treating malignant tumor, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations.
XX
PS Example 2; Page 12; 34pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in
CC the treatment of cancer, haemopathy, HIV infection, development
CC disorders, immunological diseases and inflammation. The present sequence
CC is a PCR primer for the coding sequence of the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 5.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2783 TTGAAAAA 2804
Db 22 TTTAAAAA 1
RESULT 309
AAD25661/c
ID AAD25661 standard; DNA; 30 BP.
XX
AC AAD25661;
XX
DT 26-MAR-2002 (first entry)
XX
DE Oligonucleotide #7 related to method for production of RNA viruses.
XX
KW Cytostatic; replication defective gene transfer; encapsidated RNA virus;
KW gene therapy; cancer therapy; ss.
XX
OS Unidentified.
XX
PN WO200190302-A2.
XX
PD 29-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US015449.
XX
PR 24-MAY-2000; 2000US-0206997P.
XX
PA (FENG/) FENG Y.
PA (TANG/) TANG H.
XX
PI Feng Y, Tang H;
XX
DR WPI; 2002-066766/09.
XX
PT Producing encapsidated RNA virus by coexpressing RNA virus genomic
PT sequence linked to bacteriophage promoter, and coding sequence for
PT bacteriophage polymerase linked to poxvirus promoter in eukaryotic cell
PT cytoplasm.
XX
PS Disclosure; Page 38; 49pp; English.
XX
CC The patent discloses methods to produce RNA viral sequences, recombinant
CC RNA viruses, mutants of RNA viruses and RNA virus-derived vectors in cell
CC culture and in vitro using non-viable, replication defective helper
CC vaccinia recombinants. These methods generate RNA viral genomes and viral
CC particles in cell culture and in vitro independent of their natural
CC replication pathways, bypassing the limitation of any cellular barriers.
CC The invention also relates to a method for producing encapsidated RNA
CC virus comprising coexpressing polypeptide coding sequence capable of
CC forming capsid and packaging RNA viral genomic sequence in eukaryotic
CC cell, a construct comprising RNA viral genomic sequence linked to
CC bacteriophage promoter and transcription terminator and bacteriophage
CC polymerase coding sequence, which is operably compatible with the

Sequence 30 BP: 2 A; 3 C; 4 G; 21 T; 0 U; 0 Other;

```
Query Match      0.7%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0
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OV 2166 TTTTTTTTTTTTTTTT 2187

Db
1 TTTT TTTT TTTT TTTT TTTT CA 22

ABL56888

XX

DT 26-JU

XX
DE Synthetic deoxyribonucleotide poly a

KW Concentra

XX

OS Synthetic

PN EP1046717-A2.

PD 25-OCT-2000.

PF 20-APR-2000

PR 20-APR-1999; 99JP-00111601

PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.

PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

PA (KANK-) KANKYO ENG CO LTD.

PI Kurane R, Kanagawa T, Kama

XX
DR WPI; 2000-657765/64.

PT Determining the conc

WT: 1997-322152/30

CC reduced fluorescence emission when

hybridisation. The new method is particularly used to quantify target nucleic acids by a real-time polymerase chain reaction, e.g. for quantifying microbial cells in co-cultures or symbiotic systems, for detecting gene mutations or polymorphisms, and for analysing melting curves of target nucleic acids to determine a T_m value. Methods of the invention allow target nucleic acids to be quantified quickly, easily and accurately. Particularly there is no need to remove unbound probe, and no materials are introduced that inhibit amplification by Taq polymerase (so conventional PCR conditions can be used). The specificity of PCR is kept

FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	FT	
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Query Match      0.7%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 4.9e+02;
Matches 20; Conservative 1; Mismatches 0; Indels
```

XX ABK86172;

XX 24-SEP-2002 (first entry)
DT Oligo dT primer #4 used in method to study gene expression.
XX
DE Oligo dT primer; gene expression analysis; primer; ss.
XX
KW Synthetic.
XX
OS WO200236828-A2.
XX
PN 10-MAY-2002.
XX
PD 01-NOV-2001; 2001WO-US045401.
XX
PF 01-NOV-2000; 2000US-0244933P.
XX
PR (GENO-) GENOMIC SOLUTIONS INC.
XX
PA Kane MD, Dombkowski AA, Nagel AC;
XX
PI WPI; 2002-508123/54.
XX
DR Identifying and characterizing gene expression in samples, for
XX identifying mRNAs expressed at different levels, comprises employing an
PT identifier having an oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end.
PT
XX Example 1; Page 15; 45pp; English.
PS
XX The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dT primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given *in vivo* or *in vitro* RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence information. The present
CC sequence represents an oligo dT primer used in the method of the
CC invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 4 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 6.1e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2165 CTTTTTTTTTTTTTTTTTTT 2185
DB 4 VTTTTTTTTTTTTTTTTTTT 24
RESULT 325
AAX84260/c
ID AAX84260 standard; DNA; 25 BP.
XX
AC AAX84260;
XX
DT 08-SEP-1999 (first entry)

XX PCR primer for human Nck associated protein 1 coding sequence.
DE
XX Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW therapy; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9931239-A1.
XX
PD 24-JUN-1999.
XX
XX 14-DEC-1998; 98WO-JP005646.
PF
XX 15-DEC-1997; 97JP-00363183.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA (SAKA/) SAKAKI Y.
XX
PI Sakaki Y;
XX
XX WPI; 1999-395181/33.
DR
XX Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT Alzheimer's disease.
PT
XX Disclosure; Page 77; 90pp; Japanese.
PS
XX This sequence represents a PCR primer used to isolate DNA encoding the
CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC apoptosis. The protein can be used in the investigation, diagnosis and
CC treatment (e.g. by gene therapy) of Alzheimer's disease
XX
SQ Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 6.8e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA AAAAAAAAAAAAAA 2804
DB 25 GAAAAA AAAAAAAAAAAAAA 1
RESULT 326
AAA47833
ID AAA47833 standard; DNA; 25 BP.
XX
AC AAA47833;
XX
DT 16-NOV-2000 (first entry)
XX
DE Adapter sequence for 3' end of lectin cDNA.
XX
KW Lectin; mannose; sugar; transgenic plant; crop protection; resistance;
KW bacteria; virus; fungus; insect; targeting; neutrophil glycoprotein;
KW polymorphonuclear cell; blood typing; primer; ss.
XX
OS Hernandia moerenhoutiana.
XX
PN WO200044780-A1.
XX
XX 03-AUG-2000.
PD
XX 28-JAN-2000; 2000WO-AU000039.
PF
XX 29-JAN-1999; 99AU-00008395.
PR
XX (AURE-) AUSTRALIAN RED CROSS BLOOD SERVICE.
PA
XX Clark TR, Minchinton RM;
PI
XX

SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 26;
Best Local Similarity 88.0%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA 2804
Db 26 GAAAAA 2
RESULT 331
ID ABX93461 standard; DNA; 26 BP.
XX ABX93461;
AC ABX93461;
XX 27-MAY-2003 (first entry)
DT
DE LS147-specific polynucleotide sequencing related universal primer #1.
XX LS147; cancer; lung cancer; gene therapy; cytostatic; ss; sequencing;
KW primer; EST clone; expressed sequence tag clone.
XX Synthetic.
OS
XX US2002188114-A1.
PN
XX 12-DEC-2002.
PD
XX 05-JUN-1998; 98US-00092296.
PF
XX 05-JUN-1997; 97US-0048810P.
PR
XX (BILL/) BILLINGEL P.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (KLAS/) KLASS M R.
PA (RUSS/) RUSSELL J C.
PA (STRO/) STROUPE S.
XX Billengel P, Cohen M, Colpitts TL, Friedman PN, Klass MR;
PI Russell JC, Stroupe S;
PI
XX WPI; 2003-341045/32.
DR
XX New LS147 polypeptide, useful for preparing a composition for treating
PT e.g., lung cancer.
PT
XX Example 2; Page 39; 47pp; English.
PS
XX The invention describes a purified polypeptide or its fragment derived
CC from the LS147 gene capable of selectively hybridizing to the nucleic
CC acid of the gene and has at least 50% identity with the polynucleotide.
CC The LS147 polypeptide is useful for preparing a composition for treating
CC cancer, e.g. lung cancer using gene therapy. This sequence represents a
CC universal primer used to sequence LS147 expressed sequence tag (EST)-
CC clones
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 26;
Best Local Similarity 88.0%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA 2804
Db 26 GAAAAA 2
RESULT 332
AAAL3806

ID XX AAAL3806 standard; DNA; 26 BP.
AC AAAL3806;
XX 27-JUL-2000 (first entry)
DT
XX Yeast DOG2 stress responsive gene PCR primer SEQ ID NO:5.
DE
XX Yeast; stress responsive gene; promoter; brewing; beer; wine; sake;
KW bread; oxidative stress; osmotic pressure; stress; glucose starvation;
KW PCR primer; ss.
XX Saccharomyces cerevisiae.
OS
XX JP2000078977-A.
PN
XX 21-MAR-2000.
PD
XX 04-SEP-1998; 98JP-00251390.
PF
XX 04-SEP-1998; 98JP-00251390.
PR (TAIF) MARUHA CORP.
XX
XX WPI; 2000-285929/25.
DR
XX A stress-responsive gene promoter.
PT
XX Example 3; Page 10; 12pp; Japanese.
PS
XX The present invention describes a stress responsive gene promoter
CC isolated from Saccharomyces cerevisiae (yeast). Also described in the
CC present invention are: (1) a promoter containing a DNA hybridizing with
CC the above DNA under a stringent condition and having stress-responsive
CC promoter activity; (2) a gene expression cassette containing the above
CC promoter; (3) an expression vector containing the above gene expression
CC cassette; (4) a recombinant vector in which a gene encoding an optional
CC polypeptide is recombined to the above expression vector; (5) a
CC transformant containing the above recombinant vector; and (6) a method
CC for the preparation of the above polypeptide in which the above
CC transformant is cultured and the polypeptide is collected from the
CC resultant culture. Saccharomyces cerevisiae is used for the brewing of
CC beer, wine and sake and production of bread. The gene is responsive to
CC the stresses such as oxidative stress, osmotic pressure stress and
CC glucose starvation stress. The present sequence represents a PCR primer
CC for the yeast DOG2 stress responsive gene, which is used in an example
CC from the present invention
XX
SQ Sequence 26 BP; 3 A; 2 C; 2 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 26;
Best Local Similarity 88.0%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2165 CTTTTTTTTTTTTTTTTTTTTTTTAAAC 2189
Db 1 CATTTCATTTTATTTTGTGAC 25
RESULT 333
AAAL2516
ID AAD12516 standard; DNA; 26 BP.
XX
AC AAD12516;
XX
DT 25-SEP-2001 (first entry)
XX
DE Thuja sp. pinoresinol/lariciresinol reductase cDNA cloning linker primer.
XX Dirigent protein; pinoresinol/lariciresinol reductase; stereospecificity;
KW lignan biosynthetic pathway; secoisolariciresinol; western red cedar;
KW PCR primer; ss.
XX

CC PCR amplification of cDNA (see ACC83474) encoding a novel rat zinc finger
CC protein, designated Czf-1 (see ABR42912). Czf-1 is expressed in
CC osteoblasts and chondrocytes, and serves as a marker for osteoarthritis.
CC Czf-1 polynucleotides, polypeptides and antibodies can be used in the
CC characterisation, diagnosis and treatment of fibroblast growth factor
CC receptor-related and skeletal diseases and disorders, such as
CC osteoarthritis, rheumatoid arthritis, and cartilage-related diseases
XX
SQ Sequence 28 BP; 2 A; 3 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 8.9e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2161 TCTCCTTTTTTTTTTTTTTTTTTTT 2185
Db 4 TCTCGAGTTTTTTTTTTTTTTTTTTT 28

RESULT 336
ABZ59816
ID ABZ59816 standard; RNA; 28 BP.

AC ABZ59816;

DT 01-APR-2003 (first entry)

DE Potato gene PCR primer DDT18AN.

XX Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
KW transferrin binding protein; receptor-like protein kinase; helicase;
KW non-long terminal repeat retroelement reverse transcriptase;
KW overwatering; transgenic; reverse transcriptase; PCR; primer; ss.

OS Synthetic.

PN DE10114063-A1.

PD 10-OCT-2002.

PF 22-MAR-2001; 2001DE-01014063.

PR 22-MAR-2001; 2001DE-01014063.

XX (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.

XX Buelow L, Tsharntke M, Haussuehl K;

PI WPI; 2003-041808/04.

XX New DNA sequences from potato, useful for producing plants with altered
XX properties, e.g. tolerance of flooding, also related proteins, antibodies
XX and inhibitory sequences.

PS Example 1; Page 8; 26pp; German.

XX The invention relates to DNA sequences (I) that encode six specific plant
CC proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
CC activity (IIa); (ii) a protein (ABP60426) with transferrin binding
CC protein activity (IIB); (iii) a protein (ABP60427) with receptor-like
CC protein kinase activity (IIC); (iv) a protein (ABP60428) with elongation
CC factor EF-2 activity (IID); (v) a protein (ABP60429) with non-long
CC terminal repeat retroelement reverse transcriptase activity (IIE); or
CC (vi) a protein (ABP60430) with helicase activity (IIF). (I), also related
CC sequences, derived ribozymes and antisense sequences, expression vectors,
CC encoded proteins and antibodies against the proteins, are used to produce
CC plants with altered properties, including tolerance of overwatering. The
CC antibodies are also used for isolation of the proteins and in
CC immunoassays. Also (I) or their primer or probe fragments are used to
CC screen for terminators and constitutively, aerobically or anaerobically
CC inducible plant promoters, specifically for use in potatoes and the
CC sequence that encodes (IID) is used to alter the translation profile in
CC plants. Since (I) are derived from potato, their promoters and

CC terminators provide high level transgene expression in potato, with
CC improved tissue specificity and inducibility, and can also be used to
CC control endogenous genes. The present sequence is that of a PCR primer
CC used in the first strand synthesis of cDNAs derived from potato
XX
SQ Sequence 28 BP; 3 A; 2 C; 2 G; 20 T; 0 U; 1 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 8.9e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2163 TCCTTTTTTTTTTTTTTTTTTTTTTTT 2187
Db 3 TCGATCTTTTTTTTTTTTTTTTTTTT 27

RESULT 337
ADD41445/C
ID ADD41445 standard; DNA; 28 BP.

XX ADD41445;

AC 15-JAN-2004 (first entry)

DE Hepatitis C virus NS3 protease/helicase related PCR primer Seq ID26.

XX NS3 protease; NS3 helicase; hepatitis C virus; HCV; hepatitis C; ss; PCR;
KW primer.

XX Unidentified.

XX JP2002345475-A.

XX 03-DEC-2002.

XX 25-MAY-2001; 2001JP-00156957.

XX 25-MAY-2001; 2001JP-00156957.

XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.

XX (MITN) MITSUBISHI GAS CHEM CO INC.

XX WPI; 2003-460881/44.

XX Functional nucleic acids targeting NS3 protease and/or helicase of
XX hepatitis C virus (HCV) for prevention, diagnosis and treatment of
XX hepatitis C.

PS Example 1; SEQ ID NO 26; 22pp; Japanese.

XX This invention relates to novel nucleic acids targeting the NS3 protease
CC and/or helicase of hepatitis C virus (HCV). The invention provides RNA
CC molecules having a base sequence with a structure given in the
CC specification and capable of inhibition of NS3 protease and/or helicase
CC of HCV, and capable of forming a secondary structure also given in the
CC specification. The invention is useful for the effective prevention,
CC diagnosis and treatment of hepatitis C. The present sequence is that of a
CC PCR primer which was used during the exemplification of the invention.

XX Sequence 28 BP; 20 A; 0 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 8.9e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2155 TTTTCTCTCTCTCTCTCTCTCTCTTTT 2179
Db 25 TTCCTCTCTCTCTCTCTCTCTCTTTT 1

RESULT 338
AAV15487/C
ID AAV15487 standard; DNA; 29 BP.

CC Chemically regulatable gene in a plant tissue. The method allows
CC isolation of sequences which will be useful for the controlled expression
CC of genes, under the control of a non-coding regulatable sequence. This is
CC useful in plants with a herbicide or pesticide detoxification mechanism
CC under the control of a chemical regulator, the regulator being applied
CC before or with the herbicide or pesticide to give optimal tolerance. The
CC promoter fragment is useful for controlling sequences which encode traits
CC such as height, shape, development, male or female sterility, and the
CC ability of the plant to withstand cold, heat, salt and drought. The
CC chemical induction of the promoter allows the regulation of production of
CC compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
CC industrial feedstocks, antimicrobials and pharmaceuticals, by
CC biosynthesis or metabolite conversion, whose biosynthesis is controlled
CC by endogenous or foreign genes. The method allows control over the time
CC and rate of gene expression either throughout the whole plant, or in
CC localized tissues, to achieve e.g. fungal or insect resistance by for
CC instance dusting the leaves with the chemical regulator. Controlling the
CC developmental processes by the application of a regulating chemical in
CC e.g. the commercial production of cultivated crops allows processes such
CC as germination, flower formation and fruit ripening to be synchronised at
CC a given time

XX Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTCAGAAAAAAGAAAAAAGAAAAA 2804
||||| ||||||| ||||||| ||||||| ||
Db 4 GAATTCAGAAAAAAGAAAAAAGAAAAA 28

RESULT 341

AAV81666

ID AAV81666 standard; DNA; 30 BP.

XX AAV81666;

DT 25-FEB-1999 (first entry)

DE Oligonucleotide SEQ ID NO:85 used in Example 72.

XX Regulation; transcription; plant tissue; chimeric construction; PR;
KW pathogenesis-related protein; anti-pathogenic; transgenic plant;
KW beta-1,3-glucanase activity; pest resistance; primer; ss.

OS Synthetic.

XX US5847258-A.

XX 08-DEC-1998.

PF 31-MAY-1995; 95US-00457364.

XX 08-MAR-1988; 88US-00165667.

PR 06-FEB-1989; 89US-00305566.

PR 24-MAR-1989; 89US-00329018.

PR 20-JUN-1989; 89US-00368672.

PR 20-OCT-1989; 89US-00425504.

PR 07-SEP-1990; 90US-00580431.

PR 21-DEC-1990; 90US-00632441.

PR 01-APR-1991; 91US-00678378.

PR 27-SEP-1991; 91US-00768122.

PR 06-MAR-1992; 92US-00848506.

PR 06-NOV-1992; 92US-00973197.

PR 06-APR-1993; 93US-00042847.

PR 12-APR-1993; 93US-00045957.

PR 16-JUL-1993; 93US-00033301.

PR 13-JAN-1994; 94US-00181271.

PR 31-MAY-1995; 95US-00457364.

XX (NOVS) NOVARTIS FINANCE CORP.

PA

XX Payne GB, Ward ER, Moyer MB, Ryals JA;
PI WPI; 1999-059180/05.

XX DNA encoding pathogenesis-related glucanase proteins - useful for
PT producing transgenic plants with enhanced disease or pest resistance.

XX Example 72; Col 93; 169pp; English.

XX The present invention describes a DNA molecule encoding a pathogenesis-
CC related (PR) protein having beta-1,3-glucanase activity selected from PR-
CC 2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described are: (i) a
CC chimeric gene comprising the above DNA molecule linked to a heterologous
CC promoter; (ii) a vector containing the chimeric gene; (iii) a host cell
CC containing the chimeric gene; (iv) a transgenic plant containing the
CC chimeric gene; and (v) a seed from the transgenic plant. The DNA molecule
CC is used to produce transgenic plants with enhanced disease or pest
CC resistance. The present sequence represents an oligonucleotide from the
CC present invention

XX Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTCAGAAAAAAGAAAAAAGAAAAA 2804
||||| ||||||| ||||||| ||||||| ||
Db 4 GAATTCAGAAAAAAGAAAAAAGAAAAA 28

RESULT 342

AAF74908/C

ID AAF74908 standard; DNA; 30 BP.

XX AAF74908;

DT 23-MAY-2001 (first entry)

DE CD40L poly-A tract sequence SEQ ID NO:5.

XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

PF 13-SEP-2000; 2000WO-US024966.

XX 13-SEP-1999; 99US-0153625P.

PR (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX Crow MK, Li Y;

XX WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.

XX Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,

CC enrichment of even very rare molecules and allowing isolation of proteins
CC that bind specifically to almost any compound or catalyse almost any
CC reaction
XX
SQ Sequence 34 BP; 22 A; 4 C; 6 G; 0 T; 1 U; 1 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 34;
Best Local Similarity 88.0%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2169 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTG 2193
Db 31 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTG 7

RESULT 345
ABK99273
ID ABK99273 standard; RNA; 36 BP.

XX
AC ABK99273;
XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #3.
XX
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.

XX Synthetic.
XX US2002064771-A1.
XX 30-MAY-2002.
XX 06-APR-2001; 2001US-00828034.
XX 07-APR-2000; 2000US-0195852P.
XX (ZHON/) ZHONG W.
XX (HONG/) HONG Z.
XX (FERR/) FERRARI E.

PI Zhong W, Hong Z, Ferrari E;
XX WPI; 2002-582330/62.
DR

XX Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT and template and primer which do not form a stable duplex in the absence
PT of HCV NS5B.

PS Example; Page 6; 17pp; English.
XX
CC The invention relates to a replicase complex comprising a hepatitis C
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC complementary nucleic acid primer which is annealed to the 3' terminus of
CC the template, where the template is at least three nucleotides and the
CC primer is two or three nucleotides, and the template and primer do not
CC form a stable duplex in solution in the absence of the HCV NS5B protein.
CC The complex is useful for detecting HCV replicase activity and permits
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC and evaluate antiviral inhibitors and to improve the specificity and
CC efficacy of the inhibitors. The complex is also useful in the development
CC of a reliable system for determining kinetic and thermodynamic constants
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC mechanistic inhibitors for mis-incorporation or chain termination.
CC Specifically, the short RNA template and primer pairs are useful in
CC screening assays which are used for determining kinetic, thermodynamic
CC and mechanistic properties of NS5B replication and ultimately in the
CC development of inhibitors of NS5B. Newly identified inhibitors of
CC replicase activity may be used for developing anti-HCV pharmaceuticals.
CC Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC templates

SQ Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 36;
Best Local Similarity 88.0%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAAATAAAAAAATAAAAAA 2804
Db 2 GAAAAAATAAAAAAATAAAAAAATAAAAAA 26

RESULT 346
AAD27117
ID AAD27117 standard; RNA; 36 BP.

XX
AC AAD27117;
XX
DT 09-APR-2002 (first entry)
XX
DE RNA template, AU used to direct RNA synthesis by HCV RNA polymerase.
XX
KW Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW lead compound; RNA polymerase; ss.

XX Unidentified.
XX US6322966-B1.
XX 27-NOV-2001.

XX 11-MAY-1999; 99US-00309670.
XX 11-MAY-1999; 99US-00309670.

XX (ZHON/) ZHONG W.
XX (HONG/) HONG Z.
XX (LAUJ/) LAU J Y N.

XX Zhong W, Hong Z, Lau JYN;
PI WPI; 2002-096587/13.

XX Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.

XX Example 1; Fig 1A; 10pp; English.

XX The present invention relates to an assay system for hepatitis C virus
CC (HCV) replicase activity. The assay system comprises an RNA template that
CC has an unstable, small stemloop at the 3' end capable of forming a copy-
CC back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC radiolabelled and an assay buffer that supports replication activity of
CC NS5B. The invention also relates to the identification of optimal
CC properties of an RNA template for copy-back self-priming RNA synthesis of
CC HCV. This activity can be used to screen for anti-HCV replicase compounds
CC or to characterise the biological relevance of lead compounds. The
CC optimal RNA templates can be used for developing a system to characterise
CC HCV NS5B polymerase mechanistically and kinetically and for designing
CC small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC system of the invention is useful for detecting HCV replicase activity.
CC The nucleic acid synthesised by NS5B is detected by evaluating an
CC autoradiograph of reaction products separated by gel electrophoresis. The
CC present sequence is RNA template, AU used to direct RNA synthesis by RNA
CC polymerase proteins of HCV, BVDV and poliovirus. This sequence is used in
CC the exemplification of the invention

XX SQ Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 36;
Best Local Similarity 88.0%; Pred. No. 1.6e+03;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 2 GAAAAA 26

RESULT 347
ABK99272
ID ABK99272 standard; RNA; 36 BP.
XX
AC ABK99272;
XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #2.
XX
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS Synthetic.
XX
PN US2002064771-A1.
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-00828034.
XX
PR 07-APR-2000; 2000US-0195852P.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (FERR/) FERRARI E.
XX
PI Zhong W, Hong Z, Ferrari E;
XX
DR WPI; 2002-582330/62.
XX
PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT and template and primer which do not form a stable duplex in the absence
PT of HCV NS5B.
XX
PS Example; Page 6; 17pp; English.
XX
CC The invention relates to a replicase complex comprising a hepatitis C
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC complementary nucleic acid primer which is annealed to the 3' terminus of
CC the template, where the template is at least three nucleotides and the
CC primer is two or three nucleotides, and the template and primer do not
CC form a stable duplex in solution in the absence of the HCV NS5B protein.
CC The complex is useful for detecting HCV replicase activity and permits
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC and evaluate antiviral inhibitors and to improve the specificity and
CC efficacy of the inhibitors. The complex is also useful in the development
CC of a reliable system for determining kinetic and thermodynamic constants
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC mechanistic inhibitors for mis-incorporation or chain termination.
CC Specifically, the short RNA template and primer pairs are useful in
CC screening assays which are used for determining kinetic, thermodynamic
CC and mechanistic properties of NS5B replication and ultimately in the
CC development of inhibitors of NS5B. Newly identified inhibitors of
CC replicase activity may be used for developing anti-HCV pharmaceuticals.
CC Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC templates
XX
SQ Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 36;
Best Local Similarity 88.0%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 2 GAAAAA 26

RESULT 349

Db 2 GAAAAA 26

RESULT 348
AAD27116
ID AAD27116 standard; RNA; 36 BP.
XX
AC AAD27116;
XX
DT 09-APR-2002 (first entry)
XX
DE RNA template, AA used to direct RNA synthesis by HCV RNA polymerase.
XX
KW Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW lead compound; RNA polymerase; ss.
XX
OS Unidentified.
XX
PN US6322966-B1.
XX
PD 27-NOV-2001.
XX
PF 11-MAY-1999; 99US-00309670.
XX
PR 11-MAY-1999; 99US-00309670.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (LAUJ/) LAU J Y N.
XX
PI Zhong W, Hong Z, Lau JYN;
XX
DR WPI; 2002-096587/13.
XX
PT Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.
XX
PS Example 1; Fig 1A; 10pp; English.
XX
CC The present invention relates to an assay system for hepatitis C virus
CC (HCV) replicase activity. The assay system comprises an RNA template that
CC has an unstable, small stemloop at the 3' end capable of forming a copy-
CC back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC radiolabelled and an assay buffer that supports replication activity of
CC NS5B. The invention also relates to the identification of optimal
CC properties of an RNA template for copy-back self-priming RNA synthesis of
CC HCV. This activity can be used to screen for anti-HCV replicase compounds
CC or to characterise the biological relevance of lead compounds. The
CC optimal RNA templates can be used for developing a system to characterise
CC HCV NS5B polymerase mechanistically and kinetically and for designing
CC small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC system of the invention is useful for detecting HCV replicase activity.
CC The nucleic acid synthesised by NS5B is detected by evaluating an
CC autoradiograph of reaction products separated by gel electrophoresis. The
CC present sequence is RNA template, AA used to direct RNA synthesis by RNA
CC polymerase proteins of HCV, BVDV and poliovirus. This sequence is used in
CC the exemplification of the invention
XX
SQ Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 36;
Best Local Similarity 88.0%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAA 2804
Db 2 GAAAAA 26

RESULT 349

AAD27121
ID AAD27121 standard; RNA; 36 BP.
XX
AC AAD27121;
XX
DT 09-APR-2002. (first entry)
XX
DE RNA template, (AU)4 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW lead compound; RNA polymerase; ss.
XX
OS Unidentified.
XX
PN US6322966-B1.
XX
PD 27-NOV-2001.
XX
PF 11-MAY-1999; 99US-00309670.
XX
PR 11-MAY-1999; 99US-00309670.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (LAUJ/) LAU J Y N.
XX
PI Zhong W, Hong Z, Lau JYN;
XX
DR WPI; 2002-096587/13.
XX
PT Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.
XX
PS Example 1; Fig 1C; 10pp; English.
XX
CC The present invention relates to an assay system for hepatitis C virus
CC (HCV) replicase activity. The assay system comprises an RNA template that
CC has an unstable, small stemloop at the 3' end capable of forming a copy-
CC back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC radiolabelled and an assay buffer that supports replication activity of
CC NS5B. The invention also relates to the identification of optimal
CC properties of an RNA template for copy-back self-priming RNA synthesis of
CC HCV. This activity can be used to screen for anti-HCV replicase compounds
CC or to characterise the biological relevance of lead compounds. The
CC optimal RNA templates can be used for developing a system to characterise
CC HCV NS5B polymerase mechanistically and kinetically and for designing
CC small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC system of the invention is useful for detecting HCV replicase activity.
CC The nucleic acid synthesised by NS5B is detected by evaluating an
CC autoradiograph of reaction products separated by gel electrophoresis. The
CC present sequence is RNA template, (AU)4 used to direct RNA synthesis by
CC RNA polymerase proteins of HCV, BVDV and poliovirus. This sequence is used
CC in the exemplification of the invention
XX
SQ Sequence 36 BP; 30 A; 0 C; 2 G; 0 T; 4 U; 0 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 36;
Best Local Similarity 88.0%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA..... 2804
Db 2 GAAAAA..... 26
RESULT 350
ABK99274
ID ABK99274 standard; RNA; 36 BP.
XX
AC ABK99274;

XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #4.
XX
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS Synthetic.
XX
PN US2002064771-A1.
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-00828034.
XX
PR 07-APR-2000; 2000US-0195852P.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (FERR/) FERRARI E.
XX
PI Zhong W, Hong Z, Ferrari E;
XX
DR WPI; 2002-582330/62.
XX
PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT and template and primer which do not form a stable duplex in the absence
PT of HCV NS5B.
XX
PS Example; Page 6; 17pp; English.
XX
CC The invention relates to a replicase complex comprising a hepatitis C
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC complementary nucleic acid primer which is annealed to the 3' terminus of
CC the template, where the template is at least three nucleotides and the
CC primer is two or three nucleotides, and the template and primer do not
CC form a stable duplex in solution in the absence of the HCV NS5B protein.
CC The complex is useful for detecting HCV replicase activity and permits
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC and evaluate antiviral inhibitors and to improve the specificity and
CC efficacy of the inhibitors. The complex is also useful in the development
CC of a reliable system for determining kinetic and thermodynamic constants
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC mechanistic inhibitors for mis-incorporation or chain termination.
CC Specifically, the short RNA template and primer pairs are useful in
CC screening assays which are used for determining kinetic, thermodynamic
CC and mechanistic properties of NS5B replication and ultimately in the
CC development of inhibitors of NS5B. Newly identified inhibitors of
CC replicase activity may be used for developing anti-HCV pharmaceuticals.
CC Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC templates
XX
SQ Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;
Query Match 0.7%; Score 20.2; DB 1; Length 36;
Best Local Similarity 88.0%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2780 GAATTGAAAAA..... 2804
Db 2 GAAAAA..... 26
RESULT 351
AAD27118
ID AAD27118 standard; RNA; 36 BP.
XX
AC AAD27118;
XX
DT 09-APR-2002 (first entry)
XX
DE RNA template, (AU)5 used to direct RNA synthesis by HCV RNA polymerase.


```
XX Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW lead compound; RNA polymerase; ss.
XX
OS Unidentified.
XX US6322966-B1.
XX
XX 27-NOV-2001.
XX
XX 11-MAY-1999; 99US-00309670.
XX
XX 11-MAY-1999; 99US-00309670.
XX
XX (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (LAUJ/) LAU J Y N.
XX
PI Zhong W, Hong Z, Lau JYN;
XX WPI; 2002-096587/13.
XX
XX Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.
XX
XX Example 1; Fig 1A; 10pp; English.
XX
XX The present invention relates to an assay system for hepatitis C virus
CC (HCV) replicase activity. The assay system comprises an RNA template that
CC has an unstable, small stemloop at the 3' end capable of forming a copy-
CC back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC radiolabelled and an assay buffer that supports replication activity of
CC NS5B. The invention also relates to the identification of optimal
CC properties of an RNA template for copy-back self-priming RNA synthesis of
CC HCV. This activity can be used to screen for anti-HCV replicase compounds
CC or to characterise the biological relevance of lead compounds. The
CC optimal RNA templates can be used for developing a system to characterise
CC HCV NS5B polymerase mechanistically and kinetically and for designing
CC small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC system of the invention is useful for detecting HCV replicase activity.
CC The nucleic acid synthesised by NS5B is detected by evaluating an
CC autoradiograph of reaction products separated by gel electrophoresis. The
CC present sequence is RNA template, (AU)5 used to direct RNA synthesis by
CC RNA polymerase proteins of HCV, BVDV and poliovirus. This sequence is used
CC in the exemplification of the invention
XX
SQ Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;
XX
XX Query Match 0.7%; Score 20.2; DB 1; Length 36;
XX Best Local Similarity 88.0%; Pred. No. 1.6e+03;
XX Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2780 GAATTGAAAAA AAAAAAAAAA 2804
Db ||| ||||| ||||| ||||| ||||| |||||
2 GAAAAA AAAAAAAAAA AAAAAAAAAA 26
XX
XX RESULT 352
XX AAD27125
XX ID AAD27125 standard; RNA; 37 BP.
XX
XX AC AAD27125;
XX
XX 09-APR-2002 (first entry)
XX
XX RNA template, (AU)2 used to direct RNA synthesis by HCV RNA polymerase.
DE Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
XX lead compound; RNA polymerase; ss.
KW
KW
XX
```

```
OS Unidentified.
XX US6322966-B1.
XX
XX 27-NOV-2001.
XX
XX 11-MAY-1999; 99US-00309670.
XX
XX 11-MAY-1999; 99US-00309670.
XX
XX (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (LAUJ/) LAU J Y N.
XX
PI Zhong W, Hong Z, Lau JYN;
XX WPI; 2002-096587/13.
XX
XX Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.
XX
XX Example 1; Fig 2A; 10pp; English.
XX
XX The present invention relates to an assay system for hepatitis C virus
CC (HCV) replicase activity. The assay system comprises an RNA template that
CC has an unstable, small stemloop at the 3' end capable of forming a copy-
CC back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC radiolabelled and an assay buffer that supports replication activity of
CC NS5B. The invention also relates to the identification of optimal
CC properties of an RNA template for copy-back self-priming RNA synthesis of
CC HCV. This activity can be used to screen for anti-HCV replicase compounds
CC or to characterise the biological relevance of lead compounds. The
CC optimal RNA templates can be used for developing a system to characterise
CC HCV NS5B polymerase mechanistically and kinetically and for designing
CC small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC system of the invention is useful for detecting HCV replicase activity.
CC The nucleic acid synthesised by NS5B is detected by evaluating an
CC autoradiograph of reaction products separated by gel electrophoresis. The
CC present sequence is RNA template, (AU)2 used to direct RNA synthesis by
CC RNA polymerase proteins of HCV, BVDV and poliovirus. This sequence is used
CC in the exemplification of the invention
XX
SQ Sequence 37 BP; 33 A; 0 C; 2 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 0.7%; Score 20.2; DB 1; Length 37;
XX Best Local Similarity 88.0%; Pred. No. 1.6e+03;
XX Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2780 GAATTGAAAAA AAAAAAAAAA 2804
Db ||| ||||| ||||| ||||| ||||| |||||
2 GAAAAA AAAAAAAAAA AAAAAAAAAA 26
XX
XX RESULT 353
XX AAD27124
XX ID AAD27124 standard; RNA; 37 BP.
XX
XX AC AAD27124;
XX
XX 09-APR-2002 (first entry)
XX
XX RNA template, (AU)3 used to direct RNA synthesis by HCV RNA polymerase.
DE Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
XX lead compound; RNA polymerase; ss.
KW
KW
XX
XX Unidentified.
XX US6322966-B1.
XX
```


CC The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 356
AAQ58578/c
ID AAQ58578 standard; RNA; 20 BP.
XX
AC AAQ58578;
XX
XX 25-MAR-2003 (revised)
DT 21-AUG-1994 (first entry)
DT
XX
DE Sequence of synthetic RNA oligo which is a target nucleotide for a novel
DE receptor.
XX

KW Novel receptor; nucleic acid; transport; oligo; ss.
XX
OS Synthetic.
XX
XX WO9404194-A1.
PN
XX
PD 03-MAR-1994.
XX

PF 13-AUG-1993; 93WO-US007603.
XX
PR 14-AUG-1992; 92US-00930087.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Usman N, Rebek J, De Mendoza J;
XX
DR WPI; 1994-082846/10.
XX

PT Transport of nucleic acid derivs. across membranes - using new receptors
PT which use salt bridging, aromatic stacking, hydrogen bonding and
PT chelation.
XX
PS Example; Table 1, page 38; 103pp; English.
XX

CC The inventors claim a method of transporting a nucleic acid deriv. across
CC a membrane which comprises using a receptor that uses salt bridgin,
CC aromatic stacking, H bonding and chelation to recognise the nucleic acid
CC deriv. AAQ56305, AAQ58577-86 are nucleic acid derivs used in the
CC examples. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 357
AAQ94205
ID AAQ94205 standard; DNA; 20 BP.
XX
AC AAQ94205;
XX
XX 25-MAR-2003 (revised)
DT 24-AUG-1995 (first entry)
DT
XX
DE Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
XX
KW Oligonucleotide ligand; steroid hormone; hapten; immobilisation;
KW immunodetection; estradiol; alpha-anomer; ss.
XX

OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .21
FT /*tag= b
FT /note= "the glycosidic bonds between nucleotides are all
FT in the alpha-anomer form"
FT modified_base 20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "carries a group derived ffrom aminopropanediol"

XX WO9429723-A1.

XX 22-DEC-1994.

PF 10-JUN-1994; 94WO-FR000689.

PR 11-JUN-1993; 93FR-00007093.

XX (CROS/) CROS P.
PA (KURF/) KURFURST R.
PA (BATT/) BATTAIL N.
PA (PIGA/) PIGA N.

PI Cros P, Kurfurst R, Battail N, Piga N;

DR WPI; 1995-036665/05.

XX Assay device for hapten or its specific antibodies - comprises support
XX having competitive reagent immobilised via nucleic acid ligand to improve
XX orientation and accessibility.

PS Example 1; Page 10; 39pp; French.

XX Oligonucleotides (AAQ94201-Q94205) were synthesised for use as ligands.
CC The ligands are covalently linked to a hapten (esp. a steroid hormone) to
CC form a conjugate which is then immobilised on a solid support for
CC interaction with antibodies against the hapten. Nucleic acid ligands are
CC less likely to be recognised by the antibodies than are peptide ligands
CC and nucleic acids are also less likely to undergo intramolecular
CC organisation which interferes with accessibility of the hapten to the
CC antibodies. For immunodiagnosis of oestradiol, the active hapten
CC oestradiol-6-carboxymethoxime-N- hydroxysuccinimide ester was used.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2166	TTTTTTTTTTTTTTTTTTTTTTT	2185
Db	1	TTTTTTTTTTTTTTTTTTTTTTT	20
RESULT	358		
AAQ75596/c			
ID	AAQ75596	standard; DNA; 20 BP.	
XX	AC	AAQ75596;	
XX	AC		
XX	XX		
DT	04-AUG-1995	(first entry)	
XX			
DE	Reverse transcription primer	used in cDNA analysis technique.	
XX			
XX	Analysis; gene expression; reverse transcription; primer; cDNA;		
KW	aggregate; restriction enzyme; ss.		
KW			
XX	Synthetic.		
OS			
XX	JP06303997-A.		
PN			
XX	01-NOV-1994.		
PD			
XX	16-APR-1993;	93JP-00112515.	
PF			
XX	16-APR-1993;	93JP-00112515.	
XX			
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.		
XX			
XX	WPI; 1995-018287/03.		
DR			
XX			
PT	Analysis of cDNA and gene expression - by amplification of mRNA followed		
PT	by digestion with restriction enzymes.		
XX			
PS	Disclosure; Page 5; 11pp; Japanese.		
XX			
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of		
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of		
CC	labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)		
CC	and using the aggregate of mRNAs as the template for each reverse		
CC	transcription primer; (b) digesting each of the prepared aggregates of		
CC	the double-stranded cDNAs with restriction enzyme and; (c)		
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The		
CC	method can be used to analyse gene expression rapidly and easily		
XX			
SQ	Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;		
Query Match	0.7%;	Score 20;	DB 1; Length 20;
Best local similarity	100.0%;	Pred. No. 4.1e+02;	
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	2783	TTGAAAAA	2802
Db	20	TTGAAAAA	1
RESULT	359		
AAQ75582			
ID	AAQ75582	standard; DNA; 20 BP.	
XX	AC	AAQ75582;	
XX	XX		
DT	04-AUG-1995	(first entry)	
XX			
DE	Reverse transcription primer	used in cDNA analysis technique.	
XX			
KW	Analysis; gene expression; reverse transcription; primer; cDNA;		
KW	aggregate; restriction enzyme; ss.		
XX	Synthetic.		
OS			
XX			

PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT and bio:polymer synthesis.
XX
PS Example 1; Page 41; 86pp; English.
XX
CC The sequences represented by, AAQ90402-15 are synthetic DNA probes
CC containing 5' amino termini. The sequences shown in AAQ90390-401 are
CC synthetic DNA probes with 3' ribonucleoside termini. These sequences were
CC specific for the polymorphisms of HLA gene dQa. The sequences were used
CC in the device of the invention. This is a self-addressable electronic
CC device (SAED) that can be used to carry out multi-step and multiplex
CC reactions, such as nucleic acid hybridisations. The advantages of this
CC method are that these reactions can be carried out with complete and
CC precise electronic control, and that the rate, specificity and
CC sensitivity of these reactions are greatly improved at micro-locations
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 361
AAV07752
ID AAV07752 standard; DNA; 20 BP.
XX
AC AAV07752;
XX
DT 07-DEC-1998 (first entry)
XX
DE Phosphorothioate oligonucleotide.
XX
KW Phosphorothioate; sulphurisation; heterocycle; automated synthesis;
KW antisense; EDITH; Beaucage reagent; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..20
FT /tag= a
FT /note= "phosphorothioate internucleotide linkages"
XX
PN WO9741130-A2.
XX
PD 06-NOV-1997.
XX
PF 29-APR-1997; 97WO-US007118.
XX
PR 30-APR-1996; 96US-00641920.
XX
PA (MINU) UNIV MINNESOTA.
PA (LOU) UNIV LOUISIANA STATE & AGRIC.
XX
PI Barany G, Musier-Forsyth K, Xu Q, Chen L, Hammer RP;
XX WPI; 1997-549671/50.
DR
XX
PT Sulphurisation of phosphorus-containing compounds, e.g.
PT oligo:nucleotide(s) - by contacting the compound with a di:sulphide-
PT containing five-membered heterocycle.
XX
PS Example 7; Page 30; 51pp; English.
XX
CC The present invention provides a method for sulphurising phosphorus-
CC containing compounds. It comprises contacting the phosphorus-containing
CC compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-
CC substituted-1,2,4-dithiazolin-5-one compound. The method is especially
CC useful for incorporation of phosphorothioate linkages into biologically

CC important molecules such as DNA, RNA and phosphopeptides. Molecules
CC containing such linkages are useful e.g. as antisense compounds for
CC inhibiting gene expression, as reagents for studying DNA-protein or RNA-
CC protein interactions, or as catalytic RNA. The present sequence
CC represents an oligonucleotide with phosphorothioate linkages prepared by
CC the method of the invention
XX
SQ Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 5.0%; Pred. No. 4.1e+02;
Matches 1; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 2168 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2187
Db 1 UUUUUUUUUUUUUUUUUUUUUUUA 20

RESULT 362
AAT63649
ID AAT63649 standard; DNA; 20 BP.
XX
AC AAT63649;
XX
DT 06-JUN-1997 (first entry)
XX
DE Anti-HTLV antisense reference oligonucleotide HT.
XX
KW antisense; complementary; tax gene; inhibit; HTLV-1;
KW human T-cell lymphotropic virus type 1; viral antigen expression; ss.
XX
OS Synthetic.
XX
PN JP09052898-A.
XX
PD 25-FEB-1997.
XX
PF 09-AUG-1995; 95JP-00224606.
XX
PR 09-AUG-1995; 95JP-00224606.
XX
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
XX
DR WPI; 1997-197252/18.
XX
PT Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region of
PT tax gene from human T-cell lymphotropic virus type 1 and inhibits viral
PT antigen expression.
XX
PS Example 1; Page 8; 10pp; Japanese.
XX
CC Oligonucleotides having a partial sequence consisting of at least 15
CC bases of AAT63641 (an antisense oligo complementary to a region of the
CC tax gene which can inhibit human T-cell lymphotropic virus type 1 (HTLV-
CC 1) viral antigen expression) are claimed. In an example, six antisense
CC oligos were designed, T1-T6 (AAT63650-55) and were compared to six oligos
CC derived from other regions of HTLV-1, i.e. SJ1 (splice junction), P1
CC (p21), R1 (rex), RR1 (rex response element), E1 (env) and G1 (gag), four
CC reference oligonucleotides T1S (tax-sense), HC (dc20), HT (dt20)
CC (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen
CC expression inhibiting test. Oligonucleotide T1 gave the best results
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 363
AAV34591/c
ID AAV34591 standard; DNA; 20 BP.
XX
AC AAV34591;
XX
DT 25-AUG-1998 (first entry)
XX
DE M. vaccae antigenic sequence hybridising oligo AD12.
XX
KW Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW mycobacteria infection; vaccine; cancer; ss.
XX
OS Synthetic.
OS Mycobacterium vaccae.
XX
PN W09808542-A2.
XX
PD 05-MAR-1998.
XX
PF 28-AUG-1997; 97WO-NZ000105.
XX
PR 29-AUG-1996; 96US-00705347.
PR 12-JUN-1997; 97US-00873970.
XX
PA (GENE-) GENESIS RES & DEV CORP.
XX
PI Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX WPI; 1998-216926/19.
DR
XX Mycobacterium vaccae polypeptides - used to develop products for use in
PT detection, therapy and prevention of mycobacteria infections or as immune
PT response enhancers.
XX
PS Example 8; Page 99; 153pp; English.
XX
CC This oligonucleotide is used in the DNA cloning strategies of the
CC Mycobacterium vaccae antigens. The invention provides M. vaccae
CC polypeptides that comprise an immunogenic portion of a soluble M. vaccae
CC antigen, or a variant, where the antigen induces an immune response in
CC patients previously exposed to a mycobacterium. Such M. vaccae
CC polypeptides can be used in methods for enhancing non-specific immune
CC response. The methods and products can be used for the detection,
CC treatment and prevention of infectious diseases caused by mycobacteria
CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
CC the ability to induce cell proliferation and cytokine production (e.g.
CC interferon-gamma and interleukin-12 production) in T cells, NK cells, B
CC cells, or macrophages. They can be used for enhancing immune responses
CC for use in vaccines or immunotherapy of infectious diseases and cancers
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 364
AAT86606
ID AAT86606 standard; DNA; 20 BP.
XX
AC AAT86606;
XX
DT 04-JUN-1998 (first entry)
XX
DE Oligonucleotide separated by capillary affinity gel electrophoresis.

Capillary affinity gel electrophoresis; separation; polymer-gel;
polyacrylamide; ss.
Synthetic.
W09745721-A1.
04-DEC-1997.
23-MAY-1997; 97WO-EP002647.
24-MAY-1996; 96CH-00001320.
(NOVS) NOVARTIS AG.
Muscate A, Paulus A, Natt F;
WPI; 1998-041763/04.
Separation of electrically charged target molecules - by capillary
affinity gel electrophoresis using polymer-gel to which receptors for
target molecules are bound.
Example D3; Page 25; 41pp; English.
A mixture of oligonucleotides (AAT86604-7) were separated by a new
process using capillary affinity gel electrophoresis. The invention
relates to selective separation of electrically charged target molecules
in an analytical mixture. It comprises capillary affinity gel
electrophoresis using a capillary tube which is at least partly filled
with a polymer gel. Receptors for target molecules are covalently bound
to the polymer. An electric field of at least 50 volts/cm is applied. The
capillary tube is charged with the analytical mixture. In a first
separation stage, the target molecules in the mixture are bound to the
receptors and the remaining components are eluted, optionally whilst
splitting open. In a second stage, the elution conditions are changed,
optionally in stages, so that the affinity of the target molecules for
the receptor is eliminated and the target molecules are eluted and
detected, optionally whilst splitting open. The process is useful for
selective separation and/or determination of charged organic compounds,
such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
for isolation of specific proteins and DNA molecules, purification of
antibodies, analysis of antisense compounds or screening for enzyme
inhibitors. The process achieves higher resolution and selectivity than
prior art processes, especially in the case of complex biological
analytical mixtures. It has high sensitivity, even with small amounts of
samples. The derivatised polymers may be synthesised specifically using
standard methods
Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 365
AAX27533
ID AAX27533 standard; RNA; 20 BP.
XX
AC AAX27533;
XX
DT 27-MAY-1999 (first entry)
XX
DE Synthetic RNA sequence produced by the method of the invention.
KW Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;
KW cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.

```

OS Synthetic.
XX PN WO9909044-A1.
XX PD 25-FEB-1999.
XX PF 17-AUG-1998; 98WO-EP005215.
XX PR 18-AUG-1997; 97CH-00001931.
XX (PITS/) PITSCH S.
XX PA (WEIS/) WEISS P A.
XX PA (JENN/) JENNY L.
XX PI Pitsch S, Weiss PA, Jenny L;
XX WPI; 1999-180963/15.
XX
XX PT 2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have
XX PT high purity, use in machine synthesis of ribonucleic acids, enable longer
XX PT oligonucleotide chain construction, and larger amounts.
XX PS Example 6; Page 25; 38pp; English.
XX
XX CC The invention relates to silyloxymethyl protected D- or L-ribonucleosides
XX CC and their phosphonates (I), and silyloxymethyl halides (II). (I) are
XX CC intermediates for synthesis of RNA-oligonucleotides with predetermined
XX CC nucleotide sequence, particularly by machine synthesis. The groups
XX CC specified above, apart from those on silyl, are those particularly for
XX CC the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide
XX CC products in diagnosis, therapy, and as research tools, are well known,
XX CC and are not dealt with in detail. (II) is an intermediate for (I). The
XX CC silyloxymethyl halide reagent is easy to prepare, and yields are high.
XX CC Introduction of the silyloxymethyl group into the ribonucleoside is
XX CC simple and rapid, and the acetal bond formed does not migrate,
XX CC eliminating particularly the prior art problem of 2' to 3' isomerisation.
XX CC The methylenedioxy group spacer between the silyl group and nucleoside
XX CC ring results in less steric hindrance than bulky direct silyloxy
XX CC linkages, enabling first, a range of choices for the silyl substituents,
XX CC to provide, e.g., acid or base stability; and second, higher yields in
XX CC coupling. Purer products are therefore obtained than in prior art,
XX CC enabling larger quantities and longer chains of oligoribonucleotides to
XX CC be synthesised successfully, and in shorter times
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 20 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 0.0%; Pred. No. 4.1e+02;
Matches 0; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2185
Db 1 UUUUUUUUUUUUUUUUUUUU 20

RESULT 366
AAZ11326/c
ID AAZ11326 standard; DNA; 20 BP.
XX AC AAZ11326;
XX DT
XX DT 25-OCT-1999 (first entry)
XX DE Mycobacterial 16S rRNA specific oligo AD12.
XX KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
XX KW dendritic cell maturation; infectious disease; immune disorder; cancer;
XX KW respiratory system; mycobacterial infection; allergy; tuberculosis;
XX KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
XX KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
XX KW squamous cell carcinoma; melanoma; PCR primer; ss.
XX OS Synthetic.

```

PF 07-JAN-2000; 2000EP-00100126.
XX
PR 06-JAN-1999; 99JP-00001111.
PR 24-MAY-1999; 99JP-00143599.
XX
PA (FUJF) FUJI PHOTO FILM CO LTD.
XX
PI Ogawa M, Takenaka S, Takagi M;
XX
DR WPI; 2000-444372/39.
XX
XX Quantitative analysis of a biochemical compound such as glucose, in body
PT a body fluid such as blood, comprising detecting enhanced electron
PT transfer between an oxidase and a DNA-immobilized electrode, useful for
PT diagnosis of disease.
XX
PS Example 1; Page 8; 14pp; English.
XX
XX This invention describes a novel method for quantitatively analysing a
CC biochemical compound (I) which comprises contacting (I) with double
CC stranded DNA fixed to the surface of an electrode at their terminals in
CC which electrochemically active threading intercalators are intercalated,
CC in an aqueous medium under application of electric potential to the
CC electrode in the presence of an oxidase which oxidizes the biochemical
CC compound and becomes reduced, and detecting electric current flowing
CC between the electrode and a second electrode in the aqueous medium. The
CC method is useful for detection of biochemical compounds such as glucose,
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
CC for diagnosis of various diseases. The method allows detection of
CC biochemical compounds quickly and easily with a high sensitivity using a
CC simple apparatus. This sequence represents DNA fragment used as a target
CC sample in the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 368
AAA40448
ID AAA40448 standard; DNA; 20 BP.
XX
AC AAA40448;
XX
DT 13-NOV-2000 (first entry)
XX
DE Electrochemical detection method fixed probe. DNA.
XX
KW Electrochemical detection; glucose; cholesterol; urea nitrogen;
KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
KW plasma; serum; urine; lymph diagnosis; probe; ss.
XX
OS Synthetic.
XX
PN EP1018646-A2.
XX
PD 12-JUL-2000.
XX
PF 07-JAN-2000; 2000EP-00100126.
XX
PR 06-JAN-1999; 99JP-00001111.
PR 24-MAY-1999; 99JP-00143599.
XX
PA (FUJF). FUJI PHOTO FILM CO LTD.
XX
PI Ogawa M, Takenaka S, Takagi M;

WPI; 2000-444372/39.
Quantitative analysis of a biochemical compound such as glucose, in body
a body fluid such as blood, comprising detecting enhanced electron
transfer between an oxidase and a DNA-immobilized electrode, useful for
diagnosis of disease.
Example 1; Page 7; 14pp; English.
This invention describes a novel method for quantitatively analysing a
biochemical compound (I) which comprises contacting (I) with double
stranded DNA fixed to the surface of an electrode at their terminals in
which electrochemically active threading intercalators are intercalated,
in an aqueous medium under application of electric potential to the
electrode in the presence of an oxidase which oxidizes the biochemical
compound and becomes reduced, and detecting electric current flowing
between the electrode and a second electrode in the aqueous medium. The
method is useful for detection of biochemical compounds such as glucose,
cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
acid in body fluids such as whole blood, plasma, serum, urine, and lymph
for diagnosis of various diseases. The method allows detection of
biochemical compounds quickly and easily with a high sensitivity using a
simple apparatus. This sequence represents DNA fragment used as fixed
probe DNA in the method of the invention
Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 369
AAZ91117
ID AAZ91117 standard; DNA; 20 BP.
XX
AC AAZ91117;
XX
DT 06-JUN-2000 (first entry)
XX
DE Oligonucleotide #5 for conjugation to abietane derivative.
XX
KW Abietane derivative; labelling; diagnostic test; biotin substitute; ss.
XX
OS Synthetic.
XX
PN FR2781802-A1.
XX
PD 04-FEB-2000.
XX
PF 31-JUL-1998; 98FR-00010084.
XX
PR 31-JUL-1998; 98FR-00010084.
XX
PA (INMR) BIO MERIEUX.
XX
PI Charles MH, Piga N, Battail PN, Veron L, Delair T, Mandrand B;
XX
DR WPI; 2000-239603/21.
XX
PT Saturated and unsaturated derivatives of abietic acid and their
PT conjugated derivatives with natural and synthetic polymers, having use in
PT diagnostics, chemical reactions and analysis.
XX
PS Example 5; Page 20; 39pp; French.
XX
CC The invention relates to novel saturated and unsaturated abietane
CC derivatives. The new compounds may be used directly or indirectly in the

development of new diagnostic tests, to follow infections, especially viral infections, to follow and/or measure chemical products, especially potential pollutants. In diagnostic tests they may be used as markers, or to form a universal solid phase after immobilization on a solid support, to produce monoclonal antibodies or polyclonal antibodies having diagnostic uses. The oligonucleotides AA291113-291117 represent examples of sequences that can be labeled with the new abietane derivatives. The new derivatives may be used to substitute for biotin in diagnostic tests, but because they are not found naturally in humans the risk of potential interactions with biological molecules is eliminated

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
| | | | | | | | | | | | | | | | | |
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 370
AAA50193
ID AAA50193 standard; DNA; 20 BP.
XX
AC AAA50193;
XX
DT 07-NOV-2000 (first entry)
XX
DE 2'-Methoxyethoxy-modified oligonucleotide.
XX
KW Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= a
FT /note= "2'-methoxyethoxy modified thymidine"

WO200047593-A1.
17-AUG-2000.
11-FEB-2000; 2000WO-US003543.
12-FEB-1999; 99US-00250075.
(ISIS-) ISIS PHARM INC.
Manoharan M, Maier MA;
WPI; 2000-558188/51.
Preparation of mixed backbone oligomeric compounds useful as e.g. primers for diagnostic tests, involves oxidation of H-phosphonate internucleoside linkages to phosphodiester internucleoside linkages.

Example 12; Page 34; 49pp; English.
The present sequence is that of a phosphodiester oligonucleotide containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group on its 5' ribosyl sugar moiety. It is an example of an oligomeric compound produced according to the methods of the invention. The invention provides compounds and methods for the preparation of mixed backbone oligomeric, or chimeric, compounds having phosphodiester internucleoside linkages in addition to phosphorothioate and/or phosphoramidate internucleoside linkages. The methods also include incorporation of boranophosphate internucleoside linkages. The methods utilise H-phosphonate intermediates that are coupled together forming contiguous regions of 1 or more H-phosphonate internucleoside linkages. Each contiguous region is subsequently oxidized to phosphodiester, phosphorothioate,

phosphoramidate or boranophosphate internucleoside linkages prior to further elongation. Mixed backbone oligomeric compounds are prepared in this manner by oxidizing adjacent regions with different reagents. Oligomeric compounds of the invention are prepared using novel oxidation steps that oxidize a region of 1 or more H-phosphonate internucleoside linkages without degrading existing linkages that have been previously oxidized. The oligonucleotides obtained are useful as primers in PCR, probes, linkers, gene fragments and for other diagnostic tests on e.g. biological tissue, fluid, cells etc., as research reagents, and as antiviral agents

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
| | | | | | | | | | | | | | | | | |
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 371
AAC87238
ID AAC87238 standard; DNA; 20 BP.
XX
AC AAC87238;
XX
DT 09-MAR-2001 (first entry)
XX
DE Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.
XX

KW Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW antagonist; mimic; inhibitor; drug screening;
KW cellular target identification; oligonucleotide optimisation;
KW immunotherapy; ss.

XX Synthetic.
OS
XX WO200067023-A1.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011697.
XX
PR 29-APR-1999; 99US-0131830P.
PR 03-MAR-2000; 2000US-0186845P.
XX
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Noll BO, Schetter C, Krieg AM;
XX
DR WPI; 2001-016002/02.

XX Immunostimulatory DNA binding proteins to identify immunostimulatory DNA functional modifiers, immunostimulatory DNA binding competitors and to optimize immunostimulatory oligodeoxynucleotides for stimulation.
PS Example 1; Page 45; 95pp; English.
XX

CC The invention relates to the use of an immunostimulatory single-stranded DNA-binding protein in screening assays to identify compounds which bind to it and thereby act as functional modifiers of immunostimulatory oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity consist of immunostimulatory DNA binding inhibitors, immunostimulatory DNA mimics, and immunostimulatory DNA agonists and antagonists. CC Immunostimulatory DNA-binding proteins can also be used in screening methods to identify immunostimulatory DNA binding competitors, and to optimize an immunostimulatory ODN for immune stimulation. Isolated CC complexes of an immunostimulatory DNA-binding protein bound to an

CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory ODN competitors allow the
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 372
AAC87230
ID AAC87230 standard; DNA; 20 BP.

XX AAC87230;

AC AAC87230;

XX 09-MAR-2001 (first entry)

DT Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.

DE Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
XX immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW antagonist; mimic; inhibitor; drug screening;
KW cellular target identification; oligonucleotide optimisation;
KW immunotherapy; ss.

XX Synthetic.

OS WO200067023-A1.

XX 09-NOV-2000.

PN 28-APR-2000; 2000WO-US011697.

PD 29-APR-1999; 99US-0131830P.

XX 03-MAR-2000; 2000US-0186845P.

XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

PA (IOWA) UNIV IOWA RES FOUND.

XX Noll BO, Schetter C, Krieg AM;

PI WPI; 2001-016002/02.

XX Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT functional modifiers, immunostimulatory DNA binding competitors and to
PT optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded
CC DNA-binding protein in screening assays to identify compounds which bind
CC to it and thereby act as functional modifiers of immunostimulatory
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC immunostimulatory DNA-binding proteins can also be used in screening

CC methods to identify immunostimulatory DNA binding competitors, and to
CC optimize an immunostimulatory ODN for immune stimulation. Isolated
CC complexes of an immunostimulatory DNA-binding protein bound to an
CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory ODN competitors allow the
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 373

AAC87241

ID AAC87241 standard; DNA; 20 BP.

XX AAC87241;

AC AAC87241;

XX 09-MAR-2001 (first entry)

DT Poly T oligonucleotide, SEQ ID NO:20.

DE Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
XX immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW antagonist; mimic; inhibitor; drug screening;
KW cellular target identification; oligonucleotide optimisation;
KW immunotherapy; ss.

XX Synthetic.

OS WO200067023-A1.

XX 09-NOV-2000.

PN 28-APR-2000; 2000WO-US011697.

PD 29-APR-1999; 99US-0131830P.

XX 03-MAR-2000; 2000US-0186845P.

XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

PA (IOWA) UNIV IOWA RES FOUND.

XX Noll BO, Schetter C, Krieg AM;

PI WPI; 2001-016002/02.

XX Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT functional modifiers, immunostimulatory DNA binding competitors and to
PT optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded
CC DNA-binding protein in screening assays to identify compounds which bind
CC to it and thereby act as functional modifiers of immunostimulatory
CC oligodeoxynucleotide (ODN) activity. Such modifiers of immunostimulatory
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC immunostimulatory DNA-binding proteins can also be used in screening

consist of immunostimulatory DNA binding inhibitors, immunostimulatory DNA mimics, and immunostimulatory DNA agonists and antagonists. Immunostimulatory DNA-binding proteins can also be used in screening methods to identify immunostimulatory DNA binding competitors, and to optimize an immunostimulatory ODN for immune stimulation. Isolated complexes of an immunostimulatory DNA-binding protein bound to an immunostimulatory ODN can additionally be used to screen a panel of candidate target molecules to identify the cellular target molecules of the immunostimulatory ODN. The immunostimulatory DNA-binding proteins used in the methods of the invention are the RNA-binding proteins nucleolin, hnRNP D, AUFL1, hnRNP A1 and lupus La protein. The screening methods are useful for identifying a compound that inhibits interaction between immunostimulatory DNA and an immunostimulatory DNA-binding protein and for identifying agonists useful in immunotherapy. The complex is useful in screening for immunostimulatory DNA cellular target molecules. The candidate immunostimulatory ODN competitors allow the investigation of structure/activity relationships of immunostimulatory DNA-binding proteins and immunostimulatory ODNs. The present sequence represents an oligonucleotide used in an exemplification of the invention

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

```

CC The method, based on the synthesis of Okazaki fragments, is useful for
CC labeling and modifying the 3'-termini of other nucleic acids such as DNA
CC fragments. The method is a simple and efficient way of labeling or
CC modifying RNA 3'-termini using DNA polymerase and a synthetic template
CC with defined overhang nucleotides
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 375
AAD16997
ID AAD16997 standard; DNA; 20 BP.
XX
AC AAD16997;
XX
DT 29-NOV-2001 (first entry)
XX
DE Capture probe CP5'.
XX
KW Scaffold protein; antibody mimic; fibronectin type III domain;
KW randomised loop; randomised beta-sheet; diagnostic purpose;
KW protein designing; probe; tenth module of human Fn3; 10Fn3;
KW fibronectin module of type III; Fn3; ss.

```

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Thu Jun 10 13:10:09 2004

CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
CC the scope of (B)) have superior uptake to corresponding fluorescein
CC conjugates
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 377

AAS63428/c

ID AAS63428 standard; DNA; 20 BP.

XX AAS63428;

AC AAS63428;

XX 29-JAN-2002 (first entry)

DE Oligonucleotide-nanoparticle probe #52.

XX Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;

KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;

KW ss.

XX Synthetic.

OS WO200173123-A2.

XX 04-OCT-2001.

XX 28-MAR-2001; 2001WO-US010071.

XX 28-MAR-2000; 2000US-0192699P.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

PR 26-JUN-2000; 2000US-0213906P.

PR 08-DEC-2000; 2000US-0254392P.

PR 11-DEC-2000; 2000US-0255235P.

PR 12-JAN-2001; 2001US-00760500.

PR 28-MAR-2001; 2001US-00820279.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA, Park S, Li Z;

XX WPI; 2001-656926/75.

DR Detecting and separating nucleic acid, useful e.g. for diagnosis,

XX comprises reaction with nanoparticles that carry oligonucleotides

XX complementary to parts of the target.

PS Example 18; Page 158; 404pp; English.

XX The invention relates to a method for detection of nucleic acid (I)

CC having at least 2 portions, comprising treatment with nanoparticles that

CC carry oligonucleotides complementary to at least 2 parts of (I), where

CC detectable change caused by hybridisation of the oligonucleotide to (I)

CC is observed. The method is used to detect (or to separate) specific (I),

CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic

CC analysis etc., and generally to detect analytes other than (I). The

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 376

AAF60896/c

ID AAF60896 standard; DNA; 20 BP.

XX AAF60896;

DT 15-MAY-2001 (first entry)

XX Conjugate forming oligonucleotide ON5 SEQ ID 5.

XX Transport; membrane; cytostatic; virucide; vasotropic; dermatological;

KW antiprosoratic; antiasthmatic; gene therapy; tumor cell; antisense;

KW tumor therapy; drug; phosphodiester linkage; ss.

XX Unidentified.

XX DE19935302-A1.

XX 08-FEB-2001.

XX 28-JUL-1999; 99DE-01035302.

XX 28-JUL-1999; 99DE-01035302.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;

XX WPI; 2001-203679/21.

XX New substituted aryl conjugates of parent molecules, especially

PT oligonucleotides, having improved transmembrane and intracellular

PT transport properties, useful as medicaments or diagnostic agents.

PS Disclosure; Page 9; 28pp; German.

XX This invention describes a novel conjugate (I) which consists of (A) a

CC molecule to be transported and (B) at least one aryl residue of formula -

CC Ar-(X-C(Y)-R₁)_n (II). Ar = group containing at least one aromatic ring;

CC X = O or N (sic); Y = O, S or NH-R₂ (sic); R₁ = optionally substituted

CC 1-23C alkyl (optionally containing double and/or triple bonds); R₂ =

CC optionally substituted 1-18C alkyl (optionally containing double and/or

CC triple bonds); n = integer of 1 or more. (A) is bonded to (B) directly or

CC via a chemical group, provided that the chemical group is other than CH₂

CC -S if the bond is via a phosphodiester linkage of (A). The invention also

CC describes (i) the preparation of a conjugate (I') of (A') a molecule to

CC be transported and (B') at least one aryl residue (not restricted to

CC (II)), by preparing (A') containing a reactive function at the position

CC at which (B') is to be bonded, preparing (B') and reacting (A') and (B'); and

CC and (ii) the use of aryl groups (II) (optionally bonded via a chemical

CC group) for transporting (A) across biological membranes. The products of

CC the invention have cytostatic, virucide, vasotropic, dermatological,

CC antiprosoratic and antiasthmatic activity and can be used for gene

CC therapy. Conjugation of (A) with (B) is useful for transporting (A)

CC across biological membranes or into eukaryotic or prokaryotic cells

CC (specifically bacterial, yeast or mammalian cells, including human cells,

CC particularly tumor cells). Medicaments, diagnostic agents and test kits

CC containing (I) are also claimed. Typically (I) are antisense

CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for

CC treating viral infections or diseases associated with integrins or cell-

CC cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma); or

CC labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ

CC hybridization. Conjugation with (B) markedly improves the cellular uptake

CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,

CC in which case the conjugates (I) are fluorescently labeled, allowing

CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)

CC is superior to that obtained using other conjugated groups related to

RESULT 382
AAAF99431/c
ID AAF99431 standard; DNA; 20 BP.
XX AC AAF99431;
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #547.
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX PN WO200122972-A2.
XX PD 05-APR-2001.
XX PF 25-SEP-2000; 2000WO-US026383.
XX PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
XX PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX PS Claim 101; Page 49; 338pp; English.
XX CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 383
AAH46465
ID AAH46465 standard; DNA; 20 BP.
XX AC AAH46465;
XX DT 14-SEP-2001 (first entry)

XX Oligonucleotide #13.
DE Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX Synthetic.
XX Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /mod_base= OTHER
FT /note= "All bases are phosphorothioate"
FT modified_base 1 /*tag= b
FT /mod_base= OTHER
FT /note= "Modified with 2'-O-methyl"
XX US6242591-B1.
XX PN 05-JUN-2001.
XX PD 11-JAN-2000; 2000US-00481486.
XX PF 15-OCT-1997; 97US-00950779.
XX PR (ISIS-) ISIS PHARM INC.
XX PA Cole DL, Ravikumar VT, Cheruvallath ZS;
PI WPI; 2001-407218/43.
XX DR Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
XX useful in biological research, comprises phosphorylating the 5'-hydroxyl
XX of a nucleic acid having a nucleoside with a 2' modification.
XX Example 23; Col 11; 7pp; English.
XX CC The present invention relates to a method for preparing phosphorothioate
CC oligonucleotides having at least one nucleoside with a 2' modification.
CC The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
CC group having at least one nucleoside with a 2' modification in an
CC acetonitrile. The present sequence was used to illustrate the method of
CC the present invention. The method is useful for synthesising sulphurised
CC 2' substituted phosphorothioate oligonucleotides, which may be used in
CC molecular biological research, in applications such as anti-viral
CC therapy, and for determining the stereochemical pathways of certain
CC enzymes which recognise nucleic acids
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 384
AAH78547/c
ID AAH78547 standard; cDNA; 20 BP.
XX AC AAH78547;
XX DT 10-DEC-2001 (first entry)
XX DE Nucleotide sequence of a cDNA sequence.
XX KW Nucleic acid identification; DNA library screening; ss.
XX OS Synthetic.
XX

XX WPI; 2002-566690/60.

DR Inhibiting angiogenesis in a subject, involves administering at least one

XX antiangiogenic nucleic acid molecule to the subject.

PT Claim 2; Page 23; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,

CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque

CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic

CC acid of the invention

XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. NO. 4.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 387

ABS78072

ID ABS78072 standard; DNA; 20 BP.

XX

AC ABS78072;

XX

DT 13-DEC-2002 (first entry)

XX

DE Angiogenesis inhibitory oligonucleotide #556.

XX

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;

KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;

KW plaque neovascularisation; telangiectasia; haemophilic joint;

KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;

KW scleroderma; hypertrophic scar.

XX

OS Synthetic.

XX

PN WO200253141-A2.

XX

PD 11-JUL-2002.

XX

PF 14-DEC-2001; 2001WO-US048458.

XX

PR 14-DEC-2000; 2000US-0255534P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PI Bratzler RL;

XX

DR WPI; 2002-566690/60.

XX

XX Inhibiting angiogenesis in a subject, involves administering at least one

PT antiangiogenic nucleic acid molecule to the subject.

XX

PS Claim 2; Page 29; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,

CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque

CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic

CC acid of the invention

XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. NO. 4.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 388

ABS78076/c

ID ABS78076 standard; DNA; 20 BP.

XX

AC ABS78076;

XX

DT 13-DEC-2002 (first entry)

XX

DE Angiogenesis inhibitory oligonucleotide #560.

XX

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;

KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;

KW plaque neovascularisation; telangiectasia; haemophilic joint;

KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;

KW scleroderma; hypertrophic scar.

XX

OS Synthetic.

XX

PN WO200253141-A2.

XX

PD 11-JUL-2002.

XX

PF 14-DEC-2001; 2001WO-US048458.

XX

PR 14-DEC-2000; 2000US-0255534P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PI Bratzler RL;

XX

DR WPI; 2002-566690/60.

XX

XX Inhibiting angiogenesis in a subject, involves administering at least one

PT antiangiogenic nucleic acid molecule to the subject.

XX

PS Claim 2; Page 29; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 391
ABL39403
ID ABL39403 standard; DNA; 20 BP.
XX
AC ABL39403;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 839.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 309; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2166 TTTTTTTTTTTTTTTTTT 2185
Db 1 TTTTTTTTTTTTTTTTTT 20

RESULT 392
ABL54775
ID ABL54775 standard; DNA; 20 BP.
XX
AC ABL54775;
XX
DT 10-JUN-2002 (first entry)

XX
DE
XX
KW CD14 receptor PCR primer SEQ ID NO 9.
KW Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;
XX single-nucleotide polymorphism; PCR; primer; ss.
OS Synthetic.
XX
PN JP2002034599-A.
XX
PD 05-FEB-2002.
XX
PF 26-JUL-2000; 2000JP-00225354.
XX
PR 26-JUL-2000; 2000JP-00225354.
XX
PA (TOYM) TOYOBO KK.
XX
DR WPI; 2002-275727/32.
XX
PT Detecting 1 base polymorphism on a sequence of a chromosome or it's
PT fragment.
XX
PS Example 2; Page 10; 10pp; Japanese.
XX
CC The invention relates to a method for detecting 1 base polymorphism on
CC the sequence of a chromosome or its fragment in which a sample nucleic
CC acid is reacted with a reaction liquor containing a nucleic acid primer
CC having a base adjacent to the polymorphic base at its 3'-end, one
CC dideoxynucleotide corresponding to a polymorphic base having a
CC distinguishable feature or its mixture, DNA polymerase and a composition
CC required for its activity expression to detect the presence of taking
CC dideoxynucleotide in the nucleic acid primer and to detect the type of
CC the base to be specified. The method is used for detecting 1 base
CC polymorphism on the sequence of a chromosome or its fragment. The present
CC sequence is that of a PCR primer, useful in examples of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2166 TTTTTTTTTTTTTTTTTT 2185
Db 1 TTTTTTTTTTTTTTTTTT 20

RESULT 393
ABK65035/c
ID ABK65035 standard; DNA; 20 BP.
XX
AC ABK65035;
XX
DT 02-JUL-2002 (first entry)
XX
DE Nanoparticle-oligonucleotide #55.
XX
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW ss.
XX
OS Synthetic.
XX
PN WO200218643-A2.
XX
PD 07-MAR-2002.
XX
PF 10-AUG-2001; 2001WO-US025237.
XX
PR 11-AUG-2000; 2000US-0224631P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
PR 12-JAN-2001; 2001US-00760500.

Thu Jun 10 13:10:09 2004

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PR 28-MAR-2001; 2001US-00820279.
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
XX WPI; 2002-258024/30.
XX
XX Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX
XX Example 18; Page 410; 412pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA; and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroid residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
RESULT 394
ABK65050/c
ID ABK65050 standard; DNA; 20 BP.
XX
XX AC ABK65050;
XX
XX DT 02-JUL-2002 (first entry)
XX
XX DE Nanoparticle-oligonucleotide #70.
XX
XX XX Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW ss.
XX OS Synthetic.
XX
XX PN WO200218643-A2.
XX
XX PD 07-MAR-2002.
XX
XX PF 10-AUG-2001; 2001WO-US025237.
XX
XX PR 11-AUG-2000; 2000US-0224631P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
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PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
XX WPI; 2002-258024/30.
XX
XX Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX
XX Example 24; Fig 44; 412pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA; and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroid residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
RESULT 395
AAL45122
ID AAL45122 standard; DNA; 20 BP.
XX
XX AC AAL45122;
XX
XX DT 24-MAY-2002 (first entry)
XX
XX DE Oligonucleotide synthesis method related DNA #1.
XX
XX XX Oligonucleotide synthesis; polynucleotide array; protecting group;
KW oxidation; ss.
XX OS Synthetic.
XX
XX PN EP1176151-A1.
XX
XX PD 30-JAN-2002.
XX
XX PF 27-JUL-2001; 2001EP-00118360.
XX
XX PR 28-JUL-2000; 2000US-00627249.
```


PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX Dellinger DJ, Perbost MGM, Betley JR, Caruthers M;
PI WPI; 2002-156732/21.
XX
PT Synthesis of polynucleotide useful during fabrication of an array
PT involves coupling nucleoside phosphoramidite and a solid-supported
PT nucleoside and treating the product with an oxidation/deprotection
PT composition.
XX
PS Example 1; Page 15; 36pp; English.
XX
CC The present invention relates to a method for the synthesis of a
CC polynucleotide which involves coupling a second nucleoside to a first
CC nucleoside through a phosphite linkage, where the second nucleoside has a
CC non-carbonate protecting group protecting a hydroxyl, and exposing the
CC product to a composition which concurrently oxidizes the phosphite formed
CC to a phosphate and deprotects the protected hydroxyl of the second
CC nucleoside. The method is useful for synthesizing the polynucleotides,
CC for carrying out either 3' to 5' or 5' to 3' synthesis and for
CC fabricating an addressable array of polynucleotides on a substrate. The
CC present sequence is an oligonucleotide produced to demonstrate the method
CC of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2185
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 396
ABL36232/c
ID ABL36232 standard; DNA; 20 BP.
XX
AC ABL36232;
XX
DT 08-APR-2002 (first entry)
XX
DE M tuberculosis rRNA probe SEQ ID NO: 83.
XX
KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; probe; ss.
XX
OS Mycobacterium tuberculosis.
XX
XX US6328978-B1.
PN
XX
PD 11-DEC-2001.
XX
PF 02-JUN-1999; 99US-00324542.
XX
PR 23-DEC-1997; 97US-00997080.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Prestidge R;
XX
DR WPI; 2002-138361/18.
XX
PT Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
PS Example 5; Col 99-100; 116pp; English.

XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC probe described in the exemplification of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2185
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 397
ABS64673/c
ID ABS64673 standard; DNA; 20 BP.
XX
AC ABS64673;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polynucleotide #55.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046418.
XX
PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-608256/65.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 18; Page 437; 442pp; English.
XX
CC The invention describes a method of detecting (M1) a nucleic acid having
CC two portions, involving providing nanoparticles having oligonucleotides
CC attached to it, which has a sequence complementary to sequence of two
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC allow hybridisation of oligonucleotides with two or more portions of
CC nucleic acid, and observing a detectable change brought about by
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide

CC conjugates (II) and the aggregate probe are useful for detecting two or
CC more nucleic acids (from a biological source) having at least two
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC with a disease, synthetic, or structurally-modified natural or synthetic
CC RNA or DNA, or a product of a polymerase chain reaction amplification.
CC (II) is useful for preparing a nanoprobe conjugate for detecting an
CC analyte, and for detecting a nucleic acid bound to an electrode surface.
CC (I) and (II) are useful for fabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. (I), (II) and
CC the aggregate probe are useful for detecting an analyte (especially
CC polyvalent analyte) in a sample. This sequence represents a
CC polynucleotide used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
|||||

RESULT 398
ABS64688/C
ID ABS64688 standard; DNA; 20 BP.
XX
AC ABS64688;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polynucleotide #70.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046418.
XX
PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-608256/65.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 24; Fig 44; 442pp; English.
XX
CC The invention describes a method of detecting (M1) a nucleic acid having
CC two portions, involving providing nanoparticles having oligonucleotides
CC attached to it, which has a sequence complementary to sequence of two
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC allow hybridisation of oligonucleotides with two or more portions of

CC nucleic acid, and observing a detectable change brought about by
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC conjugates (II) and the aggregate probe are useful for detecting two or
CC more nucleic acids (from a biological source) having at least two
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC with a disease, synthetic, or structurally-modified natural or synthetic
CC RNA or DNA, or a product of a polymerase chain reaction amplification.
CC (II) is useful for preparing a nanoprobe conjugate for detecting an
CC analyte, and for detecting a nucleic acid bound to an electrode surface.
CC (I) and (II) are useful for fabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. (I), (II) and
CC the aggregate probe are useful for detecting an analyte (especially
CC polyvalent analyte) in a sample. This sequence represents a
CC polynucleotide used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1
|||||

RESULT 399
ABN87103
ID ABN87103 standard; DNA; 20 BP.
XX
AC ABN87103;
XX
DT 30-JUL-2002 (first entry)
XX
DE Capture probe CP5' SEQ ID NO:23.
XX
KW Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.
XX
OS Synthetic.
XX
PN WO200232925-A2.
XX
PD 25-APR-2002.
XX
PF 16-OCT-2001; 2001WO-US032233.
XX
PR 16-OCT-2000; 2000US-00688566.
XX
PA (PHYL-) PHYLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX
DR WPI; 2002-444238/47.
XX
PT New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.
XX
PS Disclosure; Page 58; 94pp; English.
XX
CC The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct sequences

immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct](ftp:wipo.int/pub/published/pct) sequences

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition,
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 404
ABZ85312/c

ID ABZ85312 standard; DNA; 20 BP.
XX
AC ABZ85312;
XX

DT 17-OCT-2003 (first entry)
XX Human oligonucleotide sequence.

DE Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX

PN WO200285308-A2.
XX

PD 31-OCT-2002.
XX

PF 23-APR-2002; 2002WO-US013135.
XX

PR 24-APR-2001; 2001US-0286137P.
XX

PA (EPIG-) EPIGENESIS PHARM INC.
XX

PPI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PPI Miller S, Tang L, Shahabuddin S;
XX

DR WPI; 2003-229219/22.
XX

PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX

PS Claim 15; SEQ ID NO 554; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 406
ABZ88881/c
ID ABZ88881 standard; DNA; 20 BP.

XX ABZ88881;
AC
XX

DT 17-OCT-2003 (first entry)
XX

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.
OS

XX WO200285308-A2.
PN

XX 31-OCT-2002.
PD

XX 23-APR-2002; 2002WO-US013135.
PF

XX 24-APR-2001; 2001US-0286137P.
PR

XX (EPIG-) EPIGENESIS PHARM INC.
PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.
DR

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 4123; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
|||||
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 407
ABZ89546/c
ID ABZ89546 standard; DNA; 20 BP.

XX ABZ89546;
AC
XX

DT 17-OCT-2003 (first entry)
XX

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.
OS

XX WO200285308-A2.
PN

XX 31-OCT-2002.
PD

XX 23-APR-2002; 2002WO-US013135.
PF

XX 24-APR-2001; 2001US-0286137P.
PR

XX (EPIG-) EPIGENESIS PHARM INC.
PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.
DR

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 4788; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

```

Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	2169	TTTTTTTTTTTTTTTTTAA	2188
Db	20	TTTTTTTTTTTTTTTTTAA	1

RESULT 408
ABZ89706/C
ID ABZ89706 standard; DNA; 20 BP.

AC ABZ89706;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence:

Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
asthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; lung; bronchoconstriction;
lung inflammation; respiratory disease; ds.

OS Homo sapiens.

PN WO200285308-A2

31-OCT-2002.
PD

23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiguinone.

PS Disclosure; SEQ ID NO 4948; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive.

immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct/sequences

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

```

Query Match          0.7%;   Score 20;   DB 1;   Length 20;
Best Local Similarity 100.0%;   Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

[illegible]

RESULT 409
ABZ88620/c
ID ABZ88620 standard; DNA; 20 BP.

AC ABZ88620;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
asthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

OS Homo sapiens.

PN WO200285308-A2.

PD 31-OCT-2002.

23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

PS Disclosure; SEQ ID NO 3862; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp:wipo.int/pub/published_pct_sequences)

```

Q      Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;

```

Qy	2166	2185
Qy	TTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTT
pb	TTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTT
	20	1

RESULT 415
ABZ99050/C
ID ABZ99050 standard: DNA: 20 BP.

ABZ99050;

17-OCT-2003 (first entry)

Human pDE4C oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WD200285308-A2.

31-OCT-2002.

23-APP-2002: 2002WO-US013135.

24 APR 2001: 2001US-02861 37P

(ERIC) ERICGENESTS PHARM INC

Condrescova A. Katz E. Pabalan J. Aquilar D.

Nyce JW, Li Y, Saurasaga H, Lippincott J, Tang I, Shabazz S:

[illegible]

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure: SEO ID NO 14292: 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 416
ABZ88815/c
ID ABZ88815 standard; DNA; 20 BP.
XX
AC ABZ88815;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX

PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX

PS Disclosure; SEQ ID NO 4057; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2185
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 417
ABZ85311
ID ABZ85311 standard; DNA; 20 BP.

XX
AC ABZ85311;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.

XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX

PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX

PS Claim 15; SEQ ID NO 553; 872pp; English.

XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 418
ABZ85435
ID ABZ85435 standard; DNA; 20 BP.
XX
AC ABZ85435;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 677; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 419
ABZ8817/C
ID ABZ8817 standard; DNA; 20 BP.
XX
AC ABZ8817;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4059; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 428
ABZ89016/c
ID ABZ89016 standard; DNA; 20 BP.
XX
AC ABZ89016;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4258; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
DB 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 429
ABZ89120/c
ID ABZ89120 standard; DNA; 20 BP.
XX
AC ABZ89120;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4362; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at fto.wipo.int/pub/published pct sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match	0.7%;	Score 20;	DB 1;	Length 20;
-------------	-------	-----------	-------	------------

Accuracy	Local Similarity	Pred. No.	Pred. No.
4.1e+02	100.0%	4.1e+02	4.1e+02

Best Local Similarity	0.967								
Matches	20	Conservative	0	Mismatches	0	Indels	0	Gaps	0

QY 2166 TTTTTTTTTTTTTTTTTT 2185
| | | | | | | | | | | | | | | |
pb 20 TTTTTTTTTTTTTTTTTT 1

RESULT 431
ACD27320/c
in ACD27320 standard: DNA: 20 BP:

ACD27320;

15-OCT-2003 (first entry)

Nanotechnology nucleic acid detection method associated #54.

Nanotechnology; ss; nucleic acid detection; nanoparticle; virus detection; human immunodeficiency virus; HIV; hepatitis; herpes; cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing sexually transmitted disease; inherited disorder; forensic; paternity testing; cell line authentication.

Synthetic.

Key	Location/Qualifiers
modified_base	1
	/+...

```

/mod_base= OTHER
/note= "OTHER= Thiol modified" "

```

11C2002155461-A1.

34-OCT-2002

• 2007-100-42

Aguilar D;

Ultrasağ A, N

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

XX
ps
Example 18: page 44: 130pp; English.

XX
ps
Example 18: page 44: 130pp; English.

XX This invention relates to a novel method for detecting a nucleic acid
CC having 2 portions. The method comprises providing nanoparticles having
CC oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC the oligonucleotide on the nanoparticle with two or more portions of
CC nucleic acid and observing a detectable change brought about by the
CC hybridisation. The method of the invention is useful for separating a
CC selected nucleic acid having 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having 2 portions. The method of the
CC invention is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus), hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication, for monitoring gene therapy, etc. This method
CC involves detecting nucleic acids based on observing a colour change with
CC the naked eye so is cheap, fast, simple and robust, and does not require
CC specialised expensive equipment. The present sequence represents a thiol
CC modified oligonucleotide sequence used to demonstrate the method of the
CC invention

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 432
ACC58867
ID ACC58867 standard; DNA; 20 BP.

AC ACC58867;

DT 08-SEP-2003 (first entry)

DE Doubly labelled DNA probe.

KW Probe; nucleic acid detection; ss.

OS Synthetic.

PN WO2003043402-A2.

PD 30-MAY-2003.

PF 21-OCT-2002; 2002WO-US033699.

PR 19-OCT-2001; 2001US-0336432P.

PA (PROL-) PROLIGO LLC.

PI Bruce I, Davies M, Wolter A;

XX WPI; 2003-505122/47.

DR

XX

PT Detection or quantification of nucleic acid analyte, by hybridizing a
PT nucleic acid probe having non-identical covalently attached dyes, with
PT nucleic acid analyte, and measuring change in fluorescence of the probes.

PS Example 9; Page 32; 110pp; English.

XX

CC The present sequence is an example of nucleic acid probes of the
CC invention. The probe may be doubly labelled with non-identical covalently
CC attached dyes, e.g. the fluorescent intercalator ethidium, which serves

CC as the detector dye and the fluorescent dye fluorescein, which serves as
CC the donor dye of a fluorescent resonance energy transfer (FRET) system. A
CC bifunctional linker was used to attach the dyes to the oligonucleotide.
CC The probe generates a fluorescent signal upon hybridisation to a
CC complementary nucleic acid based on the interaction of the intercalator
CC with the formed double-stranded DNA. Nucleic acid probes of the invention
CC can be used in homogeneous assays, real-time PCR monitoring,
CC transcription assays, expression analysis on nucleic acid microarrays and
CC other microarray applications such as genotyping

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 433
ABZ22916
ID ABZ22916 standard; DNA; 20 BP.

AC ABZ22916;

DT 08-APR-2003 (first entry)

DE Phosphorothioate 20-mer oligonucleotide #1.

KW Chiral; phosphorothioate; oligonucleotide synthesis; enantiomer; ss.
OS Synthetic.

FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"

PN WO2002102815-A2.

PD 27-DEC-2002.

PF 13-JUN-2002; 2002WO-US018581.

PR 14-JUN-2001; 2001US-00881535.

XX (ISIS-) ISIS PHARM INC.

PA Ravikumar VT;

PI WPI; 2003-157021/15.

DR

PT Preparing internucleotide phosphorothioate linkage enhanced in Sp/Rp
PT enantiomer, by coupling a synthon with 2'-substituted nucleoside in
PT presence of coupling agent having a pKa that enhances linkage in Sp/Rp
PT enantiomer.

PS Example 1; Page 31; 65pp; English.

XX

CC The present invention describes a method (M1) for preparing an
CC internucleotide phosphorothioate linkage enriched in the Sp or Rp
CC enantiomer between a synthon having a hydroxyl moiety at the 5' position
CC and a 2'-substituted nucleoside having an activated phosphate moiety at
CC the 3'-position, comprising coupling a synthon with a 2'-substituted
CC nucleoside in the presence of coupling agent that is selected to enhance
CC either the Rp or Sp enantiomer according to its pKa. This method is
CC useful for preparing an oligonucleotide having at least one region of
CC internucleotide linkages that is enhanced in the Sp or Rp enantiomer,
CC which involves providing a nucleotide having a hydroxyl moiety at the 5'-
CC position or a growing oligonucleotide chain having a hydroxyl moiety at

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2185
| | | | | | | | | | | | | | | | | |
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 436
ABX79181/c
ID ABX79181 standard; DNA; 20 BP.
XX
AC ABX79181;
XX
DT 15-APR-2003 (first entry)
XX
DE Thio-modified 20da oligonucleotide.
XX

KW Nanoparticle; ss; nucleic acid detection; viral disease; probe;
KW human immunodeficiency virus infection; hepatitis virus infection;
KW herpes virus infection; cytomegalovirus infection; forensic science;
KW Epstein-Barr virus infection; bacterial disease; gene therapy;
KW sexually transmitted disease; inherited disorder; DNA sequencing;
KW paternity testing; cell line authentication.
XX
OS Synthetic.
XX
PN US2002155462-A1.
XX
PD 24-OCT-2002.
XX
PF 12-OCT-2001; 2001US-00976577.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-198491/19.
XX

PT Detecting nucleic acids having at least 2 portions comprises use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the nucleic acid sequence.
PS Example 18; Page 44; 130pp; English.
XX

CC The invention relates to detecting a nucleic acid (NA) having at least 2
CC portions, comprises providing a type of nanoparticles (NP) having
CC attached to oligonucleotides (O) ((O) on each NP has a sequence
CC complementary to sequence of at least 2 portions of NA), contacting NA
CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
CC and observing a detectable change brought about by hybridisation of (O)
CC on NP with NA. The nanoparticle is useful for separating a selected
CC nucleic acid having at least 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having at least 2 portions. The method of
CC using NP is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication and for monitoring gene therapy. The method is
CC useful in research and analytical laboratories in DNA sequencing and in

CC the field to detect the presence of specific pathogens. Detecting nucleic
CC acids based on observing a colour change with the naked eye is cheap,
CC fast, simple and robust, and do not require specialised expensive
CC equipment. The present sequence is a nanoparticle (e.g. gold particles)
CC labelled probe used to demonstrate the method of the invention

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2185
| | | | | | | | | | | | | | | | | |
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 437
ABX92177/c
ID ABX92177 standard; DNA; 20 BP.
XX
AC ABX92177;
XX
DT 12-MAY-2003 (first entry)
XX
DE Nanoparticle-associated oligonucleotide SEQ ID 55.
XX

KW Nanoparticle; nucleic acid detection; hybridisation; diagnosis;
KW sequencing; viral infection; human immunodeficiency virus; HIV;
KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;
KW bacterial infection; sexually transmitted disease; inherited disorder;
KW forensic; paternity testing; cell line authentication; gene therapy; ss.
XX
OS Synthetic.
XX
PN US2002155458-A1.
XX
PD 24-OCT-2002.
XX
PF 28-SEP-2001; 2001US-00967409.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-182627/18.
XX

PT Detecting nucleic acids having at least two portions involves use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the nucleic acid sequence.
PS Disclosure; Page 59; 130pp; English.
XX

CC This invention describes a novel method of detecting nucleic acid having
CC at least two portions. The method involves providing nanoparticles
CC attached to oligonucleotides, where the oligonucleotide on each
CC nanoparticle have a sequence complementary to a sequence of at least two
CC portions of nucleic acid, contacting nucleic acid and nanoparticle to
CC allow hybridisation of the oligonucleotide on the nanoparticle with two
CC or more portions of nucleic acid and observing a detectable change
CC brought about by hybridisation of the oligonucleotide nanoparticle with
CC nucleic acid. The method is useful for separating a selected nucleic acid
CC having at least two portions, from other nucleic acids and for detecting
CC nucleic acids having at least two portions. The method is useful for
CC detecting any type of nucleic acids which may be used for diagnosis of

CC disease and in sequencing of nucleic acids. Preferably, the method is
CC useful for detecting nucleic acids for diagnosis and/or monitoring of
CC viral infections (human immunodeficiency virus (HIV), hepatitis virus,
CC herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial
CC diseases, sexually transmitted diseases, inherited disorders, in
CC forensics, in DNA sequencing, for paternity testing, for cell line
CC authentication, and for monitoring gene therapy. The method is useful in
CC research and analytical laboratories in DNA sequencing, in the field to
CC detect the presence of specific pathogens. Detecting nucleic acids based
CC on observing a colour change with the naked eye is cheap, fast, simple
CC and robust and does not require specialised expensive equipment. ABX92123
CC -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the
CC method of the invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 438
ACD27255/c
ID ACD27255 standard; DNA; 20 BP.

XX ACD27255;

XX 15-OCT-2003 (first entry)

DE Nanotechnology nucleic acid detection method associated #54.

XX Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW sexually transmitted disease; inherited disorder; forensic;
KW paternity testing; cell line authentication.

XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "

XX US2002155459-A1.

XX 24-OCT-2002.

XX 11-OCT-2001; 2001US-00975062.

XX 29-JUL-1996; 96US-0031809P.

XX 21-JUL-1997; 97WO-US012783.

XX 29-JAN-1999; 99US-00240755.

XX 25-JUN-1999; 99US-00344667.

XX 26-APR-2000; 2000US-0200161P.

XX 26-JUN-2000; 2000US-00603830.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;

XX WPI; 2003-228114/22.

XX Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT comprises use of nanoparticles which have oligonucleotides attached to
PT them that are complementary to portions of the nucleic acid sequence.

XX

PS Example 18; Page 43; 129pp; English.

XX This invention relates to a novel method for detecting a nucleic acid
CC having 2 portions. The method comprises providing nanoparticles having
CC oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC the oligonucleotide on the nanoparticle with two or more portions of
CC nucleic acid and observing a detectable change brought about by the
CC hybridisation. The method of the invention is useful for separating a
CC selected nucleic acid having 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having 2 portions. The method of the
CC invention is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication, for monitoring gene therapy, etc. This method
CC involves detecting nucleic acids based on observing a colour change with
CC the naked eye so is cheap, fast, simple and robust, and does not require
CC specialised expensive equipment. The present sequence represents a thiol
CC modified oligonucleotide sequence used to demonstrate the method of the
CC invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 439

ACD27125/c

ID ACD27125 standard; DNA; 20 BP.

XX ACD27125;

XX 15-OCT-2003 (first entry)

DE Nanotechnology nucleic acid detection method oligonucleotide #54.

XX Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
KW DNA sequencing; paternity testing; cell line authentication.

XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "

XX US2002164605-A1.

XX 07-NOV-2002.

XX 28-SEP-2001; 2001US-00966312.

XX 29-JUL-1996; 96US-0031809P.

XX 21-JUL-1997; 97WO-US012783.

XX 29-JAN-1999; 99US-00240755.

XX 25-JUN-1999; 99US-00344667.

XX 26-APR-2000; 2000US-0200161P.

XX 26-JUN-2000; 2000US-00603830.

XX (NANO-) NANOSPHERE INC.

XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-247253/24.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change,
PT useful in forensics.
XX
PS Example 18; Page 44; 130pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acid
CC sequences having two portions. The method involves providing
CC nanoparticles having oligonucleotides attached to them, which has a
CC sequence complementary to sequence of two portions of nucleic acid,
CC contacting nucleic acid and nanoparticles, to allow hybridisation of
CC oligonucleotides with two or more portions of nucleic acid, and observing
CC a detectable change brought about by hybridisation. The method of the
CC invention and the aggregate probes are useful for detecting two or more
CC nucleic acids (from a biological source) having at least two portions,
CC such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with
CC a disease, synthetic, or structurally- modified natural or synthetic RNA
CC or DNA, or a product of a polymerase chain reaction amplification.
CC Nanoparticles and nanoparticle- oligonucleotide conjugates of the
CC invention are useful for nanofabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. The method of
CC the invention is useful in forensics, DNA sequencing, for paternity
CC testing, cell line authentication, and monitoring gene therapy.
CC Diagnostic assays employing the nanoparticle-oligonucleotide conjugates
CC of the invention improve the sensitivity of the nucleic acid detection
CC assay. The present sequence represents a thiol modified oligonucleotide
CC sequence used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 440
ACD27385/c
ID ACD27385 standard; DNA; 20 BP.
XX
AC ACD27385;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KW pathogen detection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "
XX
PN US2002182611-A1.
XX
PD 05-DEC-2002.
XX
PF 28-SEP-2001; 2001US-00966491.
XX
PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-596264/56.
XX
PT Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.
XX
PS Example 18; Page 43; 109pp; English.
XX
CC This invention relates to a novel method for detecting a nucleic acid by
CC contacting a nucleic acid with at least two types of nanoparticles having
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides
CC on the nanoparticles, and observing a detectable change. The
CC oligonucleotides on each nanoparticle have a sequence complementary to
CC its respective portion of the sequence of the nucleic acid to be
CC detected. The method of the invention may be used for the detection of a
CC nucleic acid used in, e.g. research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens, in
CC the doctor's office for quick identification of an infection to assist in
CC prescribing a drug for treatment, and in homes and health centres for
CC inexpensive first-line screening. The method of the invention detects
CC nucleic acids based on observing a colour change with the naked eye. This
CC method is cheap, fast, simple, robust and does not require specialised or
CC expensive equipment. The present sequence represents a thiol modified
CC oligonucleotide sequence used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 441
ACD27190/c
ID ACD27190 standard; DNA; 20 BP.
XX
AC ACD27190;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "
XX
PN US2002182613-A1.
XX
PD 05-DEC-2002.
XX
PF 12-OCT-2001; 2001US-00976971.

06-MAR-2003.

XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP-2 gamma; AP-2.2;
KW strc2. activating enhancer-binding protein 2 gamma; antisense therapy;
WW strc2. activating enhancer-binding protein 2 gamma; antisense therapy;
XX strc2. activating enhancer-binding protein 2 gamma; antisense therapy;

KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
XX 26-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX Example 15; Page 79; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX The invention is useful for inhibiting the expression of TFAP2C in cells
XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX prophylaxis and as research reagents and kits. It is also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targeted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
SQ Sequence 20 BP; 1 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 GTGACCCGACAGCAAGGCC 45
Db 20 GTGACCCGACAGCAAGGCC.1
RESULT 444
AAL62303/c
ID AAL62303 standard; DNA; 20 BP.
XX
AC AAL62303;
XX

DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128157.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
XX WO2003051308-A2.
XX
XX 26-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX Example 15; Page 80; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX The invention is useful for inhibiting the expression of TFAP2C in cells
XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX prophylaxis and as research reagents and kits. It is also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targeted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
SQ Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1029 ATCTCCGCGCGGAGGCGG 1048
Db 20 ATCTCCGCGCGGAGGCGG 1

RESULT 445
AAL62320/c
ID AAL62320 standard; DNA; 20 BP.
XX
AC AAL62320;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128174.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1733 TCAGAAGGTGACAAAGTACTG 1752
|||
Db 20 TCAGAAGGTGACAAAGTACTG 1
|||
RESULT 446
AAL62343/c
ID AAL62343 standard; DNA; 20 BP.
XX
AC AAL62343;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128197.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention

XX
SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2653 CTAAGGTGAGTGTGCAGTAC 2672
Db 20 CTAAGGTGAGTGTGCAGTAC 1

RESULT 447
AAL622284/c
ID AAL622284 standard; DNA; 20 BP.
XX
AC AAL622284;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128138.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 79; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder

CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 CCTACTCGCATCTGGGGGAA 409
Db 20 CCTACTCGCATCTGGGGGAA 1

RESULT 448
AAL622290/c
ID AAL622290 standard; DNA; 20 BP.
XX
AC AAL622290;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128144.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods

CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 3 A; 8 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 630 CCTGGATGCCGCGGCCTG 649
Db 20 CCTGGATGCCGCGGCCTG 1
|||||
AAL62301 standard; DNA; 20 BP.
AAL62301;
06-OCT-2003 (first entry)
Human transcription factor-2 gamma antisense oligo, ISIS 128155.
Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
breast; colon; developmental disorder; human; phosphorothioate backbone;
antisense; ss.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
modified_base 1..20
/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidines are 5-
methylcytidines"
modified_base 1..5
/*tag= b
/mod_base= OTHER
/note= "2'methoxyethyl nucleotides"
modified_base 16..20
/*tag= c
/mod_base= OTHER
/note= "2'methoxyethyl nucleotides"
WO2003051308-A2.
26-JUN-2003.
12-DEC-2002; 2002WO-US040100.
17-DEC-2001; 2001US-00023782.
(ISIS-) ISIS PHARM INC.
Cowser LM, Freier SM;
WPI; 2003-569107/53.
New antisense compound targeted to a nucleic acid molecule encoding

PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 981 AAAATGGAGGCGGTCCTTG 1000
Db 20 AAAATGGAGGCGGTCCTTG 1
|||||
AAL62306 standard; DNA; 20 BP.
AAL62306;
06-OCT-2003 (first entry)
Human transcription factor-2 gamma antisense oligo, ISIS 128160.
Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
breast; colon; developmental disorder; human; phosphorothioate backbone;
antisense; ss.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
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methylcytidines"
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WO2003051308-A2.
26-JUN-2003.
12-DEC-2002; 2002WO-US040100.
17-DEC-2001; 2001US-00023782.
(ISIS-) ISIS PHARM INC.
PA

XX
PI Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
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PS Claim 3; Page 80; 107pp; English.
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CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
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QY 1170 CCAGACCTCATCTTGGAGGA 1189
DB 20 CCAGACCTCATCTTGGAGGA 1

RESULT 451
AAL62312/c
ID AAL62312 standard; DNA; 20 BP.
XX
AC AAL62312;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128166.
DE
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
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FT methylcytidines"
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PN WO2003051308-A2.
XX
PD 26-JUN-2003.

XX
PF 12-DEC-2002; 2002WO-US040100.
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PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
XX WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
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CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
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CC such as cancer e.g. breast cancer or colon cancer and a developmental
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CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
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QY 1393 GTCTGCCCTGCAGAACTACA 1412
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RESULT 452
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ID AAL62325 standard; DNA; 20 BP.
XX
AC AAL62325;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128179.
DE
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowser LM, Freier SM;
XX
XX WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
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XX Example 15; Page 80; 107pp; English.
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XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX prophylaxis and as research reagents and kits. It is also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
XX
SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2021 CCTCTGTTAGGAGGCAAAGG 2040
Db 20 CCTCTGTTAGGAGGCAAAGG 1
RESULT 453
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ID AAL62327 standard; DNA; 20 BP.
XX
XX AAL62327;
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XX 06-OCT-2003 (first entry)
XX
XX Human transcription factor-2 gamma antisense oligo, ISIS 128181.
XX
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
XX oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
XX breast; colon; developmental disorder; human; phosphorothioate backbone;
XX antisense; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
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XX WO2003051308-A2.
XX
XX 26-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowser LM, Freier SM;
XX
XX WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX Claim 3; Page 80; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
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XX or tissues. It is useful for treating an animal having a disease or
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XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX prophylaxis and as research reagents and kits. It is also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
XX
SQ Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2068 AGTGGTATCTGACACACTCT 2087
Db 20 AGTGGTATCTGACACACTCT 1
RESULT 454
AAL62341/c
ID AAL62341 standard; DNA; 20 BP.
XX
XX AAL62341;
XX
XX 06-OCT-2003 (first entry)
XX
XX Human transcription factor-2 gamma antisense oligo, ISIS 128195.
XX
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
XX oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
XX breast; colon; developmental disorder; human; phosphorothioate backbone;
XX antisense; ss.
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XX Homo sapiens.
XX Synthetic.
XX
XX
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FH Key Location/Qualifiers
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FT methylcytidines"
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FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16. .20
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FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
for modulating the expression of transcription factor-2 gamma (TFAP2C).
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or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2630 TCTCGTTCCTGTTGGGCTGA 2649
Db 20 TCTCGTTCCTGTTGGGCTGA 1

RESULT 455
AAL62272/c
ID AAL62272 standard; DNA; 20 BP.
XX
AC AAL62272;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128126.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;

KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
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PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
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PS Example 15; Page 79; 107pp; English.
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CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
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QY 19 GTGTCCAGTGACCCGGACAG 38
Db 20 GTGTCCAGTGACCCGGACAG 1

RESULT 456
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ID AAL62288 standard; DNA; 20 BP.
XX
AC AAL62288;
XX
DT 06-OCT-2003 (first entry)

XX DE Human transcription factor-2 gamma antisense oligo, ISIS 128142.
XX KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX OS Homo sapiens.
OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
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FT /note= "phosphorothioate backbone; All cytidines are 5-methylcytidines"
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XX PN WO2003051308-A2.
XX PD 26-JUN-2003.
XX PF 12-DEC-2002; 2002WO-US040100.
XX PR 17-DEC-2001; 2001US-00023782.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
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XX SQ Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
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Db 20 CCGCAGGGATGCCTACCGCC 1

AAL62292/c
ID AAL62292 standard; DNA; 20 BP.
XX AC AAL62292;
XX DT 06-OCT-2003 (first entry)
XX DE Human transcription factor-2 gamma antisense oligo, ISIS 128146.
XX KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX OS Homo sapiens.
OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
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FT /note= "Phosphorothioate backbone; All cytidines are 5-methylcytidines"
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XX PN WO2003051308-A2.
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XX PF 12-DEC-2002; 2002WO-US040100.
XX PR 17-DEC-2001; 2001US-00023782.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
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XX SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 CCTCACCAGATGGACGAGGT 696
Db 20 CCTCACCAGATGGACGAGGT 1

RESULT 458
AAL62307/C
XX AAL62307 standard; DNA; 20 BP.
AC AAL62307;
XX 06-OCT-2003 (first entry)
DT Human transcription factor-2 gamma antisense oligo, ISIS 128161.
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
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FT /*tag= b
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XX WO2003051308-A2.
PN 26-JUN-2003.
PD 12-DEC-2002; 2002WO-US040100.
XX 17-DEC-2001; 2001US-00023782.
PR (ISIS-) ISIS PHARM INC.
PA Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
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XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
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CC such as cancer e.g. breast cancer or colon cancer and a developmental
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CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention

SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1188 GACGAAATGAGATGGCAGCT 1207
Db 20 GACGAAATGAGATGGCAGCT 1

RESULT 459
AAL62314/C
ID AAL62314 standard; DNA; 20 BP.
XX AAL62314;
AC AAL62314;
XX 06-OCT-2003 (first entry)
DT Human transcription factor-2 gamma antisense oligo, ISIS 128168.
DE Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
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XX WO2003051308-A2.
PN 26-JUN-2003.
PD 12-DEC-2002; 2002WO-US040100.
XX 17-DEC-2001; 2001US-00023782.
PR (ISIS-) ISIS PHARM INC.
PA Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
DR New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
PS Claim 3; Page 80; 107pp; English.
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental

CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1426 GATTGTCTATAGACAAATCCT 1445
Db 20 GATTGTCTATAGACAAATCCT 1
RESULT 460
AAL62313/c
ID AAL62313 standard; DNA; 20 BP.
XX
AC AAL62313;
XX 06-OCT-2003 (first entry)
XX Human transcription factor-2 gamma antisense oligo, ISIS 128167.
DE
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
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XX
PN WO2003051308-A2.
XX
XX 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targetted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).

CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1419 AAGCCCTGATTGTCATAGAC 1438
Db 20 AAGCCCTGATTGTCATAGAC 1
RESULT 461
AAL62331/c
ID AAL62331 standard; DNA; 20 BP.
XX
AC AAL62331;
XX 06-OCT-2003 (first entry)
XX Human transcription factor-2 gamma antisense oligo, ISIS 128185.
DE
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
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FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT 16..20
FT /*tag= c
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FT /note= "2'methoxyethyl nucleotides"
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PN WO2003051308-A2.
XX
XX 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targetted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the

PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2231 CATGTTCCCTTAAGGTACTG 2250
Db |||||
20 CATGTTCCCTTAAGGTACTG 1
RESULT 462
AAL62286/c
ID AAL62286 standard; DNA; 20 BP.
XX
AC AAL62286;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128140.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylecytidines"
FT modified_base 1..5
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FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
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XX WO2003051308-A2.
XX
XX 26-JUN-2003.
PD
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PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX

PI Cowsert LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 79; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 0 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 441 AGCCGGCGCCACAGGCAGC 460
Db |||||
20 AGCCGGCGCCACAGGCAGC 1
RESULT 463
AAL62339/c
ID AAL62339 standard; DNA; 20 BP.
XX
AC AAL62339;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128193.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylecytidines"
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FT /*tag= b
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FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
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XX WO2003051308-A2.
XX
XX 26-JUN-2003.
PD
XX

PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 7 A; 2 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2504 TAACACATCATAAGGTTT 2523
Db 20 TAACACATCATAAGGTTT 1

RESULT 464
AAL62340/C
ID AAL62340 standard; DNA; 20 BP.
XX
AC AAL62340;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128194.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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WO2003051308-A2.
26-JUN-2003.
12-DEC-2002; 2002WO-US040100.
17-DEC-2001; 2001US-00023782.
(ISIS-) ISIS PHARM INC.
Cowsert LM, Freier SM;
WPI; 2003-569107/53.
New antisense compound targeted to a nucleic acid molecule encoding
transcription factor-2 gamma, useful for inhibiting expression of the
nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
Example 15; Page 80; 107pp; English.
The invention relates to antisense compounds, compositions and methods
for modulating the expression of transcription factor-2 gamma (TFAP2C).
TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
The invention is useful for inhibiting the expression of TFAP2C in cells
or tissues. It is useful for treating an animal having a disease or
condition associated with TFAP2C, e.g., a hyperproliferative disorder
such as cancer e.g. breast cancer or colon cancer and a developmental
disorder. The invention is also useful for diagnostics, therapeutics,
prophylaxis and as research reagents and kits. It is also used in
antisense therapy. The present sequence is an antisense oligonucleotide
targeted to human TFAP2C DNA. This sequence is used to illustrate the
method of the invention
XX
SQ Sequence 20 BP; 9 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2593 TTAATTGAAACTCTCTGTT 2612
Db 20 TTAATTGAAACTCTCTGTT 1

RESULT 465
AAL62348/C
ID AAL62348 standard; DNA; 20 BP.
XX
AC AAL62348;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128202.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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PN      WO2003051308-A2.
XX
PD      26-JUN-2003.
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PF      12-DEC-2002; 2002WO-US040100.
XX
PR      17-DEC-2001; 2001US-00023782.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Cowsert LM, Freier SM;
XX
DR      WPI; 2003-569107/53.
XX
CC      New antisense compound targeted to a nucleic acid molecule encoding
CC      transcription factor-2 gamma, useful for inhibiting expression of the
CC      nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
CC      Example 15; Page 81; 107pp; English.
CC
CC      The invention relates to antisense compounds, compositions and methods
CC      for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC      TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC      enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC      The invention is useful for inhibiting the expression of TFAP2C in cells
CC      or tissues. It is useful for treating an animal having a disease or
CC      condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC      such as cancer e.g. breast cancer or colon cancer and a developmental
CC      disorder. The invention is also useful for diagnostics, therapeutics,
CC      prophylaxis and as research reagents and kits. It is also used in
CC      antisense therapy. The present sequence is an antisense oligonucleotide
CC      targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC      method of the invention
XX
SQ      Sequence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2756 TGTATAATAAAAGTATTCTT 2775
Db      |||||
        20 TGTATAATAAAAGTATTCTT 1

RESULT 466
AAL62293/c
ID      AAL62293 standard; DNA; 20 BP.
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AC      AAL62293;
XX
DT      06-OCT-2003 (first entry)
XX
DE      Human transcription factor-2 gamma antisense oligo, ISIS 128147.
XX
KW      Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW      Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW      oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW      breast; colon; developmental disorder; human; phosphorothioate backbone;
KW      antisense; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key Location/Qualifiers
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methylcytidines"
1. .5
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16. .20
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WO2003051308-A2.
26-JUN-2003.
12-DEC-2002; 2002WO-US040100.
17-DEC-2001; 2001US-00023782.
(ISIS-) ISIS PHARM INC.
Cowsert LM, Freier SM;
WPI; 2003-569107/53.
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The invention is useful for inhibiting the expression of TFAP2C in cells
or tissues. It is useful for treating an animal having a disease or
condition associated with TFAP2C, e.g., a hyperproliferative disorder
such as cancer e.g. breast cancer or colon cancer and a developmental
disorder. The invention is also useful for diagnostics, therapeutics,
prophylaxis and as research reagents and kits. It is also used in
antisense therapy. The present sequence is an antisense oligonucleotide
targetted to human TFAP2C DNA. This sequence is used to illustrate the
method of the invention
XX
SQ      Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match
Best Local Similarity 0.7%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      684 AGATGGACGAGGTGCAGAAAT 703
Db      |||||
        20 AGATGGACGAGGTGCAGAAAT 1

RESULT 467
AAL62308/c
ID      AAL62308 standard; DNA; 20 BP.
XX
AC      AAL62308;
XX
DT      06-OCT-2003 (first entry)
XX
DE      Human transcription factor-2 gamma antisense oligo, ISIS 128162.
XX
KW      Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW      Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW      oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW      breast; colon; developmental disorder; human; phosphorothioate backbone;
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Thu Jun 10 13:10:09 2004

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KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
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FT /note= "2'methoxyethyl nucleotides"
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XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
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PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
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CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
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CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1308 TCTTGGAGACGACATACAG 1327
Db 20 TCTTGGAGACGACATACAG 1
RESULT 468
AAL62316/c
IC AAL62316 standard; DNA; 20 BP.
XX
AC AAL62316;
XX
DT 06-OCT-2003 (first entry)
XX
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```
DE Human transcription factor-2 gamma antisense oligo, ISIS 128170.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
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FT modified_base 16..20
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PN WO2003051308-A2.
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PD 26-JUN-2003.
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PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 3 A; 8 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1529 GAAGAAAGGTTAGGAGAGTA 1548
Db 20 GAAGAAAGGTTAGGAGAGTA 1
RESULT 469
AAL62294/c
```

ID XX AAL62294 standard; DNA; 20 BP.
AC XX AAL62294;
DT XX 06-OCT-2003 (first entry)
DE XX Human transcription factor-2 gamma antisense oligo, ISIS 128148.
KW KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW KW antisense; ss.
XX XX
OS OS Homo sapiens.
OS OS Synthetic.
XX XX
FH FH Key Location/Qualifiers
FT FT modified_base 1..20
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT FT methylcytidines"
FT FT 1..5
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FT FT /note= "2'methoxyethyl nucleotides"
FT FT 16..20
FT FT /*tag= c
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FT FT /note= "2'methoxyethyl nucleotides"
XX XX
PN PN WO2003051308-A2.
XX XX
PD PD 26-JUN-2003.
XX XX
PF PF 12-DEC-2002; 2002WO-US040100.
XX XX
PR PR 17-DEC-2001; 2001US-00023782.
XX XX (ISIS-) ISIS PHARM INC.
PA PA
PI PI Cowser LM, Freier SM;
XX XX
DR DR WPI; 2003-569107/53.
XX XX
CC CC The invention relates to antisense compounds, compositions and methods
CC CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC CC or tissues. It is useful for treating an animal having a disease or
CC CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC CC disorder. The invention is also useful for diagnostics, therapeutics,
CC CC prophylaxis and as research reagents and kits. It is also used in
CC CC antisense therapy. The present sequence is an antisense oligonucleotide
CC CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC CC method of the invention
XX XX
SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AATGTCGACGACCACCT 720

Db 20 AATGTCGACGACCACCT 1
RESULT 470
AAL62298/c
ID AAL62298 standard; DNA; 20 BP.
XX XX
AC AAL62298;
XX XX
DT 06-OCT-2003 (first entry)
XX XX
DE XX Human transcription factor-2 gamma antisense oligo, ISIS 128152.
XX XX
KW KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW KW antisense; ss.
XX XX
OS OS Homo sapiens.
OS OS Synthetic.
XX XX
FH FH Key Location/Qualifiers
FT FT modified_base 1..20
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT FT methylcytidines"
FT FT 1..5
FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "2'methoxyethyl nucleotides"
FT FT 16..20
FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'methoxyethyl nucleotides"
XX XX
PN PN WO2003051308-A2.
XX XX
PD PD 26-JUN-2003.
XX XX
PF PF 12-DEC-2002; 2002WO-US040100.
XX XX
PR PR 17-DEC-2001; 2001US-00023782.
XX XX (ISIS-) ISIS PHARM INC.
PA PA
PI PI Cowser LM, Freier SM;
XX XX
DR DR WPI; 2003-569107/53.
XX XX
CC CC New antisense compound targeted to a nucleic acid molecule encoding
CC CC transcription factor-2 gamma, useful for inhibiting expression of the
CC CC nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
PS PS Claim 3; Page 80; 107pp; English.
XX XX
CC CC The invention relates to antisense compounds, compositions and methods
CC CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC CC or tissues. It is useful for treating an animal having a disease or
CC CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC CC disorder. The invention is also useful for diagnostics, therapeutics,
CC CC prophylaxis and as research reagents and kits. It is also used in
CC CC antisense therapy. The present sequence is an antisense oligonucleotide
CC CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC CC method of the invention
XX XX
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1093 AGCTGTTTCATTGGCTAGGG 1112
Db 20 AGCTGTTTCATTGGCTAGGG 1

RESULT 472
AAL62305/c
ID AAL62309 standard; DNA; 20 BP.
XX
AC AAL62309;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128163.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX
PH Key Location/Qualifiers
FT modified_base 1..20
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
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FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
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FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PS New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX The invention is useful for inhibiting the expression of TFAP2C in cells
XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX

CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGCTCAGTCCCTGGAAGATT 858
Db 20 TGCTCAGTCCCTGGAAGATT 1

RESULT 471
AAL62305/c
ID AAL62305 standard; DNA; 20 BP.
XX
AC AAL62305;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128159.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
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FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
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FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PS New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
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XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX The invention is useful for inhibiting the expression of TFAP2C in cells
XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX

CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1365 TTGGCAGCCAGGCCATCTGT 1384
Db 20 TTGGCAGCCAGGCCATCTGT 1

RESULT 473
AAL62315/c
ID AAL62315 standard; DNA; 20 BP.
XX
AC AAL62315;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128169.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT 1..5
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FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.

XX
PS
XX Claim 3; Page 80; 107pp; English.
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CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
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CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 3 A; 4 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 ACAGGAAATAAAATTGGAAC 1528
Db 20 ACAGGAAATAAAATTGGAAC 1

RESULT 474
AAL62333/c
ID AAL62333 standard; DNA; 20 BP.
XX
AC AAL62333;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128187.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT methylcytidines"
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PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;

XX WPI; 2003-569107/53.
XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX Example 15; Page 80; 107pp; English.
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
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CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX Sequence 20 BP; 4 A; 7 C; 1 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2286 GTAACTTGAAAGGGTAGG 2305
Db 20 GTAACTTGAAAGGGTAGG 1
RESULT 475
AAL62278/c
ID AAL62278 standard; DNA; 20 BP.
XX AAL62278;
XX 06-OCT-2003 (first entry)
XX Human transcription factor-2 gamma antisense oligo, ISIS 128132.
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20 /*tag= a
FT /mod_base= OTHER
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FT methylcytidines"
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FT 16..20
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XX WO2003051308-A2.
XX 26-JUN-2003.
XX 12-DEC-2002; 2002WO-US040100.

XX 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX Example 15; Page 79; 107pp; English.
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
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CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 CCTGGATTAACTGGCGACT 144
Db 20 CCTGGATTAACTGGCGACT 1
RESULT 476
AAL62310/c
ID AAL62310 standard; DNA; 20 BP.
XX AAL62310;
XX 06-OCT-2003 (first entry)
XX Human transcription factor-2 gamma antisense oligo, ISIS 128164.
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20 /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT 1..5
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FT 16..20
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FT /note= "2'methoxyethyl nucleotides"

XX PN WO2003051308-A2.
XX PD 26-JUN-2003.
XX PF 12-DEC-2002; 2002WO-US040100.
XX PR 17-DEC-2001; 2001US-00023782.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowser LM, Freier SM;
XX DR WPI; 2003-569107/53.
XX PF New antisense compound targeted to a nucleic acid molecule encoding transcription factor-2 gamma, useful for inhibiting expression of the nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX PS Example 15; Page 80; 107pp; English.
XX CC The invention relates to antisense compounds, compositions and methods for modulating the expression of transcription factor-2 gamma (TFAP2C). TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1. The invention is useful for inhibiting the expression of TFAP2C in cells or tissues. It is useful for treating an animal having a disease or condition associated with TFAP2C, e.g., a hyperproliferative disorder such as cancer e.g. breast cancer or colon cancer and a developmental disorder. The invention is also useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is also used in antisense therapy. The present sequence is an antisense oligonucleotide targeted to human TFAP2C DNA. This sequence is used to illustrate the method of the invention
XX SQ Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1375 GGCCATCTGTGCCGCGGTGT 1394
Db 20 GGCCATCTGTGCCGCGGTGT 1
RESULT 477
AAL62319/c
ID AAL62319 standard; DNA; 20 BP.
XX AC AAL62319;
XX DT 06-OCT-2003 (first entry)
XX DE Human transcription factor-2 gamma antisense oligo, ISIS 128173.
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone; antisense; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-methylcytidines"
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FT FT /mod_base= OTHER
FT modified_base /note= "2'methoxyethyl nucleotides"
FT 16..20
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XX FT /note= "2'methoxyethyl nucleotides"
PN WO2003051308-A2.
XX PD 26-JUN-2003.
XX PF 12-DEC-2002; 2002WO-US040100.
XX PR 17-DEC-2001; 2001US-00023782.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowser LM, Freier SM;
XX DR WPI; 2003-569107/53.
XX PF New antisense compound targeted to a nucleic acid molecule encoding transcription factor-2 gamma, useful for inhibiting expression of the nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX PS Claim 3; Page 80; 107pp; English.
XX CC The invention relates to antisense compounds, compositions and methods for modulating the expression of transcription factor-2 gamma (TFAP2C). TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1. The invention is useful for inhibiting the expression of TFAP2C in cells or tissues. It is useful for treating an animal having a disease or condition associated with TFAP2C, e.g., a hyperproliferative disorder such as cancer e.g. breast cancer or colon cancer and a developmental disorder. The invention is also useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is also used in antisense therapy. The present sequence is an antisense oligonucleotide targeted to human TFAP2C DNA. This sequence is used to illustrate the method of the invention
XX SQ Sequence 20 BP; 8 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1712 CTCCTAACTTTGGACCTATT 1731
Db 20 CTCCTAACTTTGGACCTATT 1
RESULT 478
AAL62336/c
ID AAL62336 standard; DNA; 20 BP.
XX AC AAL62336;
XX DT 06-OCT-2003 (first entry)
XX DE Human transcription factor-2 gamma antisense oligo, ISIS 128190.
XX KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone; antisense; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX Key Location/Qualifiers
FT modified_base 1..20

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FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidines are 5-
FT      methylcytidines"
FT      modified_base
FT      1. .5
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "2'methoxyethyl nucleotides"
FT      modified_base
FT      16. .20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'methoxyethyl nucleotides"
XX      WO2003051308-A2.
PN
XX
XX      26-JUN-2003.
XX
XX      12-DEC-2002; 2002WO-US040100.
XX
XX      17-DEC-2001; 2001US-00023782.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Cowsert LM, Freier SM;
XX
XX      WPI; 2003-569107/53.
XX
XX      New antisense compound targeted to a nucleic acid molecule encoding
XX      transcription factor-2 gamma, useful for inhibiting expression of the
XX      nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX      Claim 3; Page 80; 107pp; English.
XX
XX      The invention relates to antisense compounds, compositions and methods
XX      for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX      TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX      enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX      The invention is useful for inhibiting the expression of TFAP2C in cells
XX      or tissues. It is useful for treating an animal having a disease or
XX      condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX      such as cancer e.g. breast cancer or colon cancer and a developmental
XX      disorder. The invention is also useful for diagnostics, therapeutics,
XX      prophylaxis and as research reagents and kits. It is also used in
XX      antisense therapy. The present sequence is an antisense oligonucleotide
XX      targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX      method of the invention
XX
XX      Sequence 20 BP; 8 A; 6 C; 1 G; 5 T; 0 U; 0 Other;
SQ
      Query Match      0.7%; Score 20; DB 1; Length 20;
      Best Local Similarity 100.0%; Pred.No. 4.1e+02;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2397 TATGCGTAATTAAATGGGT 2416
      |||||||
Db      20 TATGCGTAATTAAATGGGT 1

RESULT 479
AAL62276/c
ID      AAL62276 standard; DNA; 20 BP.
XX
XX      AAL62276;
XX
XX      06-OCT-2003 (first entry)
XX
XX      Human transcription factor-2 gamma antisense oligo, ISIS 128130.
XX
XX      Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX      Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
XX      oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
XX      breast; colon; developmental disorder; human; phosphorothioate backbone;
XX      antisense; ss.
```

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XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key      Location/Qualifiers
FH      modified_base
FT      1. .20
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidines are 5-
FT      methylcytidines"
FT      modified_base
FT      1. .5
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "2'methoxyethyl nucleotides"
FT      modified_base
FT      16. .20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'methoxyethyl nucleotides"
XX      WO2003051308-A2.
PN
XX
XX      26-JUN-2003.
XX
XX      12-DEC-2002; 2002WO-US040100.
XX
XX      17-DEC-2001; 2001US-00023782.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Cowsert LM, Freier SM;
XX
XX      WPI; 2003-569107/53.
XX
XX      New antisense compound targeted to a nucleic acid molecule encoding
XX      transcription factor-2 gamma, useful for inhibiting expression of the
XX      nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX      Example 15; Page 79; 107pp; English.
XX
XX      The invention relates to antisense compounds, compositions and methods
XX      for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX      TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX      enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX      The invention is useful for inhibiting the expression of TFAP2C in cells
XX      or tissues. It is useful for treating an animal having a disease or
XX      condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX      such as cancer e.g. breast cancer or colon cancer and a developmental
XX      disorder. The invention is also useful for diagnostics, therapeutics,
XX      prophylaxis and as research reagents and kits. It is also used in
XX      antisense therapy. The present sequence is an antisense oligonucleotide
XX      targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX      method of the invention
XX
XX      Sequence 20 BP; 9 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
SQ
      Query Match      0.7%; Score 20; DB 1; Length 20;
      Best Local Similarity 100.0%; Pred.No. 4.1e+02;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      91 GATTTTGGATTACCGCTTG 110
      |||||||
Db      20 GATTTTGGATTACCGCTTG 1

RESULT 480
AAL62282/c
ID      AAL62282 standard; DNA; 20 BP.
XX
XX      AAL62282;
XX
XX      06-OCT-2003 (first entry)
XX
XX      Human transcription factor-2 gamma antisense oligo, ISIS 128136.
DE
```


XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX WO2003051308-A2.
XX 26-JUN-2003.
XX 12-DEC-2002; 2002WO-US040100.
XX 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX Example 15; Page 79; 107pp; English.
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
SQ Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 ATGTTGCGAAATAACCGA 186
Db 20 ATGTTGCGAAATAACCGA 1
RESULT 481
AAL62285/c
ID AAL62285 standard; DNA; 20 BP.

XX AAL62285;
AC 06-OCT-2003 (first entry)
XX Human transcription factor-2 gamma antisense oligo, ISIS 128139.
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX WO2003051308-A2.
XX 26-JUN-2003.
XX 12-DEC-2002; 2002WO-US040100.
XX 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX Claim 3; Page 79; 107pp; English.
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
SQ Sequence 20 BP; 1 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 405 GCGAAGCGTACGCCGCCGCC 424
|||||

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1013 GACAAGATCGGGTTGAATCT 1032
| | | | | | | | | | | | | | | | | | | |
Db 20 GACAAGATCGGGTTGAATCT 1

RESULT 483
AAL62347/C
ID AAL62347 standard; DNA; 20 BP.
XX
AC AAL62347;
XX
DT 06-OCT-2003 (first entry)
DE Human transcription factor-2 gamma antisense oligo, ISIS 128201.
XX

KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"

WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.

XX
PT New antisense compound targeted to a nucleic acid molecule encoding transcription factor-2 gamma, useful for inhibiting expression of the nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.

PS Example 15; Page 81; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells or tissues. It is useful for treating an animal having a disease or condition associated with TFAP2C, e.g., a hyperproliferative disorder such as cancer e.g. breast cancer or colon cancer and a developmental disorder. The invention is also useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is also used in

Db 20 GGAAGCGTACGCCGCCGCC 1

RESULT 482
AAL62302/C
ID AAL62302 standard; DNA; 20 BP.
XX
AC AAL62302;
XX
DT 06-OCT-2003 (first entry)
DE Human transcription factor-2 gamma antisense oligo, ISIS 128156.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.

XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"

WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.

XX
PT New antisense compound targeted to a nucleic acid molecule encoding transcription factor-2 gamma, useful for inhibiting expression of the nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.

PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells or tissues. It is useful for treating an animal having a disease or condition associated with TFAP2C, e.g., a hyperproliferative disorder such as cancer e.g. breast cancer or colon cancer and a developmental disorder. The invention is also useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is also used in antisense therapy. The present sequence is an antisense oligonucleotide targeted to human TFAP2C DNA. This sequence is used to illustrate the method of the invention

XX
SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2754 CGTGTATAATAAAAGTATTC 2773
Db 20 CGTGTATAATAAAAGTATTC 1
RESULT 484
AAL62283/c
ID AAL62283 standard; DNA; 20 BP.
XX
AC AAL62283;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128137.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT 1. .5
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 79; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.

CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 352 TCCCTACCAGCAGCTGGCCT 371
Db 20 TCCCTACCAGCAGCTGGCCT 1
RESULT 485
AAL62323/c
ID AAL62323 standard; DNA; 20 BP.
XX
AC AAL62323;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128177.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX

WPI; 2003-569107/53.

New antisense compound targeted to a nucleic acid molecule encoding transcription factor-2 gamma, useful for inhibiting expression of the nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.

Example 15; Page 80; 107pp; English.

The invention relates to antisense compounds, compositions and methods for modulating the expression of transcription factor-2 gamma (TFAP2C). TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1. The invention is useful for inhibiting the expression of TFAP2C in cells or tissues. It is useful for treating an animal having a disease or condition associated with TFAP2C, e.g., a hyperproliferative disorder such as cancer e.g. breast cancer or colon cancer and a developmental disorder. The invention is also useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is also used in antisense therapy. The present sequence is an antisense oligonucleotide targeted to human TFAP2C DNA. This sequence is used to illustrate the method of the invention

Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2220 CTTTGAATGACATGTTCCC 2239
Db 20 CTTTGAATGACATGTTCCC 1

RESULT 487
AAL62342/c
ID AAL62342 standard; DNA; 20 BP.
XX
AC AAL62342;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128196.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX

Claim 3; Page 80; 107pp; English.

The invention relates to antisense compounds, compositions and methods for modulating the expression of transcription factor-2 gamma (TFAP2C). TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1. The invention is useful for inhibiting the expression of TFAP2C in cells or tissues. It is useful for treating an animal having a disease or condition associated with TFAP2C, e.g., a hyperproliferative disorder such as cancer e.g. breast cancer or colon cancer and a developmental disorder. The invention is also useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. It is also used in antisense therapy. The present sequence is an antisense oligonucleotide targeted to human TFAP2C DNA. This sequence is used to illustrate the method of the invention

Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1864 ACACTTAGCCATTGAAATGT 1883
Db 20 ACACTTAGCCATTGAAATGT 1

RESULT 486
AAL62330/c
ID AAL62330 standard; DNA; 20 BP.
XX
AC AAL62330;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128184.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
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XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX

PR 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2638 CTGTTGGGCTGAACCCCTAAG 2657
Db 20 CTGTTGGGCTGAACCCCTAAG 1

RESULT 488
AAL62346/c
ID AAL62346 standard; DNA; 20 BP.
XX
AC AAL62346;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128200.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
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FT methylcytidines"
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PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
PA
XX Cowsert LM, Freier SM;
PI
XX WPI; 2003-569107/53.
DR
XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 81; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TCTCTGCCTGTAAATGTTC 2728
Db 20 TCTCTGCCTGTAAATGTTC 1

RESULT 489
AAL62277/c
ID AAL62277 standard; DNA; 20 BP.
XX
AC AAL62277;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128131.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
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FT modified_base 1..20
FT /*tag= a
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FT /note= "2'methoxyethyl nucleotides"
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XX
PN WO2003051308-A2.
XX
XX 26-JUN-2003.
PD
XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
DR
XX New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX Example 15; Page 79; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX The invention is useful for inhibiting the expression of TFAP2C in cells
XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX prophylaxis and as research reagents and kits. It is also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targeted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
XX
XX Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 GATTACCGCTGGGGCTG 117
Db 20 GATTACCGCTGGGGCTG 1
RESULT 490
AAL62287/c
ID AAL62287 standard; DNA; 20 BP.
XX
XX AAL62287;
XX
XX 06-OCT-2003 (first entry)
XX
XX Human transcription factor-2 gamma antisense oligo, ISIS 128141.
XX
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
XX oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
XX breast; colon; developmental disorder; human; phosphorothioate backbone;
XX antisense; ss.
XX
XX Homo sapiens.
XX Synthetic.
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XX Key Location/Qualifiers
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FT methylcytidines"
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FT modified_base 16. .20
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XX WO2003051308-A2.
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XX 26-JUN-2003.
PD
XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
DR
XX New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX Example 15; Page 79; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX The invention is useful for inhibiting the expression of TFAP2C in cells
XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX prophylaxis and as research reagents and kits. It is also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targeted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
XX
XX Sequence 20 BP; 3 A; 7 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 544 CCACCTCTCCGGGCTGGAGG 563
Db 20 CCACCTCTCCGGGCTGGAGG 1
RESULT 491
AAL62300/c
ID AAL62300 standard; DNA; 20 BP.
XX
XX AAL62300;
XX
XX 06-OCT-2003 (first entry)
XX
XX Human transcription factor-2 gamma antisense oligo, ISIS 128154.
XX
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
XX oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
XX breast; colon; developmental disorder; human; phosphorothioate backbone;
XX antisense; ss.
XX
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OS Homo sapiens.
XX Synthetic.
FH Key
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FT Location/Qualifiers
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FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
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FT 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base
FT 16. .20
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PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
XX WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 928 TGAATGCTTAAATGCCTCGT 947
Db 20 TGAATGCTTAAATGCCTCGT 1
RESULT 492
AAL62304/c
ID AAL62304 standard; DNA; 20 BP.
XX
AC AAL62304;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128158.
XX

KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
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FT methylcytidines"
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PN WO2003051308-A2.
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PD 26-JUN-2003.
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PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
XX WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 7 A; 2 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1064 ACTCTCCTGACATCCTTAGT 1083
Db 20 ACTCTCCTGACATCCTTAGT 1

RESULT 493
AAL62317/c
ID AAL62317 standard; DNA; 20 BP.
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AC AAL62317;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128171.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT methylcytidines"
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FT modified_base 16..20
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PD 26-JUN-2003.
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PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PS New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 5 A; 1 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1564 TGC AAAAATCCTTCTCCACC 1583
DB 20 TGC AAAAATCCTTCTCCACC 1
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RESULT 494
AAL62334/C
ID AAL62334 standard; DNA; 20 BP.
XX
AC AAL62334;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128188.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
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XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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PN WO2003051308-A2.
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PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PS New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.
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CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 9 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 GTGGAGGTTCTGTATTTAA 2365
Db 20 GTGGAGGTTCTGTATTTAA 1

RESULT 495
AAL62337/c

ID AAL62337 standard; DNA; 20 BP.
XX
AC AAL62337;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128191.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT 1. .5
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PN WO2003051308-A2.
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PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide

CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 9 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2474 ATTAACCTTTTAATGGTGATG 2493
Db 20 ATTAACCTTTTAATGGTGATG 1

RESULT 496
AAL62289/c

ID AAL62289 standard; DNA; 20 BP.
XX
AC AAL62289;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128143.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
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FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT 16. .20
FT /tag= c
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XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells

CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 624 CACACGCCCTGGATGCGCG 643
Db 20 CACACGCCCTGGATGCGCG 1
RESULT 497
AAL62291/c
ID AAL62291 standard; DNA; 20 BP.
XX
AC AAL622291;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128145.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
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FT methylcytidines"
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FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16. .20
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XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
PI WPI; 2003-569107/53.
XX
DR New antisense compound targetted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.

XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 669 ACGACATGCCTCACCAGATG 688
Db 20 ACGACATGCCTCACCAGATG 1
RESULT 498
AAL62296/c
ID AAL62296 standard; DNA; 20 BP.
XX
AC AAL622296;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128150.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1. .5
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FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
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FT /note= "2'methoxyethyl nucleotides"
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PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
PI WPI; 2003-569107/53.
XX
DR

XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Example 15; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 753 GTCCCATTTCCATGACCAAG 772
Db 20 GTCCCATTTCCATGACCAAG 1

RESULT 499
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ID AAL62321 standard; DNA; 20 BP.
XX AAL62321;
AC
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128175.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT methylecytidines"
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FT 16..20
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XX
PN WO2003051308-A2.
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PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.

XX (ISIS-) ISIS PHARM INC.
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PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 9 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1751 TGGCTCTTTATTTCATTAGC 1770
Db 20 TGGCTCTTTATTTCATTAGC 1

RESULT 500
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ID AAL62324 standard; DNA; 20 BP.
XX AAL62324;
AC
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128178.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylecytidines"
FT 1..5
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FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
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PN WO2003051308-A2.


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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
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XX WO2003051308-A2.
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PD 26-JUN-2003.
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XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX Example 15; Page 80; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, AP2-gamma, AP2-gamma, AP-2.2, Stra2, activating
XX The invention is useful for inhibiting the expression of TFAP2C in cells
XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX prophylaxis and as research reagents and kits. It is also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
XX
XX Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2195 AAGTTAACTCTTCAAAATGGG 2214
Db |||||
20 AAGTTAACTCTTCAAAATGGG 1
XX
XX RESULT 503
AAL62344/c
ID AAL62344 standard; DNA; 20 BP.
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XX AAL62344;
XX
XX 06-OCT-2003 (first entry)
XX
XX Human transcription factor-2 gamma antisense oligo, ISIS 128198.
XX
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
XX oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
XX breast; colon; developmental disorder; human; phosphorothioate backbone;
XX antisense; ss.
XX
XX Homo sapiens.
OS
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OS Synthetic.
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XX Key Location/Qualifiers
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FT 1..5
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FT /note= "2'methoxyethyl nucleotides"
FT 16..20
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FT /note= "2'methoxyethyl nucleotides"
XX WO2003051308-A2.
XX
XX 26-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
XX Claim 3; Page 80; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of transcription factor-2 gamma (TFAP2C).
XX TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
XX enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
XX The invention is useful for inhibiting the expression of TFAP2C in cells
XX or tissues. It is useful for treating an animal having a disease or
XX condition associated with TFAP2C, e.g., a hyperproliferative disorder
XX such as cancer e.g. breast cancer or colon cancer and a developmental
XX disorder. The invention is also useful for diagnostics, therapeutics,
XX prophylaxis and as research reagents and kits. It is also used in
XX antisense therapy. The present sequence is an antisense oligonucleotide
XX targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
XX
XX Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2672 CAGTGTGTGTGGTGAATG 2691
Db |||||
20 CAGTGTGTGTGGTGAATG 1
XX
XX RESULT 504
AAL62279/c
ID AAL62279 standard; DNA; 20 BP.
XX
XX AAL62279;
XX
XX 06-OCT-2003 (first entry)
XX
XX Human transcription factor-2 gamma antisense oligo, ISIS 128133.
XX
XX Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
```

KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1. .5
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FT /note= "2'methoxyethyl nucleotides"
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XX WO2003051308-A2.
PN
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PD 26-JUN-2003.
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XX 12-DEC-2002; 2002WO-US040100.
PF
XX 17-DEC-2001; 2001US-00023782.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Cowdert LM, Freier SM;
PI
XX WPI; 2003-569107/53.
DR
XX New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
PT
XX
PS Claim 3; Page 79; 107pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 147 TTGGGGGACCGCGACGCC 166
DB 20 TTGGGGGACCGCGACGCC 1
RESULT 505
AAL62280/c
ID AAL62280 standard; DNA; 20 BP.
XX
AC AAL62280;

XX
DT 06-OCT-2003 (first entry)
XX Human transcription factor-2 gamma antisense oligo, ISIS 128134.
DE
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
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FT methylcytidines"
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XX WO2003051308-A2.
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PD 26-JUN-2003.
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XX 12-DEC-2002; 2002WO-US040100.
PF
XX 17-DEC-2001; 2001US-00023782.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Cowdert LM, Freier SM;
PI
XX WPI; 2003-569107/53.
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XX New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
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XX Example 15; Page 79; 107pp; English.
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XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 158 CCGGACGCCCATGTTGTGGAA 177
DB 20 CCGGACGCCCATGTTGTGGAA 1

RESULT 506
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ID AAL62281 standard; DNA; 20 BP.
XX
AC
XX AAL62281;
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128135.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
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FN WO2003051308-A2.
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PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
DR WPI; 2003-569107/53.
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PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
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CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
method of the invention
XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 159 CGGACGCCCATGTTGTGGAAA 178
Db 20 CGGACGCCCATGTTGTGGAAA 1
RESULT 507
AAL62297/c
ID AAL62297 standard; DNA; 20 BP.
XX
AC AAL62297;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128151.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
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FN WO2003051308-A2.
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XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT transcription factor-2 gamma, useful for inhibiting expression of the
PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS Claim 3; Page 80; 107pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the

CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1645 AGAGCCTTCACTGGTCTGC 1664
Db 20 AGAGCCTTCACTGGTCTGC 1

RESULT 509
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ID AAL62322 standard; DNA; 20 BP.
XX
AC AAL62322;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128176.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
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FT modified_base 1..20
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
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XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX
PS New antisense compound targetted to a nucleic acid molecule encoding
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XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX Example 15; Page 80; 107pp; English.

CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 789 CCTGTCAGAGGAGCTGGTG 808
Db 20 CCTGTCAGAGGAGCTGGTG 1

RESULT 508
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ID AAL62318 standard; DNA; 20 BP.
XX
AC AAL62318;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128172.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
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FT /note= "2'methoxyethyl nucleotides"
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PN WO2003051308-A2.
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PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
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CC or tissues. It is useful for treating an animal having a disease or

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CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 8 A; 0 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1827 AATCTTTTAAATACATCCCC 1846
Db 20 AATCTTTTAAATACATCCCC 1

RESULT 510
AAL62274/c
ID AAL62274 standard; DNA; 20 BP.
XX
AC AAL62274;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128128.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
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FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
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FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM, Freier SM;
XX
DR WPI; 2003-569107/53.
XX

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PT nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
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CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 2 A; 9 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 GCGGGCGGCGAGCGCTGGTC 79
Db 20 GCGGGCGGCGAGCGCTGGTC 1

RESULT 511
AAL62299/c
ID AAL62299 standard; DNA; 20 BP.
XX
AC AAL62299;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128153.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
methylethylnucleotides"
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FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
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PN WO2003051308-A2.
XX
PD 26-JUN-2003.
XX
PF 12-DEC-2002; 2002WO-US040100.
XX
PR 17-DEC-2001; 2001US-00023782.
XX

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PA (ISIS-) ISIS PHARM INC.
XX Cowsert LM, Freier SM;
XX WPI; 2003-569107/53.
DR
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CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 856 ATTGTCGCTCCTCAGCTCTA 875
DB 20 ATTGTCGCTCCTCAGCTCTA 1

RESULT 512
AAL62332/c
ID AAL62332 standard; DNA; 20 BP.
XX
AC AAL62332;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128186.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT 1..5
FT /*tag= b
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FT /note= "2'methoxyethyl nucleotides"
FT 16..20
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FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003051308-A2.
XX

PD 26-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-US040100.
XX
XX 17-DEC-2001; 2001US-00023782.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Cowsert LM, Freier SM;
PI
XX WPI; 2003-569107/53.
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CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2241 TAAGGTACTGAAGCTTTATT 2260
DB 20 TAAGGTACTGAAGCTTTATT 1

RESULT 513
AAL62338/c
ID AAL62338 standard; DNA; 20 BP.
XX
AC AAL62338;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human transcription factor-2 gamma antisense oligo, ISIS 128192.
XX
KW Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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PN      WO2003051308-A2.
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PD      26-JUN-2003.
XX
PF      12-DEC-2002; 2002WO-US040100.
XX
PR      17-DEC-2001; 2001US-00023782.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Cowsert LM, Freier SM;
XX
DR      WPI; 2003-569107/53.
XX
PT      New antisense compound targeted to a nucleic acid molecule encoding
PT      transcription factor-2 gamma, useful for inhibiting expression of the
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CC      or tissues. It is useful for treating an animal having a disease or
CC      condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC      such as cancer e.g. breast cancer or colon cancer and a developmental
CC      disorder. The invention is also useful for diagnostics, therapeutics,
CC      prophylaxis and as research reagents and kits. It is also used in
CC      antisense therapy. The present sequence is an antisense oligonucleotide
CC      targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC      method of the invention
XX
SQ      Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2491 ATGGGTAATCTATAACACA 2510
Db      20 ATGGGTAATCTATAACACA 1

RESULT 514
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ID      AAL62271 standard; DNA; 20 BP.
XX
AC      AAL62271;
XX
DT      06-OCT-2003 (first entry)
XX
DE      Human transcription factor-2 gamma antisense oligo, ISIS 128125.
XX
KW      Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW      Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW      oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW      breast; colon; developmental disorder; human; phosphorothioate backbone;
KW      antisense; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
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FH      Key      Location/Qualifiers
FT      modified_base 1..20
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FT      methylcytidines"
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XX
PN      WO2003051308-A2.
XX
PD      26-JUN-2003.
XX
PF      12-DEC-2002; 2002WO-US040100.
XX
PR      17-DEC-2001; 2001US-00023782.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Cowsert LM, Freier SM;
XX
DR      WPI; 2003-569107/53.
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PT      New antisense compound targeted to a nucleic acid molecule encoding
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CC      method of the invention
XX
SQ      Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 GCCGCCGATCGGTGTCAGT 27
Db      20 GCCGCCGATCGGTGTCAGT 1

RESULT 515
AAL62275/c
ID      AAL62275 standard; DNA; 20 BP.
XX
AC      AAL62275;
XX
DT      06-OCT-2003 (first entry)
XX
DE      Human transcription factor-2 gamma antisense oligo, ISIS 128129.
XX
KW      Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW      Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW      oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW      breast; colon; developmental disorder; human; phosphorothioate backbone;
KW      antisense; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
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XX Key Location/Qualifiers
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FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
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FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16. .20
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XX WO2003051308-A2.
PN 26-JUN-2003.
XX PD
XX 12-DEC-2002; 2002WO-US040100.
XX PF 17-DEC-2001; 2001US-00023782.
XX PR (ISIS-) ISIS PHARM INC.
XX PA Cowser LM, Freier SM;
XX PI WPI; 2003-569107/53.
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CC antisense therapy. The present sequence is an antisense oligonucleotide
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XX
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 ACGCCTGGTCACCGTGACCC 89
DB 20 ACGCCTGGTCACCGTGACCC 1
RESULT 516
ID AAL62295/c
XX AAL62295 standard; DNA; 20 BP.
XX AAL62295;
AC
XX 06-OCT-2003 (first entry)
DT Human transcription factor-2 gamma antisense oligo, ISIS 128149.
XX
DE Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW
XX

oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
breast; colon; developmental disorder; human; phosphorothioate backbone;
antisense; ss.
XX Homo sapiens.
OS Synthetic.
OS
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX WO2003051308-A2.
PN 26-JUN-2003.
XX PD
XX 12-DEC-2002; 2002WO-US040100.
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XX PR (ISIS-) ISIS PHARM INC.
XX PA Cowser LM, Freier SM;
XX PI WPI; 2003-569107/53.
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CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 727 GCACGATCAGACAGTCATTC 746
DB 20 GCACGATCAGACAGTCATTC 1
RESULT 517
ID AAL62311/c
XX AAL62311 standard; DNA; 20 BP.
XX AAL62311;
AC
XX

DT 06-OCT-2003 (first entry)
XX Human transcription factor-2 gamma antisense oligo, ISIS 128165.
DE Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX WO2003051308-A2.
PN 26-JUN-2003.
XX 12-DEC-2002; 2002WO-US040100.
XX 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX Cowsert LM, Freier SM;
PI WPI; 2003-569107/53.
DR New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
PS Claim 3; Page 80; 107pp; English.
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
SQ Sequence 20 BP; 6 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1377 CCATCTGTGCCGGGTGCT 1396
Db 20 CCATCTGTGCCGGGTGCT 1

RESULT 518
AAL62328/c
ID AAL62328 standard; DNA; 20 BP.
XX
AC AAL62328;
XX 06-OCT-2003 (first entry)
XX Human transcription factor-2 gamma antisense oligo, ISIS 128182.
DE Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
XX Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW breast; colon; developmental disorder; human; phosphorothioate backbone;
KW antisense; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX WO2003051308-A2.
PN 26-JUN-2003.
XX 12-DEC-2002; 2002WO-US040100.
XX 17-DEC-2001; 2001US-00023782.
XX (ISIS-) ISIS PHARM INC.
XX Cowsert LM, Freier SM;
PI WPI; 2003-569107/53.
DR New antisense compound targeted to a nucleic acid molecule encoding
XX transcription factor-2 gamma, useful for inhibiting expression of the
XX nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
PS Example 15; Page 80; 107pp; English.
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC The invention is useful for inhibiting the expression of TFAP2C in cells
CC or tissues. It is useful for treating an animal having a disease or
CC condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
XX method of the invention
SQ Sequence 20 BP; 8 A; 2 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

schultz782-3.rng

Thu Jun 10 13:10:09 2004

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XX
SQ      Sequence 20 BP; 9 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
      Query Match      0.7%; Score 20; DB 1; Length 20;
      Best Local Similarity 100.0%; Pred. No. 4.1e+02;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2379 GAGTGTACAGATTTTATTTA 2398
      |||||
Db      20 GAGTGTACAGATTTTATTTA 1

RESULT 520
AAL62345/c
ID      AAL62345 standard; DNA; 20 BP.
XX
AC      AAL62345;
XX
DT      06-OCT-2003 (first entry)
XX
DE      Human transcription factor-2 gamma antisense oligo, ISIS 128189.
XX
KW      Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW      Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW      oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW      breast; colon; developmental disorder; human; phosphorothioate backbone;
KW      antisense; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key
FT      modified_base      Location/Qualifiers
FT      1..20      /*tag= a
FT      /*mod_base= OTHER
FT      /*note= "Phosphorothioate backbone; All cytidines are 5-
FT      methylcytidines"
FT      1..5
FT      /*tag= b
FT      /*mod_base= OTHER
FT      /*note= "2'methoxyethyl nucleotides"
FT      16..20
FT      /*tag= c
FT      /*mod_base= OTHER
FT      /*note= "2'methoxyethyl nucleotides"
XX
PN      WO2003051308-A2.
XX
PD      26-JUN-2003.
XX
PF      12-DEC-2002; 2002WO-US040100.
XX
PR      17-DEC-2001; 2001US-00023782.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Cowsert LM, Freier SM;
XX
DR      WPI; 2003-569107/53.
XX
XX      New antisense compound targeted to a nucleic acid molecule encoding
PT      transcription factor-2 gamma, useful for inhibiting expression of the
PT      nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS      Example 15; Page 80; 107pp; English.
XX
XX      The invention relates to antisense compounds, compositions and methods
CC      for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC      TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC      enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC      The invention is useful for inhibiting the expression of TFAP2C in cells
CC      or tissues. It is useful for treating an animal having a disease or
CC      condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC      such as cancer e.g. breast cancer or colon cancer and a developmental
CC      disorder. The invention is also useful for diagnostics, therapeutics,
CC      prophylaxis and as research reagents and kits. It is also used in
CC      antisense therapy. The present sequence is an antisense oligonucleotide
CC      targeted to human TFAP2C DNA. This sequence is used to illustrate the
CC      method of the invention
```

CC such as cancer e.g. breast cancer or colon cancer and a developmental
CC disorder. The invention is also useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. It is also used in
CC antisense therapy. The present sequence is an antisense oligonucleotide
CC targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 6 A; 6 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2689 ATGGAGATTGGAATTGAAC 2708
Db 20 ATGGAGATTGGAATTGAAC 1

RESULT 521
ACH00064/c
ID ACH00064 standard; DNA; 20 BP.
XX
AC ACH00064;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "
XX
PN US2003049631-A1.
XX
PD 13-MAR-2003.
XX
PF 10-OCT-2001; 2001US-00974500.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-634854/60.
XX
PT Detection of nucleic acid having at least two portions, by contacting
PT nucleic acid and nanoparticles under conditions, which allows
PT hybridization of oligonucleotides on nanoparticles with at least two
PT portions of nucleic acid.
XX
PS Example 18; Page 44; 108pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acids. The
CC method comprises providing nanoparticles with oligonucleotides attached
CC to them, which have a sequence complementary to a sequence of two
CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC to allow hybridisation of the oligonucleotides with two or more portions
CC of the nucleic acid, and observing a detectable change brought about by
CC the hybridisation. The nucleic acid to be detected must have at least two
CC portions and the distances between these are chosen so that when the

CC nanoparticle-oligonucleotide conjugate binds the target sequence a
CC detectable change occurs. The method of the invention is useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic, or structurally- modified natural
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC and for detecting a nucleic acid bound to an electrode surface.
CC Nanoparticles and nanoparticle conjugates of the invention are useful for
CC nanofabrication and for separating a selected nucleic acid having two
CC portions from other nucleic acids. Diagnostic assays employing
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC nucleic acid detection methods and can be used to detect nucleic acids
CC that are present in only small amounts in a sample. The invention also
CC provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC conjugates are stable with tailored hybridisation abilities. The present
CC sequence represents a thiol modified oligonucleotide sequence used to
CC demonstrate the method of the invention
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 522

ACD99851/c

ID ACD99851 standard; DNA; 20 BP.

XX ACD99851;

AC ACD99851;

XX 25-SEP-2003 (first entry)

DT Immunostimulatory nucleic acid #537.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

OS Synthetic.

XX US2003050268-A1.

PN 13-MAR-2003.

PD 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.

PA (BERG/) BERG D J.

PI Krieg AM, Berg DJ;

XX WPI; 2003-521815/49.

DR Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX allergic contact dermatitis, latex dermatitis or inflammatory bowel
XX disease by administering an immunostimulatory nucleic acid.

PS Disclosure; Page 23; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is

CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 523
ACD99847
ID ACD99847 standard; DNA; 20 BP.
XX
AC ACD99847;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #533.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX allergic contact dermatitis, latex dermatitis or inflammatory bowel
XX disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 23; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 525
ADA14838/c
ID ADA14838 standard; DNA; 20 BP.
XX
AC ADA14838;
XX
DT 06-NOV-2003 (first entry)
XX
DE Hairpin target sequence, #2, used in an example of the invention.
XX
KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW rhodamine B-labelled dye; detection; gold support; ss.
XX

RESULT 524
ACD99532
ID ACD99532 standard; DNA; 20 BP.
XX
AC ACD99532;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #218.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX allergic contact dermatitis, latex dermatitis or inflammatory bowel
XX disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 14; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 525
ADA14838/c
ID ADA14838 standard; DNA; 20 BP.
XX
AC ADA14838;
XX
DT 06-NOV-2003 (first entry)
XX
DE Hairpin target sequence, #2, used in an example of the invention.
XX
KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW rhodamine B-labelled dye; detection; gold support; ss.
XX

OS Synthetic.
XX Key Location/Qualifiers
FH misc_binding 1..20
FT /*tag= a
FT /bound_moiety= "Hairpin oligonucleotide #2"
FT /note= "Forms a double-stranded region with the hairpin
FT oligonucleotide shown in examples 3, 4 and 5"
XX
XX
PN US2003013109-A1.
XX
XX 16-JAN-2003.
XX
XX 21-JUN-2002; 2002US-00176055.
XX
XX 21-JUN-2001; 2001US-0299460P.
XX (BALL/) BALLINGER C T.
PA (LOCA/) LOCASCIO M.
PA (LAND/) LANDRY D P.
XX
PI Ballinger CT, Locascio M, Landry DP;
XX
XX WPI; 2003-596312/56.
DR
XX
XX
PT Hairpin sensor useful for detecting a target nucleotide sequence in a
PT sample, comprises a hairpin loop assembly including a complementary probe
PT and a quenchable fluorescing agent.
XX
PS Example 3; Page 11; 16pp; English.
XX
CC The invention discloses a hairpin sensor comprising a hairpin loop
CC assembly including a complementary probe positioned between a first
CC inverse repeat arm and a second inverse repeat arm, and a quenchable
CC fluorescing agent joined, directly or indirectly, to the end of the
CC second inverse repeat arm of the hairpin loop assembly opposite the
CC complementary probe. Also claimed is a microarray comprising the hairpin
CC sensor, where the end of the first inverse repeat arm opposite the
CC complementary probe is bound, directly or indirectly, to a support, a kit
CC for detecting a target nucleotide sequence in a sample comprising the
CC hairpin sensor, and a support, and a hairpin sensor system, in which the
CC particle is conductive or semi-conductive, including at least one of the
CC above hairpin sensor assemblies. The hairpin sensor further comprises a
CC functional group joined to the end of the first inverse repeat arm
CC opposite the complementary probe, or first spacer opposite the first
CC inverse repeat arm, the functional group selected from amino, carboxyl,
CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC between the second inverse repeat arm and the quenchable fluorescing
CC agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC second spacer is positioned between the second inverse repeat arm and the
CC quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC or rhodamine B-labelled dye. Within the microarray the support is capable
CC of accepting a charge. At least one hairpin sensor comprises two or more
CC hairpin sensors. The two or more hairpin sensors include complementary
CC probes that are the same or different and respective quenchable
CC fluorescing agents that are the same or different. The two or more
CC hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC and system are useful for detecting a target nucleotide sequence in a
CC sample. Further, the method involves identifying the target nucleotide
CC sequence by the location of the complementary probe to which the target
CC nucleotide sequence binds. The two or more hairpin sensors include
CC complementary probes or quenchable fluorescing agents, that are
CC different. The sequence presented is the hairpin oligonucleotide target
CC sequence, #2, used in an example of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2185

Db 20 TTTT TTTT TTTT TTTT TTTT 1
RESULT 526
ADA06159/c
ID ADA06159 standard; DNA; 20 BP.
XX
AC ADA06159;
XX
DT 06-NOV-2003 (first entry)
XX
DE Nanoparticle labelled oligonucleotides, spacer DNA #2.
XX
KW ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;
KW nanostructure; viral disease; human immunodeficiency virus infection;
KW hepatitis virus infection; herpes virus infection;
KW cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;
KW sexually transmitted disease; inherited disorders; paternity testing;
KW cell line authentication; gene therapy.
XX
OS Synthetic.
XX
XX US2003068622-A1.
XX
PD 10-APR-2003.
XX
XX 12-OCT-2001; 2001US-00976863.
XX
XX 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
XX WPI; 2003-576420/54.
XX
PT Detecting nucleic acids having at least 2 portions comprises use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the target nucleic acid sequence.
XX
XX Example 18; Page 44; 130pp; English.
XX
CC The invention relates to detecting a nucleic acid (NA) having at least 2
CC portions comprising providing a type of nanoparticles (NP. e.g. colloidal
CC gold) having oligonucleotides (O) attached (where (O) on each NP has a
CC sequence complementary to sequence of at least two portions of NA),
CC contacting NA and NP to allow hybridisation of (O) on NP with 2 or more
CC portions of NA, and observing a detectable change brought about by
CC hybridization of (O) on NP with NA. Also included are aggregate probes,
CC core probes, substrate having NP attached to it, a metallic or
CC semiconductor NP having (O) attached to it, nanomaterials/nanostructures
CC comprising nanoparticles and methods of nanofabrication utilising
CC nanoparticles and satellite probes. The methods, probes nucleic acids,
CC nanoparticles and oligonucleotides are useful for separating a selected
CC nucleic acid having at least two portions, from other nucleic acids, and
CC for detecting nucleic acids having at least two portions, for detecting
CC NA having at least two portions. The method is useful for detecting any
CC type of nucleic acids which may be used for diagnosis of disease and in
CC sequencing of nucleic acids. Preferably, the method is useful for
CC detecting nucleic acids for diagnosis and/or monitoring of viral diseases
CC (human immunodeficiency virus, hepatitis virus, herpes virus,
CC cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually
CC transmitted diseases, inherited disorders, in forensics, in DNA
CC sequencing, for paternity testing, for cell line authentication, for
CC monitoring gene therapy, etc. The method is useful in research and
CC analytical laboratories in DNA sequencing, in the field to detect the

		Best Local Similarity	100.0%; Pred.No.	4.1e+02;	Mismatches	0; Indels	0; Gaps	0;
		Matches	20; Conservative	0; Mismatches	0; Indels	0; Gaps	0;	
QY	2166	TTTTTTT	TTTTTTTTTTTTTTTT	T T T T T	2185			
D b	20	TTTTTTT	TTTTTTTTTTTTTT	T T T	1			
 RESULT 529 ADB36601								
ID	ADB36601 standard; DNA; 20 BP.							
XX AC ADB36601;								
DT	04-DEC-2003 (first entry)							
DE	Immunostimulatory nucleic acid #215.							
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;								
KW hypo-responsive subject; immunostimulatory.								
OS Synthetic.								
P N US2003087848-A1.								
P D 08-MAY-2003.								
P F 02-FEB-2001; 2001US-00776479.								
P R 03-FEB-2000; 2000US-0179991P.								
PA (BRAT/) BRATZLER R L.								
PA (PETE/) PETERSEN D M.								
PA (FOUR/) FOURON Y.								
P I Bratzler RL, Petersen DM, Fouron Y;								
D R WPI; 2003-657977/62.								
P T Treating and/or preventing allergy or asthma using an immunostimulatory								
X X nucleic acid alone or in combination with an asthma/allergy medicament.								
P S Disclosure; Page 8; 22lpp; English.								
C C The invention relates to a method of treating or preventing allergy or								
C C asthma which comprises administering to a subject a poly-G nucleic acid								
C C in an aerosol formulation. The methods and compositions of the present								
C C invention are useful for diagnosing and/or treating asthma and allergy								
C C especially in a hypo-responsive subject. The present sequence represents								
C C an immunostimulatory nucleic acid of the invention.								
S Q Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;								
 Query Match 0.7% ; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred.No. 4.1e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
QY	2166	TTTTTTT	TTTTTTTTTTTTTTTT	T T T T T	2185			
D b	1	TTTTTTT	TTTTTTTTTTTTTT	T T T	20			
 RESULT 530 ADB36929								
ID	ADB36929 standard; DNA; 20 BP.							
XX AC ADB36929;								
DT	04-DEC-2003 (first entry)							
DE Immunostimulatory nucleic acid #543.								
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;								

Qy 2783 TTGAAAAAAAAAAAAAAA 2802
|||
Db 20 TTGAAAAAAAAAAAAAAA 1

16-APR-1993:

PI Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
XX WPI; 1999-385567/32.
XX
PT New microelectronic device designed to carry out and control multi-step
PT and multiplex molecular biological reactions in microscopic format.
XX
PS Example 1; Page 89; 179pp; English.
XX
CC The specification describes a self-addressable, self-assembling
CC microelectronic device which is designed to actively carry out and
CC control multi-step and multiplex molecular biological reactions in
CC microscopic formats. A key aspect of this invention is played by the ion
CC -permeable permeation layer which overlies the electrode. This permeation
CC layer allows attachment of nucleic acids to permit immobilization but
CC also separates the attached oligonucleotides and hybridized target DNA
CC sequences from the highly reactive electrochemical environment generated
CC immediately at the electrode surface. The microelectronic device is
CC designed and fabricated to actively carry out and control reactions such
CC as nucleic acid hybridizations, antibody/antigen reactions, sample
CC preparation, diagnostics and biopolymer synthesis. The device can
CC electronically control the transport and attachment of specific binding
CC entities, such as nucleic acids and polypeptides, to specific micro-
CC locations. The device can subsequently control the transport and reaction
CC of analytes or reactants at the addressed specific micro-locations. The
CC device is able to concentrate analytes and reactants, remove non-
CC specifically bound molecules, provide stringency control for DNA
CC hybridization reactions and improve the detection of analytes. The
CC present sequence represents a probe used to exemplify the invention
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 540
AAQ30432/c
ID AAQ30432 standard; DNA; 23 BP.
XX
AC AAQ30432;
XX
DT 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX
XX
DE Oligomer IL6805 for forming triplex with HUMIL6 target duplex.
XX
KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW malignancy; hepatitis; inflammation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /tag= a /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT misc_feature 11. .12 /tag= d
FT /note= "O-xyloso dimer synthon linkage"
FT misc_feature 12. .23 /tag= c
FT /label= inverted_polarity_region
FT /note= "see comments"
FT modified_base 23 /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"

XX WO9209705-A1.
PN
XX
PD 11-JUN-1992.
XX
PF 25-NOV-1991; 91WO-US008811.
XX
PR 23-NOV-1990; 90US-00617907.
PR 18-JAN-1991; 91US-00643382.
PR 08-APR-1991; 91US-00683420.
PR 17-APR-1991; 91US-00686544.
PR 17-APR-1991; 91US-00686546.
PR 17-APR-1991; 91US-00686547.
PR 27-SEP-1991; 91US-00766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
PI WPI; 1992-217083/26.
XX
DR New oligomers contg. modified bases - which form a triplex with G-C
XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX herpes malignancy and inflammation.
PT Claim 12; Page 71; 77pp; English.
PT
XX The synthetic oligomer is capable of forming a triplex at physiological
CC pH with a purine rich target sequence by coupling into the major groove
CC of the duplex. The specific target sequence of this oligomer is the human
CC interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC concd. on one strand of the duplex. The oligomer, and others like it are
CC useful in diagnosis and therapy of diseases characterised by specific DNA
CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC tumours and inflammation. The triple helices form under mild conditions
CC thus assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer contains an inverted polarity region
CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC (nucleotides have the 3'positions of xylose sugars linked via the o-
CC xylene ring). Two nucleotides are coupled through a xylene residue to
CC form the dimer synthon. This additional modifications may render the
CC oligomer stable to nuclease activity. The oligomer is able to inhibit
CC gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804
Db 23 GAAAAAAAAAAAAAAAAAAAAA 4

RESULT 541
ABX79809/c
ID ABX79809 standard; cDNA; 24 BP.
XX
AC ABX79809;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #134.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX

XX PI Kambara H, Okano K, Uematsu C;
XX XX WPI; 1997-300347/28.
XX XX Nucleic acid assay methods - based on restriction fragment length
PT PT determination.
XX XX Example 1; Page 7; 21pp; English.
XX XX The present sequence is a DNA probe used in a novel method of analysis or
CC assay for nucleotides, which comprises: (i) digesting DNA with a
CC restriction enzyme; (ii) discriminating a difference in sequences of the
CC DNA fragments obtained around the 3' termini with a DNA probe and
CC extending the DNA probe by a complementary strand synthesis to
CC fractionate the DNA fragments into groups; and (iii) measuring lengths of
CC the DNA fragments which belong to the groups, or length of the extended
CC DNA probe, and using the lengths obtained for the fragments around the 3'
CC termini as fingerprints. Where polyA is present, the presence of
CC recognition sequence GCG is critical for clarifying the terminal site,
CC this is because the length of polyA cannot be controlled. The method is
CC useful for assaying a large number of cDNA molecules or DNA fragments and
CC for assaying long DNA sequences
XX SQ Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 0 U; 2 Other;
Query Match 0.7%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2785 GAAAAA... 2804
Db 20 GAAAAA... 1
RESULT 543
ABK12409/c
ID ABK12409 standard; DNA; 24 BP.
XX AC ABK12409;
XX DT 18-JUN-2002 (first entry)
XX DE RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.
XX KW Polypeptide-laminin B210.67; embryo development teratogenesis;
KW cytotostatic; reverse transcriptase-PCR; RT-PCR; primer; ss.
XX OS Unidentified.
XX PN CN1328013-A.
XX PD 26-DEC-2001.
XX PF 14-JUN-2000; 2000CN-00116514.
XX PR 14-JUN-2000; 2000CN-00116514.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-270054/32.
XX XX Polypeptide-laminin B210.67, useful for treating diseases such as embryo
PT development teratogenesis.
XX PS Example 2; Page 18 (disclosure); 33pp; Chinese.
XX CC The present invention relates to the isolation of polypeptide-laminin
CC B210.67, and the polynucleotide encoding it. Also described is the
CC process for preparing the protein by DNA recombination. The polypeptide
CC is useful for treating diseases such as embryo development teratogenesis.

OS Homo sapiens.
XX PN US6472154-B1.
XX PD 29-OCT-2002.
XX PF 31-DEC-1999; 99US-00475947.
XX PR 31-DEC-1999; 99US-00475947.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX XX Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX XX Example; Col 579; 588pp; English.
XX XX The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX SQ Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2785 GAAAAA... 2804
Db 24 GAAAAA... 5
RESULT 542
AAT68615/c
ID AAT68615 standard; DNA; 24 BP.
XX AC AAT68615;
XX DT 20-FEB-1998 (first entry)
XX DE DNA probe used in fingerprinting technique.
XX KW probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.
XX OS Synthetic.
XX PN EP778351-A2.
XX PD 11-JUN-1997.
XX PF 26-NOV-1996; 96EP-00118921.
XX PR 30-NOV-1995; 95JP-00311949.
XX PA (HITA) HITACHI LTD.

RESULT 546	
ACF79235	
ID	ACF79235 standard; DNA; 25 BP.
XX	
XX	ACF79235;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Calix(a)arene-oligonucleotide hybrid.
XX	
KW	Calix(4)arene; triplex; gene therapy; DNA sensor; ss.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	stem_loop 1..25
FT	/*tag= a
FT	modified_base 13
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= calix(4)arene nucleoside"

WO2003059925-A1.

24-JUL-2003.

19-JUN-2002; 2002WO-KR001160.

15-JAN-2002; 2002KR-00002316.

(POST-) POSTECH FOUND.

Kim BH, Kim SJ;

WPI: 2003-627375/59.

New calix(4)arene-nucleoside hybrid useful in gene therapy has at least one nucleoside attached to a calix(4)arene group through amide bonding, and is derived from a calix(4)arene having amino groups.

Claim 7: Page 20: 16pp: English.

The present sequence is that of a calix(4)arene-oligonucleotide hybrid of the invention, which includes a calix(4)arene-nucleoside (preferably thymidine) derivative. The calix(4)arene-oligonucleotide hybrid functions as a DNA hairpin structure mimic. It effectively recognises DNA or RNA through triplex formation by bonding between the calix(4)arene-containing cavity and a biologically active substance. The hybrid has a certain level of both rigidity and flexibility, is stable *in vivo*, has high cell permeability and can be mass-produced. It can be used as a DNA sensor or for gene therapy.

Sequence 25 BP: 0 A: 0 C: 0 G: 24 T: 0 U: 1 Other;

```
Query Match      0.7%   Score 20; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 7.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY	2166	TTTTTTTTTTTTTTTTTTTT	2186
db	1	TTTTTTTTTTTTTTTTTTTT <td>21</td>	21

RESULT 547
AAT94842
in AAT94842 standard: DNA: 27 BP.

AC AAT94842;

27-MAR-1998 (first entry)

Human ESF I 3' PCR primer.

XX

Endometrial specific steroid-binding factor I; ESF I; human;
inflammation; asthma; rhinitis; cystic fibrosis; airway disease;
neoplasia; atopy; therapy; diagnosis; primer; PCR; ss.
Synthetic.
Homo sapiens.
WO9734997-A1.
25-SEP-1997.
21-MAR-1996; 96WO-US003857.
21-MAR-1996; 96WO-US003857.
(HUMA-) HUMAN GENOME SCI INC.
Ni J, Yu G, Gentz RL;
WPI; 1997-480206/44.
Human endometrial specific steroid-binding factor I, II and III - used to
treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease,
neoplasia, atopy etc.

Example 2: Page 52-53: 92pp; English.

This oligonucleotide contains an Asp718 site followed by 18 nucleotides complementary to a polyA tail. It was used with a 5' primer (see AAT94839), containing a BamHI site and 20 bases of the human endometrial specific steroid binding factor I (ESF I) coding sequence (see AAT94830), to amplify ESF I cDNA deposited as ATCC 97401. The PCR product was incorporated into baculovirus vector pRG1 and recombinant ESF I was expressed in *Spodoptera frugiperda* Sf9 cells. Human ESF I (see AAW35802) can be used to treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease, neoplasia, atopy etc.

Sequence 27 BP: 1 A: 5 C: 2 G: 19 T: 0 U: 0 Other:

Query Match 0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels

QY	2164	CCCTTTT	TTTTTTTTT	2183
dh	8	CCCTTTT	TTTTTTTTT	27

RESULT 548

AAA59740

ID AAA59740 standard; DNA; 27 BP.

AC AAA59740:

06-OCT-2000 (first entry)

XX DE PCR primer for hESF I cDNA sequence amplification.

XX Endometrial specific steroid-binding factor; human; hESF; inflammation;
KW asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy;
KW eicosanoid level regulator; chemotaxis inhibitor; endometrial cancer;
KW PCR primer; ss.

Homo sapiens.

US6066724-A.

23-MAY-2000

31-MAP-1997. 97IIS-00821451.

31 MAR 1996 96US-0014724P

XX
PK

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Gentz R, Ni J;
XX
DR WPI; 2000-375600/32.
XX
PT Novel gene encoding human endometrial specific steroid-binding factor I,
PT II and III which is useful for treating asthma, rhinitis, cystic
PT fibrosis, airway disease and neoplasia.
XX
PS Example 2; Col 34; 36pp; English.
XX
CC This invention relates to nucleic acid molecules encoding portions of the
CC human endometrial specific steroid-binding factors I, II, and III. Also
CC included in the invention are hESF I, II, and III polypeptide sequences.
CC The nucleotide sequence exhibit antiasthmatic, antiinflammatory,
CC antiallergic, and cytostatic properties. The polynucleotides are used in
CC gene therapy to express hESF I, II and III polypeptides in vivo to treat
CC and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way
CC disease, neoplasia and atopy. The polynucleotides are also used to
CC inhibit phospholipase A2 activity, bind polychlorinated biphenyls, reduce
CC foreign protein antigenicity, inhibit monocyte and neutrophil chemotaxis
CC and phagocytosis, inhibit platelet aggregation, regulate eicosanoid
CC levels in the human uterus and control the growth of endometrial cells.
CC The polynucleotides are also useful for detecting complementary
CC polynucleotides as a diagnostic reagent. The hESF I, II and III
CC polynucleotides are used to detect complementary polynucleotides such as
CC a diagnostic reagent. Detection of a mutated form of hESF I, II and III
CC associated with a dysfunction will provide a diagnostic tool that can
CC define diagnosis of a disease or susceptibility to a disease which
CC results from under-expression, over-expression or altered expression of
CC hESF I, II and III e.g. a susceptibility to inherited asthma and
CC endometrial cancer. They are also useful for chromosome identification.
CC The present sequence represents a PCR primer used to amplify the hESF I
CC cDNA sequence
XX
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2183
Db ||||||| 8 CCTTTTCTTTTCTTTTCTTTT 27

RESULT 549
AAF25224
ID AAF25224 standard; DNA; 27 BP.
XX
AC AAF25224;
XX
DT 30-APR-2001 (first entry)
XX
DE 3' primer for an endometrial specific steroid binding factor I cDNA.
XX
KW Human; endometrial specific steroid binding factor; hESF; hESFI; hESFII;
KW hESFIII; inflammation; asthma; rhinitis; cystic fibrosis; airway disease;
KW neoplasia; atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis;
KW phagocytosis; platelet aggregation; eicosanoid; endometrial cell;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6174992-B1.
XX
PD 16-JAN-2001.
XX
PF 08-MAR-1999; 99US-00263810.
XX
PR 21-MAR-1996; 96US-0014724P.
PR 21-MAR-1997; 97US-00821451.

XX (HUMA-) HUMAN GENOME SCI INC.
PA Ni J, Yu G, Gentz R;
XX
PI WPI; 2001-158477/16.
XX
DR New human endometrial specific steroid binding factors, useful for
XX treating and preventing inflammation, asthma, rhinitis, cystic fibrosis,
PT airway disease, neoplasia and atopy.
PT
XX Example 2; Col 33; 36pp; English.
PS
XX PCR primers AAF25221 and AAF25224 were used to amplify cDNA encoding a
CC human endometrial specific steroid binding factor (hESF). The
CC specification describes hESFI, hESFII, and hESFIII. hESFI, II and III
CC polypeptides, and polynucleotides encoding them are useful for treating
CC and preventing inflammation, asthma, rhinitis, cystic fibrosis, airway
CC disease, neoplasia and atopy, inhibiting phospholipase A2 activity,
CC binding polychlorinated biphenyls, reducing foreign protein antigenicity,
CC inhibiting monocyte and neutrophil chemotaxis and phagocytosis,
CC inhibiting platelet aggregation, regulating eicosanoid levels in the
CC human uterus, and for controlling the growth of endometrial cells. hESF
CC polypeptides and nucleotides are also useful for research, biological,
CC clinical or therapeutic purposes
XX
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2183
Db ||||||| 8 CCTTTTCTTTTCTTTTCTTTT 27

RESULT 550
ABL41793
ID ABL41793 standard; DNA; 27 BP.
XX
AC ABL41793;
XX
DT 29-MAY-2002 (first entry)
XX
DE Primer for human endometrial specific steroid-binding factor I cDNA.
XX
KW Human; endometrial specific steroid-binding factor; ESF;
KW prostatic steroid-binding protein; hESF I; hESF II; hESF III; asthma;
KW PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6338948-B1.
XX
PD 15-JAN-2002.
XX
PF 30-MAY-2000; 2000US-00583169.
XX
PR 21-MAR-1996; 96US-0014724P.
PR 21-MAR-1997; 97US-00821451.
PR 08-MAR-1999; 99US-00263810.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz R;
XX
DR WPI; 2002-215019/27.
XX
PT New antibody specific for human endometrial specific steroid-binding
PT factor (hESF) III, useful for detecting hESF III protein in biological
PT sample and to isolate or identify clones expressing the protein.

XX Example 2; Col 33; 36pp; English.

PS

XX

CC PCR primers ABL41790 and ABL41793 were used to amplify cDNA encoding

CC human endometrial specific steroid-binding factor (hESF) I. The primers

CC were used to introduce restriction sites for cloning. The full length

CC hESF I protein has a molecular weight of 9.8 kDa. The protein which bind

CC homology to rat prostatic steroid-binding protein. Antibodies which bind

CC hESF proteins, such as hESF I, hESF II, and hESF III are useful for

CC isolating or to identify clones expressing the polypeptides or to purify

CC the polypeptides by affinity chromatography. Agonists and antagonists of

CC hESF proteins are useful for treating and/or preventing susceptibility to

CC asthma

XX

XX Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

SO

```

Query Match      0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY

2164 CCCCCCCCCCCCCCCCCC
| | | | | | | | | |
2183 CCCCCCCCCCCCCCCCCC

PB

8 CCCCCCCCCCCCCCCCCC
| | | | | | | | | |
27 CCCCCCCCCCCCCCCCCC

RESULT 551
ABX14927
ID ABX14927 standard; DNA: 27 BP.

AC ABX14927;

08-APR-2003 (first entry)

XX
DE
best amplifying 3' PCR primer for expression using baculovirus.

XX Human; PCR; ss; endometrial specific steroid-binding factor; hESF;
KW Clara cell 10 kDa; secretory protein; asthma; primer;
KW CC10; secretory protein; asthma; primer;
KW prostatic steroid-binding protein; hormone; lung; uterus; gene therapy.

OS	Homo sapiens.
OS	Synthetic.

PN US2002151012-A1;

17-OCT-2002

06-NOV-2007 : 2001US-00985911.

XX
DB 31-MAP-1996. 96US-0014724P.

21-MAR-1997; 97US-00821431.
PR
08-MAR-1998; 99US-00263810
PR

30-MAY-2000; 2000US-00383169.

PA (HUMA-) HUMAN GENOME SCI. INC. 3737

PI · Ni J, Yu G, Gentz R;

DR. WPI; 2003-182506/18.

PT New human endometrial specific steroid-binding factor (hESF) proteins and
PT genes, useful for treating or diagnosing a disease or susceptibility to a
PT disease, particularly asthma.

PS Example 2; Page 18; 37pp; English.

The invention discloses isolated polypeptides, which comprise human endometrial specific steroid-binding factors I, II and III (hESF I, II and III), and the nucleic acids encoding them. The hESF polypeptide has homologies to mammalian Clara cell 10 kDa (CC10) secretory protein and rat prostatic steroid-binding protein which are factors which modulate or mediate the action of hormones involved in the regulation of functions of the lung and uterus. The nucleic acids and polypeptides can be used to identify compounds that bind to and inhibit activation, raise antibodies

or develop antagonists against the isolated hESF polypeptide. The polypeptides or polynucleotides are useful for treating a patient having a need of hESF I, hESF II, hESF III or for treating a patient having to need to inhibit hESF. The polypeptide is administered by providing to the patient the DNA encoding the hESF polypeptide in vivo (gene therapy). In particular, the disease is asthma. The hESF polypeptides or polynucleotides are also useful for diagnosing a disease or a susceptibility to the disease. The sequence presented is the 3' PCR primer which was used to amplify hESF I cDNA for expression using baculovirus expression system ^T

Sequence 27 BP: 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

```
Query Match      0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20: Conservative 0; Mismatches 0; Indels
```

QY	2164	CCTTTTTTTTTTTTTTTTTT	2183
ph	8	CCCCCCCCCCCCCCCCCCCC	27

RESULT 552
ADD35234
TD ADD35234 standard; DNA; 28 BP.

AC ADD35234:

15--JAN-2004 (first entry)

XX
DE Mouse mitochondrial DNA sequence SEO ID NO: 3014.

XX ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
KW mitochondrial disease; oxidative phosphorylation dysfunction;
KW oxidative stress; apoptosis; aging.

XX סגור ונעול מיד

XX
W0000000-00

[illegible]

XX
110037985

XX

PR 31-AUG-2001; 2001CA-02356540.

PA (UYEM-) UNIV EMORY.

PI Wallace DC, Levy S, Kerstann K, Procaccio V;

DR WPI; 2003-300821/29.

Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles for use in diagnosing pathologies and identifying biochemical pathways.

PS Claim 2; SEQ ID NO 3014; 201pp; English.

The invention relates to a novel array comprising at least two isolated nucleotide molecules, each molecule having a sequence capable of uniquely hybridising to a nucleic acid molecule which is an expression product of a gene involved in mitochondrial biology. The array comprises two or more isolated nucleic acid molecules or spots, each molecule having a sequence chosen from sequence of 994 human probes and 2046 mouse probes. An array of the invention is useful for determining an expression profile of a mouse or human sample containing nucleic acid, by contacting the array with the sample under conditions allowing selective hybridisation, and measuring hybridisation of nucleic acid in the sample to the array to produce an expression profile. The array is also useful for determining an expression profile of a first labelled sample containing nucleic acid relative to a second, differently labelled sample containing nucleic acid. The second sample is a reference or a standard. An array is useful

the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACACAAUAUCUAGUUACAGAAAUC (II). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

SQ Sequence 29 BP; 22 A; 1 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 29;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels

Qy	2169	TTTTTTTTTTTTTTTTTTTAACTTGAAA	2196
Dd	29	TTTTTTTTTTTTTTTTTCACTTCTACA	2

RESULT 554
AAA71173/C

ID AAA71173 standard; DNA; 29 BP.

AC AAA71173;

DT 27-APR-2001 (first entry)

DE Molecular interaction site DNA #154.

Modulator; identification; molecular interaction; virtual library; ss.
KW
xy

OS Canis familiaris.

PN WO9958947-A2.

PD 18-NOV-1999.

PF 12-MAY-1999; 99WO-US010361.

PR 12-MAY-1998; 98US-00076404.

[illegible]

PA (ISIS-) ISIS PHARM INC.

PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;

DR WPI; 2000-086439/07.

Identifying compounds which modulate activity of target biomolecules, used to provide compounds which can be used as pharmacological, agricultural and industrial compounds.

Example 8; Fig 134; 405pp; English.

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds

predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified nucleotides forming a second side of the first ds region; (3) a purified and isolated RNA fragment comprising the human sequence UUUACACCAUAUUCAGUUUACAGAAAAUUC (II). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

```

SQ      Sequence 29 BP; 22 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

      Query Match      0.7%;      Score 20;      DB 1;      Length 29;
      Best Local Similarity 82.1%;      Pred. No. 1.1e+03;
      Matches 23;      Conservative 0;      Mismatches 5;      Indels 0;      Gaps 0;

```

QY
2169 TTTTCTTTTTTTTTTTTTTAACCTTGAAA 2196

nb
29 TTTTCTTTTTTTTTTTTTTCAGTTCTACA 2

RESULT 555
AAQ85070
ID AAQ85070 standard; DNA; 29 BP.

AA	AAQ85070;
AC	
XX	25-MAR-2003 (revised)
DT	28-SEP-1995 (first entry)
DT	
XX	Oligonucleotide clamp.
DE	
XX	Oligonucleotide clamp; diagnosis; therapeutic agents; herpes virus;
KW	cytomegalovirus; human papilloma virus; HIV; oncogenes;
KW	bromoacetylamidated; ss.
KW	

OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	modified_base	1	
FT		/*tag= a	
FT		/note= "covalently bound cholesterol group"	
FT		15. .16	
FT	misc_feature	/*tag= b	
FT		/note= "linkage or monomer containing a bromoacetyl amino functionality"	
FT		29	
FT	modified_base	/*tag= c	
FT		/note= "covalently bound cholesterol group"	

XX	WO9501456-A1.
PN	
XX	
XX	
PD	12-JAN-1995.
XX	
PF	01-JUL-1994; 94WO-US007541.
XX	
PR	02-JUL-1993; 93US-00087387.

XX (LYNX-) LYNX THERAPEUTICS INC.
PA
XX
XX
PI Gryaznov SM, Lloyd DH;
XX
XX WPI: 1995-061019/08.
DP

XX New oligo:nucleotide clamps that stably bind to target polynucleotide(s)
PT - may be used in diagnosis and therapy to inhibit genes or mRNA of, e.g.,
PT herpes:virus. HIV, oncogene(s), etc.

PS Example 10: Page 28; 44pp; English.

The oligonucleotide clamps AAQ85069 and AAQ85070 are specific for a ss, or ds target nucleotide. When bound to the target sequence the two oligonucleotides form a stable non-covalent link, clamping the target sequence. This technique may be used to inhibit the expression, or function of an exogenous gene in a host (pref. human). The gene may be from herpes virus, cytomegalovirus, human papilloma virus, HIV or an oncogene. Therefore the clamps may be used in the treatment and diagnosis of human viral diseases (updated on 25-MAR-2003 to correct PN field.)

XX
50
Sequence 29 RP: 2 A: 3 C: 0 G: 24 T: 0 U: 0 Other;

```

Query Match          0.7%; Score 20; DB 1; Length 29;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

Qy 2151 TTGATTTTTTCTCCCTTTTTTTTTTTT 2178
 || ||||| | |||||
 2 TTTTTTTTTTCACTTTTTTTTTTTT 29

RESULT 556
AAQ83933
IN AAQ83933 standard: DNA: 29 BP.

AC AAQ83933;

DT	25-MAR-2003	(revised)
DT	04-OCT-1995	(first entry)

oligonucleotide clamp containing free amines in the hinge region.

XX

vrv. vol. ref. oligonucleotide clamp: branched; macromolecule; ss.

OS Synthetic.

Key	Location/Qualifiers
FT modified_base 1	/*tag= a
FT	/note= "Modified with cholesterol"
FT modified_base 15. .16	/*tag= b
FT	/note= "C(pnp)A, pnp = a linkage of
FT	bromoacetyl amino functionality, an
FT modified_base 29	linkage"
FT	/*tag= c
FT	/note= "Modified with cholesterol"

PN W09501365-A1.

PD 12-JAN-1995.

05-JUL-1994: 94WO-US007557.

XX 02-JUL-1993: 93US-00087386.

PA (LYNX-) LYNX THERAPEUTICS INC.

PT Grvaznov SM:

WPI: 1995-060944/08.

Synthesis of branched polymers and novel branched polymeric structures - used as molecular probes esp. for detecting poly-nucleotide(s).

XX Example 5; Page 31; 52pp; English. PS

gene expression in the fields of molecular biology. They can also be used for the diagnosis and treatment of autoimmune disorders, and as research tools and in transgenic animals. This sequence represents human zinc finger binding motif DNA used in the scope of the invention

Sequence	29	BP;	0	A;	2	C;	4	G;	23	T;	0	U;	0	Other;
Query Match								0.7%	Score	20;	DB	1;	Length	29;
Best Local Similarity								82.1%	Pred. No.	1.1e+03;				
Matches	23;	Conservative						0;	Mismatches	5;	Indels		Gaps	0;

Qy 2155 TTTTCTCTCCTTTT 2182
pb 2 TTTTCTTGGCTGTTGGT 29

RESULT 559
ABL56892
ID ABL56892 standard; DNA; 30 BP.
XX AC ABL56892;

XX
PT 26-JUL-2002 (first entry)

DE Synthetic deoxyribonucleotide poly e.

xx Concentration; quantification; mutation detection; polymorphic;
 kw polymerase chain reaction; PCR; ss.
 xx Concentration; quantification; mutation detection; polymorphic;

OS Synthetic.

PN EP1046717-A2.

PD 25-OCT-2000.

20-APR-2000: 2000EP-00108643.

20-APR-1999: 99JP-00111601.

ALA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
DA

XX	Kurane R,	Kanagawa T,	Kamagata Y,	Kurata S,	Yamada K,	Yokomaku T;
PI						
PI	Kovama O,	Furusho K;				

WPT: 2000-657765/64.

XX Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.

Example 5: page 21: 55pp: English: ps

The invention relates to the determination of the concentration of a nucleic acid target, using a fluorescently labeled probe which produces reduced fluorescence emission when hybridised to the target nucleic acid. The method comprises measuring the reduction in emission caused by hybridisation. The new method is particularly used to quantify target nucleic acids by a real-time polymerase chain reaction, e.g. for quantifying microbial cells in co-cultures or symbiotic systems, for detecting gene mutations or polymorphisms, and for analysing melting curves of target nucleic acids to determine a T_m value. Methods of the invention allow target nucleic acids to be quantified quickly, easily and accurately. Particularly there is no need to remove unbound probe, and no materials are introduced that inhibit amplification by Taq polymerase (so conventional PCR conditions can be used). The specificity of PCR is kept high (amplification of primer dimers is delayed), and the limit of quantitation is reduced. Complex probes are not needed, and amplification can be monitored in real time. The working graph for data analysis (automatically generated by a computer) has a higher correlation coefficient than conventional graphs so more accurate quantitation is possible. The current sequence represents a synthetic

CC deoxyribonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match	0.7%;	Score 20;	DB 1;	Length 30;
Best Local Similarity	82.1%;	Pred. No. 1.1e+03;		
Matches 23;	Conservative	0;	Mismatches 5;	Indels 0;
				Gaps 0;

Qy

2159 TTCTCCTTTTTTTTTTTTTTTTTTT 2186
| | | | | | | | | | | | | | | |

pB

2 TATATAATTTTTTTTTTTGTTTTTTT 29
| | | | | | | | | | | | | | | |

RESULT 560
ABL56896
ID ABL56896 standard; DNA; 30 BP.
XX
AC ABL56896;
XX
DT 26-JUL-2002 (first entry)

synthetic deoxyribonucleotide poly i.

xx	Concentration; quantification; mutation detection; polymorphic;
kw	Kw
xw	polymerase chain reaction; PCR; ss.

XX QS Synthetic.

XX PN EP1046717-A2.

25-OCT-2000.

20-APR-2000:

PR 20-APR-1999: 99JP-00111601.

PA (NIBI-) JAPAN BIOINDUSTRY ASS

PA (KANK-) KANKYO ENG CO LTD.

xx Kurane R, Kanagawa T, Ka

XX
For your[illegible]

PT probe in which emission is reduced by binding to the target nucleic acid.

Example 5: Page 21; 55pp; English.

The invention relates to the determination of the concentration of a nucleic acid target, using a fluorescently labeled probe which produces reduced fluorescence emission when hybridised to the target nucleic acid. The method comprises measuring the reduction in emission caused by hybridisation. The new method is particularly used to quantify target nucleic acids by a real-time polymerase chain reaction, e.g. for quantifying microbial cells in co-cultures or symbiotic systems, for detecting gene mutations or polymorphisms, and for analysing melting curves of target nucleic acids to determine a T_m value. Methods of the invention allow target nucleic acids to be quantified quickly, easily and accurately. Particularly there is no need to remove unbound probe, and no materials are introduced that inhibit amplification by Taq polymerase (so conventional PCR conditions can be used). The specificity of PCR is kept high (amplification of primer dimers is delayed), and the limit of quantitation is reduced. Complex probes are not needed, and amplification can be monitored in real time. The working graph for data analysis (automatically generated by a computer) has a higher correlation coefficient than conventional graphs so more accurate quantitation is possible. The current sequence represents a synthetic deoxyribonucleotide that was used for investigating the base selectivity of a target nucleic acid


```
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match      0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
    ||| ||||| ||||| ||||| ||||| |||||
Db 2 TATATATTTT TTTT TTTT TTTT TTTT TTTT TTTT 29

RESULT 561
ABL56890
ID ABL56890 standard; DNA; 30 BP.
XX
AC ABL56890;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribonucleotide poly c.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
WPI; 2000-657765/64.

Determining the concentration of a target nucleic acid, useful e.g. for
detecting genetic mutations, comprises using a fluorescently labeled
probe in which emission is reduced by binding to the target nucleic acid.

Example 5; Page 21; 55pp; English.

The invention relates to the determination of the concentration of a
nucleic acid target, using a fluorescently labeled probe which produces
reduced fluorescence emission when hybridised to the target nucleic acid.
The method comprises measuring the reduction in emission caused by
hybridisation. The new method is particularly used to quantify target
nucleic acids by a real-time polymerase chain reaction, e.g. for
quantifying microbial cells in co-cultures or symbiotic systems, for
detecting gene mutations or polymorphisms, and for analysing melting
curves of target nucleic acids to determine a Tm value. Methods of the
invention allow target nucleic acids to be quantified quickly, easily and
accurately. Particularly there is no need to remove unbound probe, and no
materials are introduced that inhibit amplification by Taq polymerase (so
conventional PCR conditions can be used). The specificity of PCR is kept
high (amplification of primer dimers is delayed), and the limit of
quantitation is reduced. Complex probes are not needed, and amplification
can be monitored in real time. The working graph for data analysis
(automatically generated by a computer) has a higher correlation
coefficient than conventional graphs so more accurate quantitation is
possible. The current sequence represents a synthetic
deoxyribonucleotide that was used for investigating the base
selectivity of a target nucleic acid

Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match      0.7%; Score 20; DB 1; Length 30;
```

```
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match      0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
    ||| ||||| ||||| ||||| ||||| |||||
Db 2 TATATATTTT TTTT TTTT TTTT TTTT TTTT TTTT 29

RESULT 562
ABL56891
ID ABL56891 standard; DNA; 30 BP.
XX
AC ABL56891;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribonucleotide poly d.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
WPI; 2000-657765/64.

Determining the concentration of a target nucleic acid, useful e.g. for
detecting genetic mutations, comprises using a fluorescently labeled
probe in which emission is reduced by binding to the target nucleic acid.

Example 5; Page 21; 55pp; English.

The invention relates to the determination of the concentration of a
nucleic acid target, using a fluorescently labeled probe which produces
reduced fluorescence emission when hybridised to the target nucleic acid.
The method comprises measuring the reduction in emission caused by
hybridisation. The new method is particularly used to quantify target
nucleic acids by a real-time polymerase chain reaction, e.g. for
quantifying microbial cells in co-cultures or symbiotic systems, for
detecting gene mutations or polymorphisms, and for analysing melting
curves of target nucleic acids to determine a Tm value. Methods of the
invention allow target nucleic acids to be quantified quickly, easily and
accurately. Particularly there is no need to remove unbound probe, and no
materials are introduced that inhibit amplification by Taq polymerase (so
conventional PCR conditions can be used). The specificity of PCR is kept
high (amplification of primer dimers is delayed), and the limit of
quantitation is reduced. Complex probes are not needed, and amplification
can be monitored in real time. The working graph for data analysis
(automatically generated by a computer) has a higher correlation
coefficient than conventional graphs so more accurate quantitation is
possible. The current sequence represents a synthetic
deoxyribonucleotide that was used for investigating the base
selectivity of a target nucleic acid

Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match      0.7%; Score 20; DB 1; Length 30;
```


Db 2 TATATATTTTTTTTGTGTTTTTTTTTT 29

RESULT 565
ABA97613
ID ABA97613 standard; DNA; 30 BP.
XX
AC ABA97613;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly b nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTCTCCTTTTTTTTTTTTTTTTTTTT 2186
Db 2 TATATATTTTTTTTGTGTTTTTTTTTT 29

RESULT 566
ABA97620
ID ABA97620 standard; DNA; 30 BP.
XX
AC ABA97620;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly i nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX

PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTCTCCTTTTTTTTTTTTTTTTTTTT 2186
Db 2 TATATATTTTTTTTCTTTTTTTTTTT 29

RESULT 567
ABA97614
ID ABA97614 standard; DNA; 30 BP.
XX
AC ABA97614;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly c nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX

CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 2 TATATATTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 29

RESULT 568
ABA97615
ID ABA97615 standard; DNA; 30 BP.
XX
AC ABA97615;
XX
DT 11-APR-2002 (first entry)
XX Poly d nucleotide sequence.
DE ss; fluorochrome; nucleic acid probe; fluorescence.
XX
KW Unidentified.
XX JP2001286300-A.
XX
OS 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
XX Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 2 TATATATTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 29

RESULT 569
ABA97616
ID ABA97616 standard; DNA; 30 BP.

XX
AC ABA97616;
XX
DT 11-APR-2002 (first entry)
XX Poly e nucleotide sequence.
DE ss; fluorochrome; nucleic acid probe; fluorescence.
XX
KW Unidentified.
XX JP2001286300-A.
XX
OS 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
XX Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186
Db 2 TATATATTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 29

RESULT 570
ABL95886
ID ABL95886 standard; DNA; 30 BP.
XX
AC ABL95886;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly b for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.

CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
CC
XX Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTTCTCCTTTTGTGTTTTTTT 2186
Db 2 TATATATTTTGTGTTTTTTT 29
RESULT 573
ABL95888
ID ABL95888 standard; DNA; 30 BP.
XX
AC ABL95888;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly d for assaying nucleic acids.
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX Unidentified.
OS WO200208414-A1.
XX
PN 31-JAN-2002.
XX
PD 27-JUN-2001; 2001WO-IB001147.
PF
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTTCTCCTTTTGTGTTTTTTT 2186
Db 2 TATATATTTTGTGTTTTTTT 29
RESULT 575
ABL95893
ID ABL95893 standard; DNA; 30 BP.
XX
AC ABL95893;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly e for assaying nucleic acids.
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX Unidentified.
OS WO200208414-A1.
XX
PN 31-JAN-2002.
XX
PD 27-JUN-2001; 2001WO-IB001147.
PF
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2159 TTTCTCCTTTTGTGTTTTTTT 2186
Db 2 TATATATTTTGTGTTTTTTT 29
RESULT 574
ABL95889
ID ABL95889 standard; DNA; 30 BP.
XX
AC ABL95889;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly e for assaying nucleic acids.
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX Unidentified.
OS WO200208414-A1.
XX
PN 31-JAN-2002.
XX
PD 27-JUN-2001; 2001WO-IB001147.
PF
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2159 TTTCTCCTTTTGTGTTTTTTT 2186
Db 2 TATATATTTTGTGTTTTTTT 29
RESULT 575
ABL95893
ID ABL95893 standard; DNA; 30 BP.
XX
AC ABL95893;

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185
Db 6 TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 577
ADA14837/c
ID ADA14837 standard; DNA; 30 BP.
XX AC ADA14837;
XX DT 06-NOV-2003 (first entry)
XX DE Hairpin oligonucleotide, #2, used in an example of the invention.
XX KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW rhodamine B-labelled dye; detection; gold support; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1 /tag= a /mod_base= OTHER
FT /note= "OTHER= thiol group"
FT 6. .25
FT /tag= b
FT /bound moiety= "Target sequence #2"
FT /note= "Forms a double-stranded region with the target
FT sequence shown in examples 3, 4 and 5"
FT 30
FT /tag= c
FT /mod_base= OTHER
FT /note= "OTHER= amino group"

US2003013109-A1.
16-JAN-2003.
21-JUN-2002; 2002US-00176055.
21-JUN-2001; 2001US-0299460P.
(BALL/) BALLINGER C T.
(LOCA/) LOCASCIO M.
(LAND/) LANDRY D P.
Ballinger CT, Locascio M, Landry DP;
WPI; 2003-596312/56.
Hairpin sensor useful for detecting a target nucleotide sequence in a sample, comprises a hairpin loop assembly including a complementary probe and a quenchable fluorescing agent.
Example 3; Page 11; 16pp; English.
The invention discloses a hairpin sensor comprising a hairpin loop assembly including a complementary probe positioned between a first inverse repeat arm and a second inverse repeat arm, and a quenchable fluorescing agent joined, directly or indirectly, to the end of the second inverse repeat arm of the hairpin loop assembly opposite the complementary probe. Also claimed is a microarray comprising the hairpin sensor, where the end of the first inverse repeat arm opposite the complementary probe is bound, directly or indirectly, to a support, a kit for detecting a target nucleotide sequence in a sample comprising the hairpin sensor, and a support, and a hairpin sensor system, in which the

particle is conductive or semi-conductive, including at least one of the above hairpin sensor assemblies. The hairpin sensor further comprises a functional group joined to the end of the first inverse repeat arm opposite the complementary probe, or first spacer opposite the first inverse repeat arm, the functional group selected from amino, carboxyl, thiol and hydroxyl. Further, the sensor comprises a ligand positioned between the second inverse repeat arm and the quenchable fluorescing agent, where the ligand is selected from mercapto, hydroxyl, amino, nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The second spacer is positioned between the second inverse repeat arm and the quenchable fluorescing agent which comprises a semiconductor nanocrystal or rhodamine B-labelled dye. Within the microarray the support is capable of accepting a charge. At least one hairpin sensor comprises two or more hairpin sensors. The two or more hairpin sensors include complementary probes that are the same or different and respective quenchable fluorescing agents that are the same or different. The two or more hairpin sensors are arranged in a spatially-defined pattern. The sensor and system are useful for detecting a target nucleotide sequence in a sample. Further, the method involves identifying the target nucleotide sequence by the location of the complementary probe to which the target nucleotide sequence binds. The two or more hairpin sensors include complementary probes or quenchable fluorescing agents, that are different. The sequence presented is the hairpin oligonucleotide, #2, used in an example of the invention.

Sequence 30 BP; 1 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 26 GAAAAA AAAAAA AAAAAA AAAAAA 7

RESULT 578
AAV09273
ID AAV09273 standard; cDNA; 44 BP.
XX AC AAV09273;
XX DT 07-JUL-1998 (first entry)
XX DE Nucleotide sequence of the 3' portion of the BG513_19 protein.
XX KW BG513 19 protein; human adult brain cDNA library; nutritional activity;
KW cytokine activity; cell proliferation/differentiation activity; homology;
KW ss.
XX OS Homo sapiens.
XX PN WO9748801-A2.
XX PD 24-DEC-1997.
XX PF 16-JUN-1997; 97WO-US010501.
XX PR 17-JUN-1996; 96US-00664596.
XX PA (GEMY) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Evans C, Spaulding V, Bowman M;
XX WPI; 1998-063142/06.
XX PT poly:nucleotide(s) and proteins obtained from human PBMC, dendritic cell,
PT adult brain, foetal brain and adult testes cDNA libraries - used in
PT research, detection and therapy of, e.g. cytokine and cell proliferation
PT or differentiation.
XX Claim 19; Page 51; 78pp; English.
PS

XX This nucleotide sequence encodes the 3' portion of the BG513_19 protein
CC which was isolated from a human adult brain cDNA library. The products of
CC the polynucleotides of the invention can be used in research, detection
CC and therapy, as they may have nutritional activity, cytokine and cell
CC proliferation/differentiation activity. A search against the Genbank
CC database demonstrated that this sequence has no homology with known
CC sequences
XX
SQ Sequence 44 BP; 44 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 44;
Best Local Similarity 65.9%; Pred. No. 2.2e+03;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2761 AATAAAAGTATTCTTGTAGAAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44

RESULT 579
ABV77669/c
ID ABV77669 standard; DNA; 24 BP.
XX
AC ABV77669;
XX
DT 03-FEB-2003 (first entry)
XX
DE Human zinc finger protein 9.79 PCR primer #1.
XX
KW Human; zinc finger protein 9.79; cancer; HIV infection; cytostatic;
KW anti-HIV; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1343710-A.
XX
PD 10-APR-2002.
XX
PF 19-SEP-2000; 2000CN-00125246.
XX
PR 19-SEP-2000; 2000CN-00125246.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-548879/59.
XX
PT A novel human zinc finger protein 9.79 polypeptide, useful for treating
PT several diseases e.g. cancer and HIV infection.
XX
PS Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
CC The present invention relates to human zinc finger protein 9.79 (see
CC ABP59011). The zinc finger protein is useful for treating several
CC diseases e.g. cancer and HIV infection. The present sequence is a PCR
CC primer, which was used in an example from the invention
XX
SQ Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 7.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAA 2804
Db 24 AATGAAAAAAGA 2

RESULT 580
AAD26900
ID AAD26900 standard; DNA; 25 BP.

XX AAD26900;
AC
XX 09-APR-2002 (first entry)
DT
XX Bacterial PNP DNA fragment with an in-frame polyA tract.
DE
XX Hypermutable organism; dominant negative allele; mismatch repair gene;
KW spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
KW bacteria; ss.
XX
OS Bacteria.
OS Unidentified.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT misc_feature 1..5
FT /*tag= a
FT /note= "Bacterial PNP gene"
FT misc_feature 6..25
FT /*tag= a
FT /note= "In-frame polyA tract"
XX
PN WO200188192-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015376.
XX
PR 17-MAY-2000; 2000US-0204769P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
PA (MORP-) MORPHOTEK INC.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
PA (KINZ/) KINZLER K W.
XX
PI Nicolaides NC, Sass PM, Grasso L, Vogelstein B, Kinzler KW;
XX WPI; 2002-083004/11.
XX
XX Generating mutation in gene using cells which contain defective mismatch
PT repair gene, useful to generate genetically altered mutations with new
PT output traits.
XX
PS Example 5; Fig 7; 59pp; English.
XX
CC The patent discloses a method for generating hypermutable organisms.
CC Dominant negative alleles of human mismatch repair genes can be used to
CC generate hypermutable cells and organisms. They increase the rate of
CC spontaneous mutations by reducing the effectiveness of DNA repair and
CC thereby render the cells or animals hypermutable. The method is used to
CC produce genetically altered organisms to produce new output traits. The
CC present sequence is a bacterial poly purine nucleotide phosphorylase
CC (polyPNP) DNA fragment containing an in-frame polyA tract. This sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 25 BP; 21 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAA 2804
Db 1 ATGGCAAAAAA 23

RESULT 581
AAC96419
ID AAC96419 standard; DNA; 25 BP.

Thu Jun 10 13:10:09 2004

```
ID  ABX12469 standard; DNA; 27 BP.
XX
AC  ABX12469;
XX
DT  10-MAY-2003 (first entry)
XX
DE  Cocksackie B virus 4 (CBV-4) strain VD2921, PCR primer dt26V.
XX
KW  Cocksackie virus strain VD2921; diabetogenic cocksackie B virus-4; CBV-4;
KW  strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW  diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW  renal failure; leg amputation; PCR; primer; ss.
XX
OS  Cocksackievirus.
XX
PN  WO2002103060-A2.
XX
XX  27-DEC-2002.
PD
XX
PF  19-JUN-2002; 2002WO-IB003278.
XX
PR  20-JUN-2001; 2001SE-00002198.
XX
PA  (INNO-) INNOVENTUS PROJECT AB.
XX
PI  Tuvemo HT, Frisk GE, Yin H;
XX
DR  WPI; 2003-278229/27.
XX
PT  polymerase chain reaction and primers for detecting nucleic acids from
PT  the diabetogenic cocksackie B virus-4 strain VD2921.
XX
PS  Example 5; Page 44; 79pp; English.
XX
CC  The invention describes a polymerase chain reaction (PCR) and primers for
CC  detecting nucleic acids from the diabetogenic cocksackie B virus-4 (CBV-4)
CC  strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC  P3C and P3D nucleic acids). The methods and primers are used for the
CC  detection of CBV-4 strain VD2921 which is associated with diabetes
CC  (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC  detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC  cells, can improve prognosis by allowing treatment e.g. with antiviral
CC  drugs, to prevent further loss of beta cells and severe long term
CC  consequences of diabetes including blindness, renal failure and leg
CC  amputations. This sequence represents a primer used to determine the
CC  genomic structure of diabetogenic cocksackie B virus 4 (CBV-4) strain
CC  VD2921
XX
SQ  Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;

Query Match      0.7%; Score 19.8; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 9.6e+02;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY  2778 TAGAATTGAAAAAATAAAAAAATAAAAAA 2804
DB  :||| ||||| ||||| ||||| ||||| |||||
    27 BAAAAAATAAAAAAATAAAAAAATAAAAAA 1

RESULT 587
ADC75074/c
ID  ADC75074 standard; DNA; 27 BP.
XX
AC  ADC75074;
XX
DT  01-JAN-2004 (first entry)
XX
DE  Biosensor related oligonucleotide of the invention SEQ ID NO:2.
XX
KW  ss; biosensor; hybridisation.
XX
OS  Synthetic.
XX
```

```
PN  JP2003172737-A.
XX
PD  20-JUN-2003.
XX
PF  07-DEC-2001; 2001JP-00374764.
XX
PR  07-DEC-2001; 2001JP-00374764.
XX
PA  (TOJO ) TOYO KOHAN CO LTD.
XX
DR  WPI; 2003-819164/77.
XX
PT  Solid support body comprising crystal resonator on which a surface
PT  treatment layer is formed, and a substrate whose surface treatment layer
PT  is chemically modified, useful as biosensor.
XX
PS  Disclosure; SEQ ID NO 2; 7pp; Japanese.
XX
CC  The invention relates to a novel solid support body comprising a crystal
CC  resonator on which a surface treatment layer is formed. The biosensor is
CC  useful for analysing biological samples e.g., gene, a protein, and a
CC  peptide, and for analysing bioactive substances. Preferably, the
CC  biosensor is useful for analysing base sequences by carrying out
CC  hybridisation. The present sequence is used in the exemplification of the
CC  invention.
XX
SQ  Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match      0.7%; Score 19.8; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 9.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2168 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    23 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 588
ADC75075
ID  ADC75075 standard; DNA; 27 BP.
XX
AC  ADC75075;
XX
DT  01-JAN-2004 (first entry)
XX
DE  Biosensor related oligonucleotide of the invention SEQ ID NO:3.
XX
KW  ss; biosensor; hybridisation.
XX
OS  Synthetic.
XX
PN  JP2003172737-A.
XX
PD  20-JUN-2003.
XX
PF  07-DEC-2001; 2001JP-00374764.
XX
PR  07-DEC-2001; 2001JP-00374764.
XX
PA  (TOJO ) TOYO KOHAN CO LTD.
XX
DR  WPI; 2003-819164/77.
XX
PT  Solid support body comprising crystal resonator on which a surface
PT  treatment layer is formed, and a substrate whose surface treatment layer
PT  is chemically modified, useful as biosensor.
XX
PS  Disclosure; SEQ ID NO 3; 7pp; Japanese.
XX
CC  The invention relates to a novel solid support body comprising a crystal
CC  resonator on which a surface treatment layer is formed. The biosensor is
CC  useful for analysing biological samples e.g., gene, a protein, and a
CC  peptide, and for analysing bioactive substances. Preferably, the
```


CC biosensor is useful for analysing base sequences by carrying out
CC hybridisation. The present sequence is used in the exemplification of the
CC invention.

XX Sequence 27 BP; 19 A; 3 C; 0 G; 5 T; 0 U; 0 Other; 0;

SQ Query Match 0.7%; Score 19.8; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 9.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAATAAAAAAAAAA 2803
Db 1 AATTCAAAAAAATAAAAAAAAAA 23

RESULT 589
AAA57856/c
ID AAA57856 standard; DNA; 28 BP.

XX AAA57856;

AC 11-OCT-2000 (first entry)

DT Deoxy-T22-tagged substrate oligonucleotide.

DE Ribozyme; catalytic RNA; analyte detection; effector molecule;
KW nucleic acid substrate; in vitro selection; ribozyme ligase;
KW conformation dependent activity; allosteric activation; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH misc_RNA 23..28
FT /*tag= a
FT misc_binding 24..28
FT /*tag= b
FT /bound_moiety= "Bases 13-17 of N90 RNA pool (AAA57851)"

XX WO200024931-A2.

PN 04-MAY-2000.

XX 22-OCT-1999; 99WO-IL000557.

PR 23-OCT-1998; 98IL-00126731.

XX (INTE-) INTELLIGENE LTD.

XX Nathan A, Ellington A;

XX WPI; 2000-350763/30.

PT Detecting an analyte in a sample comprises providing nucleic acid
PT sequence which is catalytically active in presence of analyte, contacting
PT catalytic nucleic acid with substrate and amplifying catalytic product.

PS Disclosure; Page; 36pp; English.

XX The invention relates to a method of detecting an analyte in a sample.
CC The method comprises providing a nucleic acid sequence which is initially
CC catalytically inactive, but which becomes catalytically active in the
CC presence of an analyte (the effector); providing a nucleic acid substrate
CC for the catalytic activity of the effector; and contacting
CC the nucleic acid sequence and the substrate with the sample under
CC conditions allowing catalytic activity of nucleic acid sequences. The
CC catalytic nucleic acid sequence will be able to convert the nucleic acid
CC substrate into a nucleic acid product only if the analyte of interest is
CC present. The nucleic acid catalytic product is then amplified, and a
CC significant increase in the amount of product indicates the presence of
CC the analyte in the sample. The method is useful for the qualitative or
CC quantitative determination of an analyte in a sample in diagnostic
CC assays. The invention describes the in vitro selection of a ribozyme
CC ligase (L1; AAA57859, AAA57860) which is catalytically active only in the

CC presence of an oligonucleotide effector (AAA57854). The L1 ribozyme
CC ligase was selected from a pool of RNA molecules comprising a central
CC randomised region 90 nucleotides in length flanked on both sides by
CC constant sequence regions (the N90 RNA pool; AAA57851). In the presence
CC of the effector, selection was performed using one of the tagged
CC substrate molecules AAA57855-A57857. RNAs with ligase activity (i.e.,
CC those which have become ligated to the substrate molecule) were reverse
CC transcribed using the effector oligo, and then PCR amplified using the
CC effector and a DNA primer identical in sequence to the substrate used for
CC the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC can only adopt its active conformation (AAA57859) in the presence of the
CC effector oligo (analyte). In the absence of the effector, L1 adopts an
CC inactive conformation (AAA57860). The present sequence represents the
CC deoxy-T22-tagged substrate oligonucleotide. The d722 tag enables
CC successfully ligated products to be isolated using oligo(dA) cellulose
CC Type 7. Note: The present sequence is not given in the specification, but
CC is created from the information given on page 11

XX Sequence 28 BP; 1 A; 2 C; 1 G; 22 T; 2 U; 0 Other;

SQ Query Match 0.7%; Score 19.8; DB 1; Length 28;
Best Local Similarity 91.3%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAATAAAAAAAAA 2804
Db 28 AGTGCAAAAAAATAAAAAAAAA 6

RESULT 590
AAA90025
ID AAA90025 standard; DNA; 29 BP.

XX AAA90025;

AC 20-DEC-2000 (first entry)

XX PCR primer for fatty acid binding protein (FABP) DNA amplification.
KW Vaccine; Japanese schistosomiasis; fatty acid binding protein; FABP;
KW PCR primer; ss.

XX Unidentified.

XX CN1255548-A.

XX 07-JUN-2000.

XX 27-NOV-1998; 98CN-00122043.

XX 27-NOV-1998; 98CN-00122043.

XX (SHAN-) SHANGHAI DOMESTIC ANIMAL PARASITOSIS INS.

XX Lin J, Wu X, Liu J;

XX WPI; 2000-524988/48.

XX Clone of Japanese schistosome fatty acid-binding protein gene and its
PT expression in Bombyx mori system.

PS Claim 3; Page 1; 12pp; Chinese.

XX The present invention relates to the preparation of a vaccine against
CC Japanese schistosomiasis. The vaccine comprises a gene encoding a fatty
CC acid binding protein (FABP). The FABP is expressed in a Bombyx mori
CC system as a fusion protein of 18kD. The fusion protein has an increased
CC immunogenicity and stronger anti-infective action than the wild-type
CC protein. The present sequence represents a PCR primer used to amplify DNA
CC encoding the FABP of the invention

XX Sequence 29 BP; 2 A; 4 C; 3 G; 20 T; 0 U; 0 Other;

The invention comprises rapid isolation and enrichment of the differences of DNA fragments between two pools of DNA, comprises converting undesirable testers (DNA being subtracted) to drivers (DNA used to subtract) and re-utilising converted drivers in repeats of subtraction to achieve double exponential elimination of undesirable tester sequences. The method comprises (a) attaching a nucleic acid fragment to 1 or more polymerase chain reaction (PCR) adapters to form an adapter-attached nucleic acid fragment, followed PCR with primers containing nucleic acid sequences complementary to nucleic acid sequences of the adapter to form an adapter-attached nucleic acid tester, (b) mixing the adapter-attached nucleic acid tester with a nucleic acid driver that contains no attached adapter or contains an attached adapter whose sequence differs from the adapter, to form a nucleic acid mixture, (c) denaturing and re-annealing the tester/driver nucleic acid mixture, (d) adding to the nucleic acid mixture an effective amount of reagents necessary for removing the adapter sequence from the tester/ driver hetero-duplex and (e) repeating step (c) to (d) at least once (no amplification takes place and no additional driver is added). The method is used for rapid isolation and enrichment of the differences of DNA fragments between two pools of DNA e.g. in the search for tumour specific sequences. The method has 2 improvements over the methods disclosed by Yang et al. (1996), Lisitsyn et al. (1993), Straus et al. (1990) by (i) bypassing the need of a polymerase chain reaction (PCR) amplification or physical separation of desirable testers from undesirable ones in each repeat of subtraction, it eliminates the necessity of tester dilution in each repeat of subtraction, and (ii) by utilising the converted driver from each repeat of subtraction, it eliminates the need for re-introducing additional driver into hybridisation in each repeat of subtraction. The present

RESULT 593
ABA01204/C
ID ABA01204 standard; DNA; 32 BP.
XX
AC ABA01204;

XX DT 11-SEP-2003 (revised)

XX DT 28-JAN-2002 (first entry)

XX DE Mamushi fibrinolytic enzyme, brevinase, PCR primer, BBRP1.

XX KW Fibrinolytic enzyme; brevinase; thermostable; thrombolytic agent;

XX KW mamushi; PCR primer; ss.

XX OS Agkistrodon blomhoffi; brevicaudus.

XX PN KR2001045716-A.

XX PD 05-JUN-2001.

XX PF 06-NOV-1999; 99KR-00049115.

XX PR 06-NOV-1999; 99KR-00049115.

XX PA (LEEJ/) LEE J W.

XX PA (PARK/) PARK W.

XX PI Lee JW, Park W;

XX DR WPI; 2001-636862/73.

XX PT Fibrinolytic enzyme, brevinase, separated from poison of viper,

XX PT agkistrodon blomhoffi brevicaudus.

XX PS Example 5; Page 6; 23pp; Korean.

XX CC The present invention relates to fibrinolytic enzyme, brevinase (see

CC AAG79000), which is separated from the poison of Agkistrodon blomhoffi

CC brevicaudus (mamushi). The enzyme shows stability at high temperatures

CC and is thus useful in developing thrombolytic agents. The present

CC sequence is a PCR primer, which was used in an example from the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 32 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 2 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 32;

Best Local Similarity 81.5%; Pred. No. 1.4e+03;

Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAAATAAAAAAAAAAAAAA 2804

Db 31 BAAAAAATAAAAAAAAAAAAAAATAAAAAA 5

RESULT 594

ADA26489

ID ADA26489 standard; DNA; 32 BP.

XX AC ADA26489;

XX DT 20-NOV-2003 (first entry)

XX DE DNA nanolithography method example oligonucleotide G1.

XX ss; direct-write nanolithography; nanoscopic tip; nanoscale pattern;

XX KW patterning; scanning probe microscopic tip; nanoparticle; nanoarray.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 32

FT /*tag= a

FT /mod_base= OTHER

FT /note= "contains a thiol group (CH2)3SH) at the 5' end"

XX PN W02003048314-A2.

XX PD 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038252.

XX 30-NOV-2001; 2001US-0337598P.

XX 07-MAR-2002; 2002US-0362924P.

XX (UYNW-) UNIV NORTHWESTERN TECHNOLOGY TRANSFER PR.

XX Mirkin CA, Demers ML, Ginger DS;

XX WPI; 2003-671287/63.

XX Depositing nucleic acid on substrate by direct-write nanolithography, by

XX positioning nanoscopic tip relative to substrate, to transfer nucleic

XX acid to substrate and generate stable nucleic acid nanoscale pattern.

XX Disclosure; Page 38; 76pp; English.

XX The invention relates to a method of depositing nucleic acid onto a

XX substrate by direct-write nanolithography, by positioning at least one

XX nanoscopic tip relative to a substrate so that the tip and substrate

XX approach each other, and the nucleic acid is transferred from the tip to

XX the substrate to generate a stable nucleic acid nanoscale pattern on the

XX substrate which is hybridizable with complementary nucleic acid. The

XX method is useful for generating nanoscale patterns of nucleic acid on a

XX substrate, in which before transfer the tip is modified to allow the

XX nucleic acid to wet the tip and the nucleic acid is modified to chemisorb

XX or covalently bond to the substrate upon transfer. The method is also

XX useful for direct patterning of modified nucleic acid onto a substrate,

XX by inking a scanning probe microscopic tip with a modified nucleic acid

XX and positioning the inked tip close enough to the substrate to effect

XX transfer of the nucleic acid to the substrate to form a nanoscale

XX pattern. Another use for the method is for assembling nanoparticles (e.g.

XX gold nanoparticles) to form nanoscale patterns, by depositing from a

XX nanoscopic tip a first nucleic acid onto a substrate to form a deposit

XX with lateral nanoscale features of 1000 nm or less by direct write

XX nanolithography, hybridizing the nucleic acid deposit with the

XX nanoparticle, where the nanoparticle is functionalized with a second

XX nucleic acid which is either complementary to the first or complementary

XX to the nucleic acid of a linking strand which links the second nucleic

XX acid to the first. Deposition of nucleic acid on the substrate is

XX repeated to form a nanoarray of the nucleic acid and the hybridization is

XX carried out with the nanoarray. The method is suitable for writing and

XX preconcepted nanoscale features directly, without use of expensive and

XX potentially destructive methods such as electron beam and

XX photolithographic methods. The structures can be built up, if desired,

XX without degrading existing structures. Complicated stamps and resists are

XX not needed. Improvements in the consistency and stability of the

XX nanolithography can be observed. This sequence represents an example of a

XX nucleic acid that can be used in the method of the invention.

XX SQ Sequence 32 BP; 23 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 32;

Best Local Similarity 77.4%; Pred. No. 1.4e+03;

Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2774 TTGTTAGATTGAAAAAATAAAAAAAAAAAAAA 2804

Db 1 TAGCTCAACTCTAAAAAATAAAAAAAAAAAAAA 31

RESULT 595

AAD03682/c

ID AAD03682 standard; DNA; 26 BP.

XX AC AAD03682;

XX DT 19-JUN-2001 (first entry)

XX DE Human full length zcytor13 cDNA isolating polyA PCR primer, ZC7764b.

XX KW Human; phosphodiesterase; PDE; zcytor13; antiasthmatic; antiarthritic;

KW antipsoriatic; cytostatic; antiatherosclerotic; antiinfectivity;
KW antibiotic; antiinflammatory; dermatological; wound healing; antiviral;
KW antibacterial; therapy; inflammatory bowel disease; diverticulitis;
KW spermatogenesis; sperm capacitation; immunocontraceptive; vaccine;
KW cancer; reperfusion ischaemia; psoriasis; melanoma; myocarditis; PID;
KW pelvic inflammatory disease; eczema; scleroderma; vasoconstriction;
KW heart arrhythmia; congestive heart disease; muscle spasm; fatigue;
KW chromosomal abnormality; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200125444-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027734.
XX
PR 07-OCT-1999; 99US-00414025.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Novak JE, Gao Z;
XX
DR WPI; 2001-266312/27.
XX
XX Novel human phosphodiesterase polypeptide, zcytor13 and polynucleotide
PT encoding it, for detecting human chromosomal abnormalities, identifying
PT modulators and treating inflammatory and cardiovascular diseases.
PT
XX
PS Example 1C; Page 118; 122pp; English.
XX

CC The patent discloses novel human phosphodiesterase (PDE), zcytor13 cDNA
CC and its corresponding protein. Zcytor13 protein is used to promote wound
CC healing in tissues, to exhibit anti-bacterial and anti-viral effects and
CC to identify modulators (e.g. agonists or antagonists). Zcytor13, its
CC agonists or antagonists are useful in the treatment of inflammatory heart
CC or cardiovascular conditions, muscle inflammation, inflammation during
CC and after surgery, arthritis, asthma, inflammatory bowel disease or
CC diverticulitis, for modulating spermatogenesis, sperm capacitation, as
CC immunocontraceptive or anti-fertility vaccine and for treating male
CC infertility. Zcytor13 protein and its antibodies are used to diagnose
CC cancer, reperfusion ischaemia, asthma, psoriasis and melanoma. Zcytor13
CC proteins are used to enhance fertilisation. Zcytor13 antagonists are used
CC to treat myocarditis, atherosclerosis, pelvic inflammatory disease (PID),
CC psoriasis, eczema, scleroderma and other inflammatory diseases. Zcytor13
CC sequences and/or its antibodies are useful for treatment of disorders
CC associated with vasoconstriction, heart arrhythmia, congestive heart
CC disease, muscle spasms and fatigue. They are used for detecting human
CC chromosomal abnormalities. Zcytor13 cDNAs are used in gene therapy.
CC Zcytor13-cytokine fusion proteins or antibody-cytokine fusion proteins
CC are useful for enhancing in vivo killing of target tissue. The present
CC sequence is a polyA PCR primer, ZC7764b which is used to isolate full
CC length zcytor13 cDNA by screening human placental cDNA library
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAAATAAAAAA 2803
DB 26 TAAAAAATAAAAAAATAAAAAA 1

RESULT 596
AAS20596/c
ID AAS20596 standard; DNA; 26 BP.
XX
AC AAS20596;
XX
DT 23-APR-2002 (first entry)
XX

DE Human zsig63 cDNA sequencing primer ZC7764a.
XX
KW Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KW gastrointestinal disease; urinary tract infection; vaginal infection;
KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
KW chronic bronchitis; gene therapy; protein therapy; primer; ZC7764a.
XX
OS Homo sapiens.
XX
PN US6331413-B1.
XX
PD 18-DEC-2001.
XX
PF 17-MAR-2000; 2000US-00527345.
XX
PR 17-MAR-1999; 99US-0124820P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2002-096707/13.
XX
XX Polynucleotides encoding salivary proteins useful as anti-microbial
PT agents.
PT
XX
PS Example 1; Col 53; 29pp; English.
XX

CC The invention relates to a polynucleotide derived from the 4q12-4q13
CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC secreted salivary protein with anti-microbial activity. Due to their
CC microbial activity, the sequences can be used in the study of microbial
CC infections, e.g. for recombinant production of anti-microbial proteins.
CC The sequences can be used in the treatment of tooth decay, periodontal
CC disease, thrush, gastrointestinal disease, urinary tract infections,
CC vaginal infections, skin infections, epithelial wounds, chronic tissue
CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC represents a sequencing primer for cDNA encoding human zsig63
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAAATAAAAAA 2803
DB 26 TAAAAAATAAAAAAATAAAAAA 1

RESULT 597
ABS52638/c
ID ABS52638 standard; DNA; 26 BP.
XX
AC ABS52638;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human secreted salivary protein zsig63 PCR primer ZC7764a.
XX
KW Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
KW antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KW fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KW tooth decay; periodontal disease; thrush; gastrointestinal disease;
KW urinary tract infection; vaginal infection; skin infection; microflora;
KW epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KW chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KW incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KW chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KW digestion; PCR; primer; ss.

XX Homo sapiens.
OS US2002081701-A1.
XX 27-JUN-2002.
PN
XX
PD
XX
PF 03-AUG-2001; 2001US-00922480.
XX
PR 17-MAR-1999; 99US-0124820P.
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLE/) ADLER D A.
PA (SHEP/) SHEPPARD P O.
XX
PI Adler DA, Sheppard PO;
XX
XX WPI; 2002-635468/68.
DR
XX
XX Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT useful for treating microbial infections, inflammatory conditions, dental
PT caries and lung infections associated with cystic fibrosis.
XX
PS Example 1; Page 29; 33pp; English.
XX
CC The present invention relates to a new secreted salivary protein, zsig63.
CC The invention is useful for detecting in a test sample, the presence of
CC an antagonist or agonist of zsig63 protein activity. The invention is
CC also useful as an immunogen for producing an antibody to zsig63
CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC protein are useful for enhancing in vivo killing of target tissues.
CC Pharmaceutical composition comprising purified zsig63 polypeptide are
CC useful in the treatment of conditions associated with pathological
CC microbes, including bacterial, fungal and viral infections. High
CC expression of zsig63 in salivary gland suggests that anti-microbial
CC polypeptides are useful for treatment of dental caries (tooth decay),
CC periodontal disease, thrush and gastrointestinal disease. Other
CC applications can be used in urinary tract infections, vaginal infections,
CC prevention of infection in skin and other epithelial wounds. The
CC polypeptides can be used to establish normal microflora and protect
CC against pathogenic colonisation and invasion. The invention is useful
CC when pro-inflammatory activity is desired. Applications for such pro-
CC inflammatory activity include the treatment of chronic tissue damage,
CC particularly in areas having a limited or damaged vascular system e.g.,
CC damage in extremities associated with diabetes. Antagonists to zsig63
CC polypeptides may be useful as anti-inflammatory agents. The invention is
CC useful for the treatment of patients having incompetent immune system,
CC such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC that have undergone chemotherapy, radiation treatment. The invention is
CC also useful for the treatment of lung infections associated with cystic
CC fibrosis and its agonists or antagonists are useful for aiding digestion.
CC The present nucleic acid sequence represents a PCR primer that was used
CC in the methods of the invention for identification of zsig63
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 2803
Db 26 TAAAAA 1

RESULT 598
AAD45055/c
ID AAD45055 standard; DNA; 26 BP.
XX
AC AAD45055;
XX
XX
DT 27-DEC-2002 (first entry)
XX

DE ZC7764a primer used in the identification of human zsig63 DNA.
XX
KW Human; secreted salivary protein; zsig63 protein; host defense protein;
KW immune modulating factor; antipathogenic; cell-cell signalling molecule;
KW growth factor; cytokine; growth factor hormone activity; dental caries;
KW infection; tooth decay; periodontal disease; gastrointestinal disease;
KW thrush; urinary tract infection; vaginal infection; diabetes; obesity;
KW anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
KW gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KW forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.
XX
OS Homo sapiens.
XX
XX US2002090677-A1.
PN
XX 11-JUL-2002.
PD
XX
XX 03-AUG-2001; 2001US-00923236.
PF
XX 17-MAR-1999; 99US-0124820P.
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLE/) ADLER D A.
PA (SHEP/) SHEPPARD P O.
XX
XX Adler DA, Sheppard PO;
PI
XX WPI; 2002-642378/69.
DR
XX
XX Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
PT agent for treating microbial infection, dental caries, periodontal
PT disease, thrush gastrointestinal disease, and for aiding digestion.
XX
PS Example 1; Page 30; 33pp; English.
XX
CC The invention relates to human secreted salivary polypeptide designated
CC as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
CC can be used in detecting agonists and antagonists of its activity, and is
CC also useful as a host defense polypeptide, immune modulating factor,
CC antipathogenic polypeptide, cell-cell signalling molecule, growth factor,
CC cytokine, or as secreted extracellular matrix associated proteins with
CC growth factor hormone activity. It is useful for treating conditions
CC associated with pathological microbes, including bacterial, fungal and
CC viral infections, for treating dental caries (tooth decay), periodontal
CC disease, thrush and gastrointestinal disease, for treating urinary tract
CC infection, vaginal infection and for preventing infection in skin and
CC other epithelial wounds. zsig63 is useful for establishing normal
CC microflora and protect against pathogenic colonisation and invasion, for
CC treating chronic tissue damage e.g. damage in extremities associated with
CC diabetes and useful as anti-inflammatory agents. It is useful as a marker
CC of lung dysfunction, salivary gland dysfunction, or dysfunction of
CC prostate gland. It is also therapeutically useful for aiding digestion.
CC Polynucleotides of the invention are used in gene therapy for increasing
CC or inhibiting zsig63 activity, for detecting abnormalities on human
CC chromosome 4 associated with disease or other human traits and as
CC diagnostics in forensic DNA profiling. Sequences of the invention are
CC useful for stimulating proliferation or differentiation of cardiac
CC myocytes, for proliferation or differentiation of adipocytes and for
CC inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The
CC present sequence is a primer used in the identification of human zsig63
CC DNA
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 2803
Db 26 TAAAAA 1

RESULT 598
AAD45055/c
ID AAD45055 standard; DNA; 26 BP.
XX
AC AAD45055;
XX
XX
DT 27-DEC-2002 (first entry)
XX

XX	ABX93599;	XX	Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
AC		PI	Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX	28-MAY-2003 (first entry)	XX	WPI; 2002-040208/05.
DT		XX	New zalphall1 ligand polypeptides and polynucleotides, useful for
XX	Human zsig63 PCR/sequencing primer ZC7764a.	PT	stimulating proliferation, activation, differentiation and/or induction
DE		PT	of inhibition of specialized cell function, or for stimulating an
XX		PT	antigenic response.
XX	ss; PCR; zsig63; adhesin; salivary gland; dental carries;	XX	Example 7; Col 139; 105pp; English.
KW	periodontal disease; thrush; gastrointestinal disease; epithelial wound;	XX	The present invention relates to the isolation of a novel cytokine,
KW	urinary tract infection; vaginal infection; skin infection; primer;	CC	zalphall1 Ligand and the polynucleotide encoding it. The invention also
KW	pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;	CC	gives the sequence for the zalphall1 receptor and the polynucleotide
KW	lung infection; cystic fibrosis; lung dysfunction; digestive;	CC	encoding it. The zalphall1 Ligand polypeptide stimulates proliferation of
KW	salivary gland carcinoma; Pneumocystis carinii infection; emphysema;	CC	natural killer (NK) cells or NK cell progenitors, the activation of NK
KW	chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;	CC	cells, proliferation of T-cells, proliferation of B-cells stimulated with
KW	cell culture media; gene therapy; human chromosome 4q12-4q13;	CC	anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
KW	dentinogenesis imperfecta; dentin dysplasia type II.	CC	reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
OS	Synthetic.	CC	zalphall1 Ligand polypeptide is also useful in preparing antibodies that
XX		CC	bind to zalphall1 Ligand epitopes. The zalphall1 Ligand polynucleotides can
PN	US2002173027-A1.	CC	be used as probes or primers to clone regions of a zalphall1 Ligand gene,
XX		CC	and in gene therapy. Zalphall1 Ligand may also be used to identify
PD	21-NOV-2002.	CC	inhibitors of its activity, to enhance the generation of anti-tumour
XX		CC	responses with or without the infusion of donor lymphocytes, and to
PF	03-AUG-2001; 2001US-00922469.	CC	activate or stimulate the immune system. The present sequence represents
XX		CC	a sequencing primer used to sequence cDNA clones in the isolation of
PR	17-MAR-1999; 99US-0124820P.	XX	human zalphall1 Ligand
PR	17-MAR-2000; 2000US-00527345.	XX	Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
XX		XX	Query Match 0.7%; Score 19.6; DB 1; Length 26;
PA	(ADLE/) ADLER D A.	XX	Best Local Similarity 84.6%; Pred. No. 9.5e+02;
PA	(SHEP/) SHEPPARD P O.	XX	Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX	Adler DA, Sheppard PO;	QY	2778 TACAATTGAAAAAATAAAAAAAAAAAAAA 2803
PI		DB	26 TAAAAAATAAAAAAAAAAAAAA 1
XX	WPI; 2003-328428/31.		
DR			
XX	Novel isolated zsig63 polypeptide, member of the adhesin family, useful		
PT	for treating dental carries, periodontal disease, thrush,		
PT	gastrointestinal disease, urinary tract infections, vaginal infections,		
PT	skin infections.		
XX			
PS	Example 1; Page 29; 32pp; English.		
XX	The invention relates to an isolated zsig63 polypeptide comprising at		
CC	least 90% identity to an amino acid sequence which comprises domain 1 of		
CC	zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also		
CC	included are the polynucleotide encoding zsig63, a zsig63 expression		
CC	vector, a cultured cell comprising the vector and expressing the protein,		
CC	a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-		
CC	126, 127-219 or 16-219 of zsig63 and an additional protein), using a		
CC	zsig63 reporter gene construct to identify zsig63 agonists, and producing		
CC	an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is		
CC	useful for detecting in a test sample, the presence of antagonist of		
CC	zsig63 protein activity. Zsig63 has antimicrobial activity and since		
CC	exhibits high expression in salivary gland, can be used for treating		
CC	dental carries, periodontal disease, thrush, and gastrointestinal		
CC	disease, urinary tract infections, vaginal infections, skin infections		
CC	and other epithelial wounds. The polypeptides can be used to establish		
CC	normal microflora and protect against pathogenic colonization and		
CC	invasion. Zsig63 can also be used for providing pro-inflammatory activity		
CC	for treating chronic, tissue damage particularly in areas having limited		
CC	or damaged vascular system, e.g. in diabetes, and for treating		
CC	immunocompromised AIDS patients or in individuals that have undergone		
CC	chemotherapy, radiation treatment, for treating lung infections e.g. in		
CC	cystic fibrosis. Detection of zsig63 polypeptide at relatively high		
CC	levels in the trachea may indicate that such polypeptides may serve as a		
CC	marker of lung dysfunction. Zsig63 is also useful in diagnosing		
CC	conditions associated with salivary gland or lung dysfunction including		
CC	salivary gland carcinoma, Pneumocystis carinii infection, emphysema,		
CC	chronic bronchitis, prostate dysfunctions such as prostate		
CC	adenocarcinoma, aiding digestion, and as components of defined cell		
CC	culture media and may be used to replace serum that is commonly used in		
CC	culture. The DNA is useful in gene therapy applications to increase or		
CC	inhibit zsig63 activity, and for detecting abnormalities on human		

```
CC chromosome 4 (e.g. 4ql2-4ql3, associated with dentinogenesis imperfecta,
CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The
CC present sequence is a primer used to isolate and sequence nucleic acids
CC encoding human zsig63
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match          0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TACAATTGAAAAA 2803
Db 26 TAAAAA 1

RESULT 601
AAN70276/c
ID AAN70276 standard; DNA; 26 BP.
XX
AC AAN70276;
XX
DT 03-OCT-2002 (revised)
DT 26-MAY-1991 (first entry)
XX
DE Sequence of scissile link probe MRC060 (HL).
XX
KW Hybridisation; probe; ss.
XX
OS Synthetic.
XX
PN EP227976-A.
XX
PD 08-JUL-1987.
XX
PF 04-DEC-1986; 86EP-00116906.
XX
PR 05-DEC-1985; 85US-00805279.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R, Crosby W, Robertson JG;
XX
DR WPI; 1987-186567/27.
XX
PT Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT linked by a scissile linkage.
XX
PS Example; p29; 46pp; English.
XX
CC The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC or RNA sequences in a test soln. The scissile link probes may be PL
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC Support). The differential liability of DNA and RNA may be exploited in a
CC heterogenous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

Query Match          0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 26 AAAAAA 1

RESULT 602
AAN70276/c
ID AAN70276 standard; DNA; 26 BP.
XX
AC AAN70276;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRC059.
XX
KW Probe MRC059; solid support; ribonuclease.
XX
OS Synthetic.
XX
FH Key
FT misc_feature 1.10
```

FT /tag= a /note= "deoxyribonucleotides."
FT /note= "deoxyribonucleotides."
FT 11. .14
FT /tag= b
FT /note= "ribonucleotides."
FT 15. .26
FT /tag= c
FT /note= "deoxyribonucleotides."
XX

PN WO8910415-A.
XX
PD 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R;
XX
PS WPI; 1989-339977/46.
XX

CC Detecting target nucleic acid molecules - using excess complementary
CC nucleic acid probes and nicking to complete a cycling sequence.
XX
PS Disclosure; Page 24; 34pp; English.

XX Probe MRCO59 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
SQ
Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA AAAAAAAAAAAAAA 2804
DE 26 AAAAAAAAAA AAAAAAAAAAAAAA 1

RESULT 604
AAN92242/c
ID AAN92242 standard; DNA; 26 BP.
XX
AC AAN92242;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)

XX SS probe MRCO60.
DE
XX Probe MRCO60; solid support; ribonuclease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .12 /tag= a
FT /note= "deoxyribonucleotides."
FT 13. .16
FT misc_feature /tag= b

FT /note= "ribonucleotides."
FT 17. .26
FT /tag= c
FT /note= "deoxyribonucleotides."
XX
PN WO8910415-A.
XX
PD 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R;
XX
PS WPI; 1989-339977/46.
XX

CC Detecting target nucleic acid molecules - using excess complementary
CC nucleic acid probes and nicking to complete a cycling sequence.
XX
PS Disclosure; Page 24; 34pp; English.

XX Probe MRCO60 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
SQ
Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA AAAAAAAAAAAAAA 2804
DB 26 AAAAAAAAAA AAAAAAAAAAAAAA 1

RESULT 605
AAF77536/c
ID AAF77536 standard; DNA; 26 BP.
XX
AC AAF77536;
XX
DT 23-MAY-2001 (first entry)
XX
DE CDNA library production method related oligonucleotide SEQ ID NO: 5.
XX
KW CDNA library production; SCLA; gene chip technology;
KW differential screening; pathological diagnosis; genetic identification;
KW single-cell cDNA library amplification; ds.
XX
OS Synthetic.
XX
PN US6197554-B1.
XX
PD 06-MAR-2001.
XX
PF 20-NOV-1998; 98US-00197951.
XX
PR 20-NOV-1998; 98US-00197951.
XX
PA (LINS/) LIN S.
PA (CHUO/) CHUONG C.

PA (YING/) YING S.
XX Lin S, Chuong C, Ying S;
PI WPI; 2001-243448/25.
XX
DR
XX
PT Generating a complete full-length cDNA library from single cells for use
PT in gene chip technology, involves reverse transcribing intracellular
PT mRNAs, adding polynucleotide tail and amplifying formed cDNAs.
XX
PS Disclosure; Col 11-12; 11pp; English.
XX
CC The present invention describes a method of producing full-length cDNA
CC libraries from single cells, designated single-cell cDNA library
CC amplification (SCLA). The method is useful in gene chip technology,
CC differential screening, pathological diagnosis, physiological prognosis
CC and genetic identification. No further information about this sequence is
CC given in the specification
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA AAAAAAAAAA AAAAAA 2804
Db ||| ||||| ||||| ||||| ||||| |||||
26 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1
RESULT 606
AAF23526/c
ID AAF23526 standard; DNA; 26 BP.
XX
AC AAF23526;
XX
DT 22-MAR-2001 (first entry)
XX
DE Primer #4.
XX
KW Primer; mRNA; amplification; ss.
XX
OS Unidentified.
XX
PN WO200075356-A1.
XX
PD 14-DEC-2000.
XX
PF 04-JUN-1999; 99WO-US012461.
XX
PR 04-JUN-1999; 99WO-US012461.
XX
PA (LINS/) LIN S.
PA (YING/) YING S.
PA (CHUO/) CHUONG C.
PA (WIDE/) WIDELITZ R B.
XX
PI Lin S, Ying S, Chuong C, Widelitz RB;
XX
DR WPI; 2001-061734/07.
XX
PT Generating amplified messenger RNA sequences from single cells, involves
PT cycling steps of reverse transcription, denaturation, double-stranded DNA
PT sequences and in vitro transcription.
XX
PS Disclosure; Page 17; 31pp; English.
XX
CC The present invention relates to generating amplified messenger RNAs with
CC polymerase reaction activity, comprising cycling steps of reverse
CC transcription, denaturation, double-stranded cDNA synthesis and in vitro
CC transcription. The invention is used for generating amplified mRNAs from
CC limited mRNAs from single cells
XX

SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA AAAAAAAAAA AAAAAA 2804
Db ||| ||||| ||||| ||||| ||||| |||||
26 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1
RESULT 607
AAD43853/c
ID AAD43853 standard; DNA; 26 BP.
XX
AC AAD43853;
XX
DT 14-NOV-2002 (first entry)
XX
DE Primer #2 used to illustrate the method of the invention.
XX
KW Single stranded polynucleotide tag; cleavage agent; gene expression;
KW primer; ss.
XX
OS Unidentified.
XX
PN WO200259357-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-DK000052.
XX
PR 24-JAN-2001; 2001DK-00000126.
PR 12-FEB-2001; 2001US-0267704P.
XX
PA (GENO-) GENOMIC EXPRESSION APS.
XX
PI Pedersen ML;
XX
DR WPI; 2002-636542/68.
XX
PT Obtaining single stranded polynucleotide tags from a biological sample,
PT for analyzing gene expression or diagnosing clinical conditions,
PT comprises employing nicking endonucleases that cleave complementary
PT strands.
XX
PS Example; Page 294; 302pp; English.
XX
CC The invention relates to a method for obtaining a single stranded
CC polynucleotide tag from a biological sample by cleaving one of the
CC complementary strands of a double stranded polynucleotide with a cleavage
CC agent capable of recognising a double stranded polynucleotide comprising
CC complementary strands and cleaving only one of the strands of the
CC polynucleotide in the process of generating a single stranded
CC polynucleotide tag. The method is useful for separating, analysing,
CC quantifying or obtaining single stranded polynucleotides comprising tags
CC originating partly, and preferably wholly from a source of DNA and/or RNA
CC in a sample comprising biological cells. The method is particularly for
CC analysing gene expression (expression profiling or differential gene
CC expression), or in diagnosing clinical conditions. The present sequence
CC is a primer used in the exemplification of the invention
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA AAAAAAAAAA AAAAAA 2804
Db ||| ||||| ||||| ||||| ||||| |||||
26 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1

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RESULT 608
ABZ24784/C
ID ABZ24784 standard; DNA; 26 BP.
XX
AC ABZ24784;
XX
DT 07-APR-2003 (first entry)
XX
DE Oligodeoxynucleic acid molecule ODN 24.
XX
KW Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
KW ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..26
FT /*tag= a
FT /mod_base= OTHER
FT /note= "thiophosphate backbone"
XX
PN WO200295027-A2.
XX
PD 28-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-EP005448.
XX
PR 21-MAY-2001; 2001AT-00000805.
XX
PA (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Lingnau K, Schellack C, Schmidt W;
XX
DR WPI; 2003-183880/18.
XX
XX New oligodeoxynucleic acid molecules useful for the preparation of
PT vaccine.
XX
PS Example 8; Page 32; 57pp; English.
XX
CC The present sequence is that of a thiosubstituted oligodeoxynucleic acid
CC (ODN) molecule, ODN 24, including deoxyuridine monophosphates. The
CC invention is based on the discovery that ODNs containing deoxyuridine
CC residues (U-ODNs) have an immunostimulatory effect comparable to, or in
CC many instances greater than, ODNs containing CpG motifs, producing higher
CC numbers of specific T cells to a given antigen. The U-ODNs do not induce
CC the systemic production of pro-inflammatory cytokines and, in contrast to
CC CpG ODNs, are not dependent on a specific motif or a palindromic
CC sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
CC Combining the U-ODN with an antigen strongly increases the potential of
CC the antigen to raise the protection/immune response of a vaccinated
CC individual. An example of the invention demonstrated the generation of a
CC specific immune response against a melanoma-derived peptide (see
CC ABP58360) by injection of mice with the peptide in combination with ODN
CC 24
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 1 T; 25 U; 0 Other;
XX
Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
DE 26 AAAAAA 1
RESULT 609
ACA62282/C
ID ACA62282 standard; DNA; 26 BP.
XX
AC ACA62282;
```

```

XX 12-AUG-2003 (first entry)
DT
XX Oligo (dT) primer #1.
DE
XX
KW ss; PCR; primer; antisense therapy; mRNA expression profile;
KW promoter containing primer.
XX
OS Synthetic.
XX
PN US2003022318-A1.
XX
PD 30-JAN-2003.
XX
PF 07-SEP-2001; 2001US-00949305.
XX
PR 25-JAN-2000; 2000US-00494212.
XX
PA (EPIC-) EPICLONE INC.
XX
PI Lin S, Ying S;
XX
DR WPI; 2003-479488/45.
XX
XX Improved polymerase thermocycling reaction for nucleic acid
PT amplification, by thermal cycling of promoter-linked nucleic acid
PT template synthesis and in vitro transcriptional amplification of nucleic
PT acid sequences.
XX
PS Example 4; Page 14; 28pp; English.
XX
CC The invention relates to an improved polymerase thermocycling reaction
CC (M1) for linear amplification of nucleic acid sequences, involves
CC denaturing a number of nucleic acid templates (I), combining the
CC denatured (I) with a promoter-containing primer (P1), a primer (P2), a
CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
CC polymerase, contacting P1 with (I) to generate a number of promoter-
CC containing templates, denaturing the promoter-containing templates to
CC generate a number of promoter-containing double-stranded DNA templates,
CC where the double-stranded nucleic acid templates are flanked by P1 in one
CC end and P2 in the other end of the other orientates, transcribing the
CC promoter-containing double-stranded DNA templates to form a number of
CC amplified RNA sequences, including the primer region of the promoter-
CC containing double-stranded DNA templates, contacting the amplified RNA
CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA
CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method
CC is useful for improved polymerase thermocycling reaction for linear
CC amplification of nucleic acid sequences, and thus for producing mRNA
CC expression profile of a cell by M1 to generate multiple copies of the
CC mRNA. M1 is also useful for determining aberrant protein production of
CC cells in a diseased state, by generating an expression profile by the
CC above method, of cells in both normal and diseased states, comparing the
CC expression profile of the cells in the normal and diseased states,
CC determining the differences in mRNA composition of the cell(s) in the
CC diseased state, isolating the mRNA sequences of cell(s) in the diseased
CC state that differ from mRNA in cell(s) in non-diseased state, amplifying
CC the isolated mRNA by M1, and determining aberrant protein function of the
CC protein coded for by the isolated mRNA. M1 is also useful for treating a
CC cell in a diseased state caused by aberrant protein production, by
CC determining protein expression of a cell in a diseased state, determining
CC the mRNA sequence for the aberrant proteins, synthesising an antisense
CC sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and
CC delivering a pharmaceutically effective dosage of a composition
CC comprising the anti-sense mRNA and a compatible lipid based biological
CC carrier. M1 is also useful for predicting the efficacy of a proposed drug
CC targeted against an aberrant protein, by determining aberrant protein
CC production of cell in a diseased state by the above method, amplifying
CC the aberrant protein by M1 and using recombinant techniques to determine
CC the effect of proposed drug on the aberrant protein. M1 is also useful
CC for differential screening of tissue-specific gene expression at a
CC cellular level, for preparing labeled RNA/DNA probes for a gene chip
```

CC technology, and for determining the efficacy of a drug regiment against a
CC gene or its cDNAs. The present sequence is an Oligo (dt) primer used to
CC produce second strand cDNA in the method of the invention
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 610
AAT99265
ID AAT99265 standard; DNA; 26 BP.
XX
AC AAT99265;

XX 15-APR-1998 (first entry)

DE Human PUR-alpha gene primer PDT-01.

XX PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW cancer; PCR; primer; amplification.
XX Synthetic.

OS Homo sapiens.

XX US5672479-A.

PN 30-SEP-1997.

XX 07-JUN-1995; 95US-00486421.

XX 28-AUG-1992; 92US-00938189.

PR 02-FEB-1993; 93US-00014943.

PR 06-JUN-1995; 95US-00470911.

XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX Bergemann AD, Johnson EM;

XX WPI; 1997-488859/45.

XX Assays for PUR protein ligands or modulators - using immobilised PUR
PT protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX Disclosure; Col 9; 64pp; English.

XX The primers AAT99265-T99269 were used to PCR amplify and isolate the
CC complete sequence of the human PUR-alpha gene (AAT99264). The PUR
CC sequence can be used to identify chemical or biological compounds that
CC bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may
CC be used to treat hyperproliferative diseases such as cancer
XX
SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2159 TTTCTCCTTTT 2184
Db 1 TATCTGCAGTTT 26

RESULT 611
AAT93819
ID AAT93819 standard; DNA; 26 BP.
XX

AC AAT93819;
XX 25-MAR-2003 (revised)
DT 24-FEB-1998 (first entry)
XX

DE Antitumoural phosphodiester oligonucleotide 9 with cytotoxic activity.
XX
KW Phosphodiester; selective binding; cell viability; growth;
KW tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW lymphoblastic tumour; ss.
XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 1..26
FT /*tag= a
FT /note= "phosphodiester oligonucleotide"

XX WO9720924-A1.

XX 12-JUN-1997.

XX 04-DEC-1996; 96WO-EP005388.

XX 04-DEC-1995; 95IT-MI002539.

XX (SAIC-) SAICOM SRL.

XX Scaggianti B, Quadrioglio F;

XX WPI; 1997-319771/29.

XX New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT selective cytotoxic effect on tumour cells, for treating both solid and
PT liquid tumours.

XX Claim 10; Page 5; 38pp; English.

XX Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC generic formula, in the 3'-5' or 5'-3' direction: (CaTa')a'-(GbTb')b'-(
CC (GcTc')c'-(GdTd')d'-(GeTe')e'-(Gftf')f'-(Ggtg')g'-'N', where: N and
CC N' = T or G, equal or different from each other; x = 0-8, equal or
CC different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC 16, equal or different from each other; The oligonucleotides are believed
CC to selectively bind and sequester some proteins which are essential to
CC the viability and growth of tumoural cell line. They have specific and
CC selective cytotoxic activity against tumour cells, and can be used for
CC treating tumours of the liquid type, in particular of lymphoblastic
CC origin, and of solid type, in particular lymphomas. The present
CC phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC reduced growth of CCRF-CEM tumoural cells by 76%, which is detectable 48
CC hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX

SQ Sequence 26 BP; 0 A; 0 C; 2 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2156 TTTTCTCCTTTT 2181
Db 1 TTTTCTGTTT 26

RESULT 612
AAV12482/c
ID AAV12482 standard; DNA; 26 BP.
XX
AC AAV12482;
XX

DT 15-MAY-1998 (first entry)

PR 28-AUG-1992; 92US-00938189.
XX 02-FEB-1993; 93US-00014943.
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX Bergemann AD, Johnson EM;
XX WPI; 1998-321632/28.
DR PUR protein and its fragments - that inhibit PUR protein binding to PUR
XX element or other proteins.
PS Disclosure; Col 9; 63pp; English.
XX
CC This is the nucleotide sequence of the PUR psecific PCR primer used for
CC amplification in the method of the invention, involving the use of the
CC PUR protein and its fragments, which inhibit PUR protein binding to PUR
CC element or other proteins. Inhibitors of PUR activity may be useful for
CC treating viral infections and hyperproliferative diseases such as cancer
XX
SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTTTTTTTTTTTTTTTTTT 2184
Db 1 TATCTGCAGTTTTTTTTTTTTTTTTTT 26

RESULT 615
AAX04087
ID AAX04087 standard; DNA; 26 BP.
XX
AC AAX04087;
XX
DT 12-APR-1999 (first entry)
DE PUR-alpha RACE reaction primer PDT-01.
XX
KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW monoclonal antibody; identification; characterisation; RACE primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5869622-A.
XX
PD 09-FEB-1999.
XX
PF 07-JUN-1995; 95US-00486809.
XX
PR 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
DR WPI; 1999-152881/13.
XX
PT Monoclonal antibody specific for PUR protein - useful for treating
PT cancer.
XX
PS Example; Col 9; 64pp; English.
XX
CC The present invention describes a monoclonal antibody that specifically
CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR
CC protein and neutralise PUR activity may be used to treat
CC hyperproliferative diseases such as cancer. PUR antibodies may be used
CC diagnostically to detect aberrant expression of the PUR protein and/or

CC mutations in the PUR gene. The present sequence represents a PUR-alpha
CC RACE primer which is used in an example from the present invention
XX
SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2159 TTCTCCTTTTTTTTTTTTTTTTTTTT 2184
Db 1 TATCTGCAGTTTTTTTTTTTTTTTTTT 26

RESULT 616
AAX30018/c
ID AAX30018 standard; DNA; 26 BP.
XX
AC AAX30018;
XX
DT 16-JUN-1999 (first entry)
XX
DE Precircle DNA oligonucleotide SEQ ID NO:5.
XX
KW Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.
XX
OS Synthetic.
XX
PN WO9909216-A2.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1998; 98WO-US016776.
XX
PR 13-AUG-1997; 97US-00910632.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Kool ET;
XX
DR WPI; 1999-181062/15.
XX
PT New detectably labelled oligonucleotide multimer, comprising multiple
PT contiguous copies of a repeated oligonucleotide - useful for detecting
PT target molecules in diagnosis and medicinal applications.
XX
PS Example 2; Page 41; 103pp; English.
XX
CC The present invention describes a detectably labelled oligonucleotide
CC multimer, comprising multiple contiguous copies of a repeated
CC oligonucleotides. The detectably labelled oligonucleotide multimer is
CC useful for detecting a target molecule. Oligonucleotide multimers may be
CC produced in sufficient quantity to be useful for diagnostic and medical
CC applications. The multimers are useful for affinity labelling of
CC proteins, and for signal amplification in highly sensitive affinity
CC capture and sequence identification applications. The method provides a
CC faster, cheaper and simpler way for large-scale production of DNA and RNA
CC oligomers and multimers. The incorporation of labels enables the
CC oligonucleotide multimers to be useful in diagnostics and medicine. The
CC present sequence represents an oligonucleotide used in an example from
CC the present invention
XX
SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2168 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2193
Db 26 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

PR 05-DEC-1985; 85US-00805279.
XX (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R, Crosby W, Robertson JG;
XX WPI; 1987-186567/27.
XX
XX Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT linked by a scissile linkage.
PT
XX Example; p29; 46pp; English.
XX
CC The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC or RNA sequences in a test soln. The scissile link probes may be PL
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC Support). The differential liability of DNA and RNA may be exploited in a
CC heterogenous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions.. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 620
AAN92240/c
ID AAN92240 standard; DNA; 27 BP.
XX
AC AAN92240;
XX
XX 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRCO46.
XX
KW Probe MRCO46; solid support; ribonuclease.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 1..10 /tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature 11..16 /tag= b
FT /note= "ribonucleotides."
FT misc_feature 17..27 /tag= c
FT /note= "deoxyribonucleotides."
XX
PN WO8910415-A.
XX
XX 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R;

XX WPI; 1989-339977/46.
XX
PT Detecting target nucleic acid molecules - using excess complementary
PT nucleic acid probes and nicking to complete a cycling sequence.
XX
PS Disclosure; Page 24; 34pp; English.
XX
CC Probe MRCO46 is bound by a permanent linkage to a solid support at its 3'
CC end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PR field.)
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 621
AAN92247/c
ID AAN92247 standard; DNA; 27 BP.
XX
AC AAN92247;
XX
XX 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRCO71.
XX
KW Probe MRCO71; solid support; ribonuclease.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 1..15 /tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature 16..17 /tag= b
FT /note= "ribonucleotides."
FT misc_feature 18..27 /tag= c
FT /note= "deoxyribonucleotides."
XX
PN WO8910415-A.
XX
XX 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R;
XX
DR WPI; 1989-339977/46.
XX
PT Detecting target nucleic acid molecules - using excess complementary

PT nucleic acid probes and nicking to complete a cycling sequence.

XX Disclosure; Page 24; 34pp; English.

PS Probe MRCO71 is bound by a hydrolysable linkage to a solid support at its

XX 3' end. It is used by reacting excess probe with a target nucleic acid;

CC nicking hybridised probe at least once within a predetermined sequence to

CC form 2 or more probe fragments hybridised to the target sequence, which

CC results in the probe fragments becoming hybridised to another probe; and

CC identifying probe fragments, so detecting the target sequence. The probe

CC can react with target sequence to complete a cycling sequence. Using this

CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can

CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg

CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

SQ Query Match 0.7%; Score 19.6; DB 1; Length 27;

Best Local Similarity 84.6%; Pred. No. 1e+03;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804

Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 622

AAQ40854

ID AAQ40854 standard; DNA; 27 BP.

XX AAQ40854;

AC 23-SEP-1993 (first entry)

XX DNA sequence used in DNA replication method.

DE ss.

XX Synthetic.

OS JP05103673-A.

PN 27-APR-1993.

XX 26-AUG-1991; 91JP-00240525.

PF 26-AUG-1991; 91JP-00240525.

XX (UYAR-) UNIV ARIZONA.

PA WPI; 1993-171830/21.

XX Replication of DNA - useful in genetic engineering and medical

XX applications.

PT Disclosure; Page 20; 20pp; Japanese.

PS The sequence is given in the disclosure to illustrate the invention

XX Sequence 27 BP; 27 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

SQ Query Match 0.7%; Score 19.6; DB 1; Length 27;

Best Local Similarity 84.6%; Pred. No. 1e+03;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 623

AAF99706/c

ID AAF99706 standard; DNA; 27 BP.

XX AAF99706;

AC 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #822.

DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;

XX immunostimulatory; tumour; viral infection; bacterial infection;

XX fungal infection; parasitic infection; cancer; asthma;

XX infectious disease; allergy; immune deficiency; phosphorothioate; ss.

OS Synthetic.

XX WO200122972-A2.

PN 05-APR-2001.

XX 25-SEP-2000; 2000WO-US026383.

PF 25-SEP-1999; 99US-0156113P.

XX 27-SEP-1999; 99US-0156135P.

PR 23-AUG-2000; 2000US-0227436P.

XX (IOWA) UNIV IOWA RES FOUND.

PA (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

PI WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma

XX using immunostimulatory Py-rich and TG nucleic acids.

PT Claim 101; Page 56; 338pp; English.

XX The present invention relates to a method for stimulating an immune

CC response. The method comprises administering an immunostimulatory nucleic

CC acid to a non-rodent subject in sufficient quantity to stimulate an

CC immune response. The present sequence is one such immunostimulatory

CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich

CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects

CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae

CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,

CC haemophilus, campylobacter, clostridium, Escherichia coli and/or

CC staphylococcus), fungal antigens and/or parasitic antigens. The method is

CC also useful for preventing cancer, asthma, infectious disease, allergy or

CC immune deficiency. The present sequence can also be used to redirect a

CC Th2 to a Th1 immune response and to activate immune cells. Note: the

CC present sequence may have a phosphorothioate backbone

XX Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

SQ Query Match 0.7%; Score 19.6; DB 1; Length 27;

Best Local Similarity 84.6%; Pred. No. 1e+03;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804

Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 624

ABS78427/c

ID ABS78427 standard; DNA; 27 BP.

XX ABS78427;

AC 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #911.

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophilic joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
PA Bratzler RL;
XX
PI WPI; 2002-566690/60.
XX
DR Inhibiting angiogenesis in a subject, involves administering at least one
XX antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 35; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAA 2
RESULT 625
ABL39406/c
ID ABL39406 standard; DNA; 27 BP.
XX
AC ABL39406;
XX
XX
DT 16-APR-2002 (first entry)
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 842.
DE Immunostimulatory nucleic acid
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..29

FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX WO200197843-A2.
XX 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 310; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAA 2
RESULT 626
ACH03245/c
ID ACH03245 standard; DNA; 27 BP.
XX
AC ACH03245;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #880.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.

XX Krieg AM, Berg DJ;
PI WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.

XX Disclosure; Page 32; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid

XX Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 4;

QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAAAAAA 2

RESULT 627
ADB37208/c
ID ADB37208 standard; DNA; 27 BP.

XX ADB37208;
AC 04-DEC-2003 (first entry)
DT Immunostimulatory nucleic acid #822.

DE ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX hypo-responsive subject; immunostimulatory.

XX Synthetic.

XX US2003087848-A1.

XX 08-MAY-2003.

XX 02-FEB-2001; 2001US-00776479.

XX 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2003-657977/62.

XX Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure; Page 17; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or

CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.

XX Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
SQ Query Match 0.7%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 4;

QY 2779 AGAATTGAAAAA 2804
Db 27 AAAAAAAAAA 2

RESULT 628
AAQ05003/c
ID AAQ05003 standard; DNA; 29 BP.

XX AAQ05003;

XX 25-MAR-2003 (revised)
DT 31-OCT-1990 (first entry)

XX Sequence binding to and inhibiting the GSTpi gene.

XX C-myc; cancer; HIV-1; AIDS; collagenase; Alzheimers disease; EGF;
KW epidermal growth factor; GSTpi; HMGCoA; thalassemia;
KW Herpes simplex virus; nerve growth factor receptor; globin; ss.

XX Synthetic.

XX EP375408-A.

XX 27-JUN-1990.

XX 20-DEC-1989; 89EP-00313391.

XX 20-DEC-1988; 88US-00287359.

XX (BAYU) BAYLOR COLLEGE MEDICINE.
PA (HOGA/) HOGAN M E.

XX Hogan ME, Kessler DJ;

XX WPI; 1990-195509/26.

XX Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-
PT linear triplex to control transcription process in gene-specific fashion.

XX Claim 39; Page 30; 40pp; English.

XX Sequence forms triplex with the double stranded target sequence with G
CC binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel
CC orientation and when targeted to a specific sequence will deactivate it.
CC This allows for growth inhibition in cancerous cells; manipulation of
CC cellular structural protein content; inhibition of IL-2 chain receptor;
CC disarming plaque formation in Alzheimer's disease; inhibiting EGF gene;
CC modulating cholesterol synthesis through the HMGCoA gene; suppressing NGF
CC gene expression; arresting HSV-1 replication and suppressing Beta- globin
CC expression in thalassemia and sickle cell anaemia patients. (Updated on
CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC field.)

XX Sequence 29 BP; 0 A; 0 C; 0 G; 29 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 29;
Best Local Similarity 84.6%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 4;

QY 2779 AGAATTGAAAAA 2804

Db 29 ||||| 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 629
AAA94315
ID AAA94315 standard; DNA; 29 BP.
XX
AC AAA94315;
XX
DT 11-JAN-2001 (first entry)
XX
DE RNA-protein fusion oligonucleotide 30-P.
XX
KW RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 29
FT /*tag= a
FT /mod_base= OTHER
FT /note= "attached to puromycin, a peptide acceptor"
XX
PN WO200047775-A1.
XX
PD 17-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US002589.
XX
PR 09-FEB-1999; 99US-00247190.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI S zostak JW, Roberts RW, Liu R;
XX
DR WPI; 2000-533022/48.
XX
PT Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
XX
PS Disclosure; Page 43; 121pp; English.
XX
CC The present sequence is one of a number of oligonucleotides which were
CC used for the generation of RNA-protein fusions, including fusions having
CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC and in vitro or in situ translation of an mRNA molecule with a peptide
CC acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC under high salt conditions to produce a protein library. This method is
CC useful for improving or altering existing proteins, as well as for
CC isolating new proteins and nucleic acid or small molecule targets. It may
CC also be used to improve human or humanised single-chain antibodies for
CC the treatment of a number of diseases. The method is useful for the
CC isolation of proteins with specific binding properties, for screening
CC cDNA libraries and cloning new genes on the basis of protein-protein
CC interactions. Unlike prior art, the new method does not rely on
CC maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC complex, which is very fragile and is therefore of limited use. The
CC method does not rely on topological links between the protein and the
CC nucleic acid so that the information of the protein is retained and can
CC be recovered in readable, nucleic acid form
XX
SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 29;
Best Local Similarity 84.6%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAAAAAAAAA 2804
||| |||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 630
AAS00066
ID AAS00066 standard; DNA; 29 BP.
XX
AC AAS00066;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synthetic branched encoding molecule sequence.
XX
KW Addressing element; microarray; protein display;
KW branched encoding molecule; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 9..10
FT /*tag= a
FT /mod_base= OTHER
FT /note= "AXA, where X is a branching monomer, linked to
FT nucleotide 16 of sequence in AAS00065 via a (Hexaethylene
FT oxide)n linkage"
FT modified_base 30
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Other= Covalently linked to puromycin"
XX
PN WO200116352-A1.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023414.
XX
PR 27-AUG-1999; 99US-0151261P.
XX
PA (PHYL-) PHYLLOS INC.
XX
PI Kuimelis RG;
XX
DR WPI; 2001-183261/18.
XX
PT Encoding and sorting in vitro translated proteins, useful for the
PT identification of desired binding partners, comprises attaching a nucleic
PT acid linker to the protein and binding an encoding molecule to the
PT linker.
XX
PS Example 3; Fig 9B; 48pp; English.
XX
CC The sequence represents part of a branched encoding molecule used in
CC methods to hybridise a capture probe to the addressing element of a DNA
CC linker attached to an in vitro translated protein, in order to immobilise
CC the protein to a solid support. The new methods are useful for tagging or
CC encoding in vitro translated proteins with unique and minimal encoding
CC molecules and sorting these molecules onto solid supports. They are also
CC useful for the identification of a desired binding partner. The method
CC allows the use of pre-made sets of universal encoding molecules, such as
CC nucleic acid(s) (analogues). These can be used in conjunction with
CC corresponding universal microarrays or sets of microparticles to create
CC new protein display systems which are flexible, modular, scalable and
CC cost effective. The method allows the use of nucleic acid analogue which
CC are not susceptible to enzymatic incorporation or polymerisation and are
CC superior to conventional DNA/RNA. The proteins can also be labelled with
CC fluorescent groups which can be used to monitor the protein in real time.
CC The absence of RNA is advantageous as they can adopt secondary structures
CC which are difficult to predict and can interfere with hybridisation steps
CC and protein folding/function
XX
SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 29;

RESULT 632
AAK98637
ID AAK98637 standard; DNA; 29 BP.
XX
XX

Sequence of scissile link probe MRC064 (HL).
Hybridisation: probe; ss.

RESULT 632
AAK98637
ID AAK98
XX

OS Synthetic.
XX EP227976-A.
PN
XX
PD 08-JUL-1987.
XX
XX
PF 04-DEC-1986; 86EP-00116906.
XX
PR 05-DEC-1985; 85US-00805279.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R, Robertson JG;
XX
DR WPI; 1987-186567/27.
XX
PT Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT linked by a scissile linkage.
XX
XX Example; p29; 46pp; English.
PS
XX The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC or RNA sequences in a test soln. The scissile link probes may be PL
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC support). The differential liability of DNA and RNA may be exploited in a
CC heterogeneous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5
RESULT 634
AAN92243/C
ID AAN92243 standard; DNA; 30 BP.
XX
AC AAN92243;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRCO64.
XX
KW Probe MRCO64; solid support; ribonuclease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .12
FT /tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature 13. .20
FT /tag= b
FT /note= "ribonucleotides."
FT misc_feature 21. .30
FT /tag= c
FT /note= "deoxyribonucleotides."
XX
PN W08910415-A.
XX
PD 02-NOV-1989.

XX 29-APR-1988; 88US-00187814.
PF
XX
PR 29-APR-1988; 88US-00187814.
XX
XX (MEIO-) MEIOGENICS INC.
PA
XX
PI Duck P, Bender R;
XX
DR WPI; 1989-339977/46.
XX
PT Detecting target nucleic acid molecules - using excess complementary
PT nucleic acid probes and nicking to complete a cycling sequence.
XX
PS Disclosure; Page 24; 34pp; English.
XX
CC Probe MRCO64 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe, and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5
RESULT 635
AAQ36302/C
ID AAQ36302 standard; DNA; 30 BP.
XX
AC AAQ36302;
XX
DT 25-MAR-2003 (revised)
DT 07-JUN-1993 (first entry)
XX
DE GST3anti, for GSTpi gene target sequence.
XX
KW Glutathione-s-transferase pi; cancer; drug resistance; chemotherapy;
KW sensitisation; triplex; target; duplex; ss.
XX
OS Synthetic.
XX
PN US5176996-A.
XX
PD 05-JAN-1993.
XX
PF 22-DEC-1989; 89US-00453532.
XX
PR 20-DEC-1988; 88US-00287359.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Hogan ME, Kessler DJ;
XX
DR WPI; 1993-035718/04.
XX
PT Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT which bind to target sequence in duplex DNA forming colinear triplex by
PT binding to major groove.
XX

KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX Synthetic.
OS
XX WO200122972-A2.
PN
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
DR
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Example 6; Page 60; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA AAAAAAAAAA AAAAAA 2804
Db 1 AAAAAAAAAA AAAAAAAAAA AAAAAA 26

RESULT 639
AAF99888/c
ID AAF99888 standard; DNA; 30 BP.
XX
AC AAF99888;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #1004.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
OS Synthetic.
XX
PN WO200122972-A2.

XX 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
DR
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Example 6; Page 60; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA AAAAAAAAAA AAAAAA 2804
Db 30 AAAAAAAAAA AAAAAAAAAA AAAAAA 5

RESULT 640
ABK10416
ID ABK10416 standard; DNA; 30 BP.
XX
AC ABK10416;
XX
DT 21-MAY-2002 (first entry)
XX
DE Synthetic primer sequence 5'-A30-3'.
XX
KW ss; 5'-A30-3'; double stranded DNA generation; promiscuous base;
KW target molecule; primer.
XX
OS Synthetic.
XX
PN US6326143-B1.
XX
PD 04-DEC-2001.
XX
PF 22-MAY-1998; 98US-00083123.
XX
PR 22-NOV-1996; 96WO-EP005149.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Orum H, Seeger C;

XX WPI; 2002-214947/27.

XX Determining an analyte in a sample, for generating multiple double

XX stranded nucleic acids, comprises employing a single primer sequence with

XX a nucleobase sequence having affinity to the sequence contained in a

XX target nucleic acid.

XX Example 1; Col 14; 25pp; English.

XX The invention relates to determining an analyte in a sample comprising

XX (a) providing a target nucleic acid comprising a region A, a nucleobase

XX sequence B, and a sequence I linked to the 5' terminus of the nucleobase

XX sequence B, where the nucleobase sequence B is not specific for the

XX analyte, and the region A specifically binds to the analyte, (b) binding

XX the target nucleic acid to the analyte, separating the analyte bound to

XX the target nucleic acid from the remaining part of the sample, (d)

XX hybridising a primer to the target nucleic acid, where the primer

XX comprises a nucleobase sequence B', and the nucleobase sequence B'

XX hybridises to the nucleobase sequence B, (e) elongating the hybridised

XX primer to produce an elongation product E using the target nucleic acid

XX as a template and using nucleotides, where at least 30 % of the

XX nucleotides contain at least one promiscuous base which is capable of

XX base pairing with each of adenine, guanine, cytosine, and thymine, (f)

XX separating the target nucleic acid from the elongation product E, (g)

XX hybridising a further primer which comprises the nucleobase sequence B'

XX to the elongation product E, where the elongation product E is capable of

XX acting as a template for the elongation of the further primer, (h)

XX elongating the hybridised further primer of step (g) to produce an

XX elongation product E' using the elongation product E as a template and

XX using nucleotides, where at least 30 % of the nucleotides contain at

XX least one promiscuous base, (i) separating the elongation product E from

XX the elongation product E', (j) hybridising a further primer comprising a

XX nucleobase sequence B' to the target nucleic acid or the elongation

XX product E, (k) elongating the further primer of step (j) to produce

XX another elongation product E using the target nucleic acid or elongation

XX product E as a template and using nucleotides, where at least 30 % of the

XX nucleotides contain at least one promiscuous base, (l) separating product

XX E of step (k) from the target nucleic acid or elongation product E, (m)

XX optionally repeating steps (g) - (l) a sufficient number of times to

XX generate a desired amount of double stranded nucleic acids and (n)

XX determining the elongation product E and/or elongation product E' as a

XX measure of the presence or amount of the analyte, where the lengths of

XX the sequence I and the nucleobase sequence B are chosen such that, when

XX the further primer hybridises to the elongation product E in step (g),

XX the further primer spans a sequence formed by elongation of the

XX hybridised primer of step (e) and overlaps at least a part of the 3'

XX region of the hybridized primer of step (e) by an overlap length. The

XX method is useful for determining an analyte in a sample. In particular, the

XX method is useful for generating multiple double stranded nucleic acids.

XX The present sequence is a primer molecule used to exemplify the method of

XX the invention

XX Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

XX Query Match 0.7%; Score 19.6; DB 1; Length 30;

XX Best Local Similarity 84.6%; Pred. No. 1.3e+03;

XX Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804

Db 1 AAAAAA 26

RESULT 641

ABK10412/c

ID ABK10412 standard; DNA; 30 BP.

XX AC ABK10412;

XX AC ABK10412;

DT 21-MAY-2002 (first entry)

XX DE Synthetic primer sequence 5'-T30-3'.

ss; 5'-T30-3'; double stranded DNA generation; promiscuous base;

target molecule; primer.

Synthetic.

US6326143-B1.

04-DEC-2001.

22-MAY-1998; 98US-00083123.

22-NOV-1996; 96WO-EP005149.

(HOFF) ROCHE DIAGNOSTICS GMBH.

Orum H, Seeger C;

WPI; 2002-214947/27.

Determining an analyte in a sample, for generating multiple double

stranded nucleic acids, comprises employing a single primer sequence with

a nucleobase sequence having affinity to the sequence contained in a

target nucleic acid.

Example 1; Col 14; 25pp; English.

The invention relates to determining an analyte in a sample comprising

(a) providing a target nucleic acid comprising a region A, a nucleobase

sequence B, and a sequence I linked to the 5' terminus of the nucleobase

sequence B, where the nucleobase sequence B is not specific for the

analyte, and the region A specifically binds to the analyte, (b) binding

the target nucleic acid to the analyte, separating the analyte bound to

the target nucleic acid from the remaining part of the sample, (d)

hybridising a primer to the target nucleic acid, where the primer

comprises a nucleobase sequence B', and the nucleobase sequence B'

hybridises to the nucleobase sequence B, (e) elongating the hybridised

primer to produce an elongation product E using the target nucleic acid

as a template and using nucleotides, where at least 30 % of the

nucleotides contain at least one promiscuous base which is capable of

base pairing with each of adenine, guanine, cytosine, and thymine, (f)

separating the target nucleic acid from the elongation product E, (g)

hybridising a further primer which comprises the nucleobase sequence B'

to the elongation product E, where the elongation product E is capable of

acting as a template for the elongation of the further primer, (h)

elongating the hybridised further primer of step (g) to produce an

elongation product E' using the elongation product E as a template and

using nucleotides, where at least 30 % of the nucleotides contain at

least one promiscuous base, (i) separating the elongation product E from

the elongation product E', (j) hybridising a further primer comprising a

nucleobase sequence B' to the target nucleic acid or the elongation

product E, (k) elongating the further primer of step (j) to produce

another elongation product E using the target nucleic acid or elongation

product E as a template and using nucleotides, where at least 30 % of the

nucleotides contain at least one promiscuous base, (l) separating product

E of step (k) from the target nucleic acid or elongation product E, (m)

optionally repeating steps (g) - (l) a sufficient number of times to

generate a desired amount of double stranded nucleic acids and (n)

determining the elongation product E and/or elongation product E' as a

measure of the presence or amount of the analyte, where the lengths of

the sequence I and the nucleobase sequence B are chosen such that, when

the further primer hybridises to the elongation product E in step (g),

the further primer spans a sequence formed by elongation of the

hybridised primer of step (e) and overlaps at least a part of the 3'

region of the hybridized primer of step (e) by an overlap length. The

method is useful for determining an analyte in a sample. In particular, the

method is useful for generating multiple double stranded nucleic acids.

The present sequence is a primer molecule used to exemplify the method of

the invention

Sequence 30 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;

Best Local Similarity 84.6%; Pred. No. 1.3e+03;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804

Db 1 AAAAAA 26

RESULT 641

ABK10412/c

ID ABK10412 standard; DNA; 30 BP.

XX AC ABK10412;

XX AC ABK10412;

DT 21-MAY-2002 (first entry)

XX DE Synthetic primer sequence 5'-T30-3'.


```
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 30 AAAAAAAAAA 5

RESULT 642
ABK70490/c
ID ABK70490 standard; DNA; 30 BP.
XX AC ABK70490;
XX DT 15-JUL-2002 (first entry)
XX DE In-situ analysis synthetic probe #58.
XX KW Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;
KW Epstein-Barr virus; lambda-immunoglobulin light chain; haptens;
KW kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;
KW Epstein-Barr early RNA; probe; ss.
XX OS Synthetic.
XX PN WO200222874-A2.
XX PD 21-MAR-2002.
XX PF 06-SEP-2001; 2001WO-US028014.
XX PR 15-SEP-2000; 2000US-0233177P.
XX PA (VENT-) VENTANA MEDICAL SYSTEMS INC.
XX PI Utermohlen JG, Connaughton J;
XX DR WPI; 2002-371972/40.
XX PT Novel oligonucleotide label-domain for incorporation into oligonucleotide
PT probes useful for detecting or localizing nucleic acid target genes
PT within a cell or tissue sample.
XX PS Disclosure; Page 69; 71pp; English.
XX CC The present invention relates to a new oligonucleotide label-domain
CC comprising the sequence (CTATTT)n and its complement (AAATAG)n, where
CC n is 1. The probe sets of the invention are useful for detecting kappa or
CC lambda-immunoglobulin light chain mRNA or corresponding heteronuclear
CC RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)
CC early RNA 1 and RNA 2, and human Alu repetitive satellite genomic
CC sequences. The invention is a useful generic sequence for incorporation
CC into oligonucleotide probes for detecting gene-specific sequences within
CC cells or tissue samples in situ hybridisation analysis and for
CC attaching a label to immunoglobulins or other proteins for detecting
CC haptens and antigens in immunohistochemical analyses. The present nucleic
CC acid sequence represents one of a collection (ABK70376-ABK70501) of
CC oligonucleotide probes that were used in the invention for detecting or
CC localising a plurality nucleic acid target gene or antigen within a cell
CC or tissue sample
XX SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 30 AAAAAAAAAA 5

RESULT 643
ABK70490/c
ID ABK70490 standard; DNA; 30 BP.
XX AC ABK70490;
XX DT 15-JUL-2002 (first entry)
XX DE In-situ analysis synthetic probe #58.
XX KW Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;
KW Epstein-Barr virus; lambda-immunoglobulin light chain; haptens;
KW kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;
KW Epstein-Barr early RNA; probe; ss.
XX OS Synthetic.
XX PN WO200222874-A2.
XX PD 21-MAR-2002.
XX PF 06-SEP-2001; 2001WO-US028014.
XX PR 15-SEP-2000; 2000US-0233177P.
XX PA (VENT-) VENTANA MEDICAL SYSTEMS INC.
XX PI Utermohlen JG, Connaughton J;
XX DR WPI; 2002-371972/40.
XX PT Novel oligonucleotide label-domain for incorporation into oligonucleotide
PT probes useful for detecting or localizing nucleic acid target genes
PT within a cell or tissue sample.
XX PS Disclosure; Page 69; 71pp; English.
XX CC The present invention relates to a new oligonucleotide label-domain
CC comprising the sequence (CTATTT)n and its complement (AAATAG)n, where
CC n is 1. The probe sets of the invention are useful for detecting kappa or
CC lambda-immunoglobulin light chain mRNA or corresponding heteronuclear
CC RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)
CC early RNA 1 and RNA 2, and human Alu repetitive satellite genomic
CC sequences. The invention is a useful generic sequence for incorporation
CC into oligonucleotide probes for detecting gene-specific sequences within
CC cells or tissue samples in situ hybridisation analysis and for
CC attaching a label to immunoglobulins or other proteins for detecting
CC haptens and antigens in immunohistochemical analyses. The present nucleic
CC acid sequence represents one of a collection (ABK70376-ABK70501) of
CC oligonucleotide probes that were used in the invention for detecting or
CC localising a plurality nucleic acid target gene or antigen within a cell
CC or tissue sample
XX SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 30 AAAAAAAAAA 5

RESULT 644
AAV48087
ID AAV48087 standard; DNA; 30 BP.
XX AC AAV48087;
XX DT 27-OCT-1998 (first entry)
XX
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```
ABS53961/c
ID ABS53961 standard; DNA; 30 BP.
XX AC ABS53961;
XX DT 26-NOV-2002 (first entry)
XX DE Method of measuring nucleic acid related oligonucleotide dT30mer.
XX KW Fluorescent intercalative dye; nucleic acid detection; gene diagnosis;
KW clinical diagnostics; Stokes shift; ds.
XX OS Synthetic.
XX PN EP1223226-A2.
XX PD 17-JUL-2002.
XX PF 11-JAN-2002; 2002EP-00000723.
XX PR 11-JAN-2001; 2001JP-00003432.
XX PA (TOYJ ) TOSOH CORP.
XX PI Tokunaga T, Ishiguro T, Horie R;
XX DR WPI; 2002-645688/70.
XX PT Fluorescent dye or its salt, hydrate, solvate or stereoisomer for nucleic
PT acid probe for measuring nucleic acid(s) containing specific nucleic acid
PT sequence in sample, has specific formula.
XX PS Example 5; Page 33; 40pp; English.
XX CC The invention describes a novel fluorescent dye and method of detecting
CC nucleic acid. The dye and method are useful for nucleic acid probes for
CC measuring nucleic acid(s) containing a specific nucleic acid sequence in
CC a sample, and for qualitative/quantitative assay of target RNA containing
CC specific base sequence anticipated in gene mixture. The assay is useful
CC in gene diagnosis and other areas of clinical diagnostics and in
CC identification/quantification microorganisms in biological samples such
CC as serum, plasma and urine, microbially contaminated samples from food,
CC rooms, soil, rivers and sea. The fluorescent intercalative dye shows a
CC large fluorescent enhancement upon intercalation into double-stranded
CC nucleic acid, and shows a great difference between excitation and
CC emission wavelengths (has a large Stokes shift) and does not have a
CC fluorescent spectrum that overlaps with those of conventionally known
CC fluorescent intercalation dyes. Viruses, microbial RNAs, specific
CC sequences in one RNA, are detected or quantified in a short time, hence
CC the detection method is applicable to clinical diagnosis which requires
CC high reliability. Amplification and extraction efficiencies of the target
CC nucleic acid, are checked. This sequence represents a synthetic DNA used
CC as the target in an assay to detect double stranded DNA
XX SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 30 AAAAAAAAAA 5

RESULT 644
AAV48087
ID AAV48087 standard; DNA; 30 BP.
XX AC AAV48087;
XX DT 27-OCT-1998 (first entry)
XX
```

Thu Jun 10 13:10:09 2004

```
DE Oligonucleotide 30-P.
XX
XX In situ translation; RNA-protein fusion; binding reagent; antibody;
KW industrial catalyst; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 30
FT /*tag= a
FT /note= "Puromycin"
FT
XX
XX WO9831700-A1.
XX
XX 23-JUL-1998.
XX
XX 14-JAN-1998; 98WO-US000807.
XX
XX 21-JAN-1997; 97US-0035963P.
PR 06-NOV-1997; 97US-0064491P.
XX
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX
XX Szostak JW, Roberts RW, Liu R;
PI
XX WPI; 1998-414032/35.
DR
XX
XX Selection of specific protein by screening protein-RNA fusions generated
PT in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
PT with altered properties, potentially useful as catalysts or for therapy
PT or diagnosis.
XX
XX Disclosure; Page 39; 94pp; English.
PS
XX The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
CC variations were used to generate RNA-protein fusions. These were used in
CC the selection of a specific protein or RNA, by in vitro or in situ
CC translation of candidate RNA molecules to produce RNA-protein fusions,
CC then selecting specific RNA protein fusions. The method is used to select
CC proteins (or DNA encoding them) having altered properties, e.g. for
CC identification of new binding reagents, to identify improved human
CC antibodies or new enzymes. These proteins are potentially useful in
CC diagnosis and therapy, or as industrial catalysts. The methods allow many
CC rounds of selection and amplification to be performed, resulting in
CC enrichment of even very rare molecules and allowing isolation of proteins
CC that bind specifically to almost any compound or catalyze almost any
CC reaction
XX
XX Sequence 30 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 1 Other;
SQ
Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAA 26

RESULT 645
AAQ83940
ID AAQ83940 standard; DNA; 30 BP.
XX
AC AAQ83940;
XX
XX 25-MAR-2003 (revised)
DT 04-OCT-1995 (first entry)
XX
XX Oligonucleotide clamp o, for producing comb-type brached polymer.
DE
XX HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
KW
XX Synthetic.
OS
```

```
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "Modified with SP(O-)(=O)-"
XX
XX WO9501365-A1.
XX
XX 12-JAN-1995.
XX
XX 05-JUL-1994; 94WO-US007557.
PF
XX
XX 02-JUL-1993; 93US-00087386.
PR
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
PA
XX
XX Gryaznov SM;
PI
XX WPI; 1995-060944/08.
XX
XX Synthesis of branched polymers and novel branched polymeric structures -
PT used as molecular probes esp. for detecting poly-nucleotide(s).
XX
XX Example 8; Page 33; 52pp; English.
PS
XX The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the
CC construction of an oligonucleotide clamp. The clamp is a comb-type
CC branched polymer which has 3' termini and was used to bind a target
CC sequence comprising a segment of the HIV pol and nef genes in single
CC stranded or double stranded forms. An oligonucleotide clamp is a compound
CC capable of forming a covalently closed macromolecule or a stable circular
CC complex after specifically binding to the target polynucleotide.
CC Oligonucleotide clamps generally comprise one or more oligonucleotide
CC moieties capable of specific binding to the target molecule and one or
CC more pairs of binding moieties covalently linked to the oligonucleotide
CC moieties. Upon annealing of the oligonucleotides moieties to the target
CC polynucleotide, the binding moieties of a pair are brought into
CC juxtaposition so that they form a stable covalent or non-covalent linkage
CC or complex. The interaction of the binding moieties effectively clamps
CC the specifically annealed oligonucleotide moieties to the target
CC polynucleotide. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 4 AAAAAA 29

RESULT 646
AAQ83940
ID AAQ83940 standard; DNA; 30 BP.
XX
AC AAQ83940;
XX
XX 27-APR-2001 (first entry)
DT
XX Oligonucleotide clamp #22.
DE
XX Oligonucleotide clamp; ds.
KW
XX Unidentified.
OS
XX US6180777-B1.
PN
XX 30-JAN-2001.
XX
XX 03-JAN-1997; 97US-00787321.
XX
```

PR 12-JAN-1996; 96US-0009918P.
XX (FARB) BAYER CORP.
XX
PI Horn T;
XX WPI; 2001-201911/20.
XX
PT Synthesizing branched nucleic acids useful as diagnostic and molecular
PT probes, involves combining first units having haloalkylamino groups and
PT second units having thiol or phosphorothioate groups.
XX
PS Example 8; Col 19; 20pp; English.
XX
CC The present invention relates to a method for synthesising a branched or
CC multiply connected macromolecular structure, comprising oligonucleotide
CC clamps (OC). The macromolecular structure is capable of specifically
CC binding to a target molecule, and can therefore be used as probes. At
CC least one OC comprises a target binding sequence that binds specifically
CC and stably with the target molecule, and at least two OCs comprise signal
CC generation moieties capable of generating a detectable signal in the
CC presence of the target molecule. In addition the OCs are connected to one
CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC present sequence is an OC used in the present invention
XX
SQ Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 4 ACACAAAAA 29

RESULT 647
AAV62858/c
ID AAV62858 standard; DNA; 30 BP.
XX
AC AAV62858;
XX
DT 05-MAR-1999 (first entry)
XX
DE Primer for PR-Q gene.
XX
KW Chemically regulatable DNA promoter; expression control; pesticide;
KW herbicide tolerance; pathogenesis-related gene; PR gene; primer; ss.
XX
OS Synthetic.
OS Nicotiana acuminata.
XX
XX US5851766-A.
PN
XX 22-DEC-1998.
PD
XX
PF 31-MAY-1995; 95US-00456262.
XX
PR 31-MAY-1995; 95US-00456262.
XX
PA (NOVS) NOVARTIS FINANCE CORP.
XX
PI Harms C, Ryals JA;
XX
DR WPI; 1999-080396/07.
XX
PT Isolating chemically regulatable DNA sequences in plants - useful for
PT chemically controlling expression in transformed plants.
XX
PS Example 72; Col 96; 175pp; English.
XX
CC This sequence represents a primer used to isolate the tobacco
CC pathogenesis-related (PR) gene. The PR gene can be isolated using the

CC method of the invention. The method is for isolating a chemically
CC regulatable DNA promoter fragment from the 5' flanking region of a
CC chemically regulatable gene in a plant tissue. The method allows
CC isolation of sequences which will be useful for the controlled expression
CC of genes, under the control of a non-coding regulatable sequence. This is
CC useful in plants with a herbicide or pesticide detoxification mechanism
CC under the control of a chemical regulator, the regulator being applied
CC before or with the herbicide or pesticide to give optimal tolerance. The
CC promoter fragment is useful for controlling sequences which encode traits
CC such as height, shape, development, male or female sterility, and the
CC ability of the plant to withstand cold, heat, salt and drought. The
CC chemical induction of the promoter allows the regulation of production of
CC compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
CC industrial feedstocks, antimicrobials and pharmaceuticals, by
CC biosynthesis or metabolite conversion, whose biosynthesis is controlled
CC by endogenous or foreign genes. The method allows control over the time
CC and rate of gene expression either throughout the whole plant, or in
CC localized tissues, to achieve e.g. fungal or insect resistance, or in
CC instance dusting the leaves with the chemical regulator. Controlling the
CC developmental processes by the application of a regulating chemical in
CC e.g. the commercial production of cultivated crops allows processes such
CC as germination, flower formation and fruit ripening to be synchronised at
CC a given time
XX
SQ Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTTTTTTTTAACT 2190
Db 30 CTTATGTTTTTTTTTTTTTTGAATT 5

RESULT 648
AAV81666/c
ID AAV81666 standard; DNA; 30 BP.
XX
AC AAV81666;
XX
DT 25-FEB-1999 (first entry)
XX
DE Oligonucleotide SEQ ID NO:85 used in Example 72.
XX
KW Regulation; transcription; plant tissue; chimeric construction; PR;
KW pathogenesis-related protein; anti-pathogenic; transgenic plant;
KW beta-1,3-glucanase activity; pest resistance; primer; ss.
XX
OS Synthetic.
XX
XX US5847258-A.
PN
XX 08-DEC-1998.
PD
XX
PF 31-MAY-1995; 95US-00457364.
XX
PR 08-MAR-1988; 88US-00165667.
PR 06-FEB-1989; 89US-00305566.
PR 24-MAR-1989; 89US-00329018.
PR 20-JUN-1989; 89US-00368672.
PR 20-OCT-1989; 89US-00425504.
PR 07-SEP-1990; 90US-00580431.
PR 21-DEC-1990; 90US-00632441.
PR 01-APR-1991; 91US-00678378.
PR 27-SEP-1991; 91US-00768122.
PR 06-MAR-1992; 92US-00848506.
PR 06-NOV-1992; 92US-00973197.
PR 06-APR-1993; 93US-00042847.
PR 12-APR-1993; 93US-00045957.
PR 16-JUL-1993; 93US-00093301.
PR 13-JAN-1994; 94US-00181271.
PR 31-MAY-1995; 95US-00457364.

CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
SQ Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 32;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7
RESULT 651
AAN92244/c
ID AAN92244 standard; DNA; 32 BP.
XX
AC AAN92244;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRCO68.
XX
KW Probe MRCO68; solid support; ribonuclease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .14
FT /*tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature 15. .22
FT /*tag= b
FT /note= "ribonucleotides."
FT misc_feature 23. .32
FT /*tag= c
FT /note= "deoxyribonucleotides."
XX
PN WO8910415-A.
XX
PD 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (MEIO-) MEIOGENICS INC.
PI Duck P, Bender R;
XX
DR WPI; 1989-339977/46.
XX
PT Detecting target nucleic acid molecules - using excess complementary
PT nucleic acid probes and nicking to complete a cycling sequence.
XX
PS Disclosure; Page 24; 34pp; English.
XX
CC Probe MRCO68 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target fragments to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX

SQ Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 32;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7
RESULT 652
ADC33445/c
ID ADC33445 standard; DNA; 32 BP.
XX
AC ADC33445;
XX
DT 18-DEC-2003 (first entry)
XX
DE Template oligonucleotide #SEQ ID 2.
XX
KW Binding; tandem repeat; label; analyte detection; ss.
XX
OS Synthetic.
XX
PN WO2003072721-A2.
XX
PD 04-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US0005301.
XX
PR 21-FEB-2002; 2002US-0359223P.
PR 08-MAY-2002; 2002US-0379360P.
XX
PA (DISC-) DISCOVERX INC.
XX
PI Wu M, Ullman E;
XX
DR WPI; 2003-712717/67.
XX
PT Detecting a label comprising employing (as the label) a reagent having a
PT 3' extendable terminus hybridized to a tandem repeat template in
PT combination with a DNA polymerase and dNTPs necessary for repetitively
PT replicating the tandem repeat.
XX
PS Example; SEQ ID NO 2; 38pp; English.
XX
CC The invention relates to a method for detecting a label, comprising
CC employing (as the label) a reagent having a 3' extendable terminus
CC hybridised to a tandem repeat template in combination with a DNA
CC polymerase and dNTPs necessary for repetitively replicating the tandem
CC repeat. The method involves detecting a binding event between the first and
CC second binding members, employing a label to determine the occurrence of
CC the binding event. The tandem repeating units are polyT. The method of
CC the invention is useful in detecting an analyte using repetitive
CC extension along a tandem repeat. The extended nucleic acid may be used
CC for detecting a moiety, particularly involved in a binding event
CC employing a reagent. The current sequence represents a template member
CC oligonucleotide containing a polyT tandem repeat that binds to the
CC extendable oligonucleotide given in ADC33444.
XX
SQ Sequence 32 BP; 0 A; 0 C; 0 G; 32 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 32;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7
RESULT 653

AAF29153/c
ID AAF29153 standard; DNA; 33 BP.
XX
AC AAF29153;
XX
DT 04-APR-2001 (first entry)
XX
DE PCR primer SEQ ID 24 used to amplify SRSV specific cDNA.
XX
KW Small round structured virus; SRSV; food poisoning; PCR primer; ss.
XX
OS Small round structured virus.
XX
PN WO200079280-A1.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-2000; 2000WO-JP004095.
XX
PR 22-JUN-1999; 99JP-00175928.
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA (DENK-) DENKA SEIKEN KK.
XX
PI Takeda N, Natori K, Miyamura T, Kamata K, Sato T, Sato S;
XX
XX WPI; 2001-080848/09.
DR
XX
XX Kit for the detection and typing of small round-structured virus (SRSV)
PT strains for investigation of food poisoning outbreaks, contains
PT antibodies.
XX
PS Example 1; Page 75; 84pp; Japanese.
XX
CC This invention relates to a kit for the detection and typing of small
CC round structured virus (SRSV) strains. The kit contains antibodies
CC directed against peptides represented in sequences AAB49700 - AAB49710,
CC which are each SRSV strain specific. Polynucleotide sequences AAF20141 -
CC AAF20151 represent cDNA encoding the strain specific proteins. The kit is
CC used for detecting and typing strains of SRSV in order to prevent the
CC spread of infection and to examine the epidemiology of outbreaks. PCR
CC primers AAF29152 - AAF29163 are used to amplify SRSV strain specific cDNA
CC sequences
XX
SQ Sequence 33 BP; 0 A; 0 C; 0 G; 33 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 33;
Best Local Similarity 84.6%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA... 2804
Db 33 AAAAAAAAAA... 8
RESULT 654
AAX88521/c
ID AAX88521 standard; DNA; 33 BP.
XX
AC AAX88521;
XX
DT 13-SEP-1999 (first entry)
XX
DE Conus stercusmuscarum contryphan PCR primer DHOG 496.
XX
KW Contryphan; leu-tryphan; anticonvulsant; neuroprotective; venom;
KW cone snail; neurodegenerative disorder; epilepsy; neurotoxic injury;
KW hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident;
KW brain trauma; spinal chord trauma; myocardial infarct; physical trauma;
KW drowning; suffocation; perinatal asphyxia; hypoglycaemia; migraine;
KW senile dementia; Alzheimer's disease; amyotrophic lateral sclerosis;
KW Parkinson's disease; Huntington's disease; Down's syndrome; PCR primer;
KW Korsakoff's disease; schizophrenia; neuronal damage; seizure; ss.

XX
OS Synthetic.
OS Conus stercusmuscarum.
XX
PN WO9933865-A1.
XX
PD 08-JUL-1999.
XX
PF 16-DEC-1998; 98WO-US026789.
XX
PR 24-DEC-1997; 97US-0068737P.
PR 16-APR-1998; 98US-00061026.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
XX Jacobsen R, Jimenez E, Cruz LJ, Olivera BM, Gray WR, Grilley M;
PI Watkins M, Hillyard DR;
XX
DR WPI; 1999-419087/35.
XX
PT New pure contryphan peptides.
XX
PS Example 3; Page 20; 48pp; English.
XX
CC The present sequence represents a PCR primer for a contryphan
CC peptide sequence. Contryphan peptides are found in the venom of cone
CC snails. The contryphan peptides are useful as anticonvulsant agents, as
CC neuroprotective agents, for managing pain, and for treating
CC neurodegenerative disorders, especially those resulting from an
CC overstimulation of excitatory amino acid receptors. The contryphans are
CC useful for the treatment and alleviation of epilepsy and as a general
CC anticonvulsant agent. The contryphans are also useful to reduce
CC neurotoxic injury associated with conditions of hypoxia, anoxia, or
CC ischaemia which typically follows stroke, cerebrovascular accident, brain
CC or spinal chord trauma, myocardial infarct, physical trauma, drownings,
CC suffocation, perinatal asphyxia, or hypoglycaemic events. The contryphans
CC are further useful for the treatment of Alzheimer's disease, senile
CC dementia, amyotrophic lateral sclerosis, Parkinson's disease,
CC Huntington's disease, Down's syndrome, Korsakoff's disease,
CC schizophrenia, AIDS dementia, multi-infarct dementia, and neuronal damage
CC associated with uncontrolled seizures. The contryphans are further useful
CC in controlling pain and are effective in the treatment of migraine. They
CC can be used prophylactically or to relieve the symptoms associated with a
CC migraine episode
XX
SQ Sequence 33 BP; 0 A; 1 C; 2 G; 30 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 33;
Best Local Similarity 84.6%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA... 2804
Db 33 AAAAAAAAAA... 8
RESULT 655
AAT93827/c
ID AAT93827 standard; DNA; 34 BP.
XX
AC AAT93827;
XX
DT 25-MAR-2003 (revised)
DT 24-FEB-1998 (first entry)
XX
DE Antitumoural phosphodiester oligonucleotide 17 with cytotoxic activity.
XX
KW Phosphodiester; selective binding; cell viability; growth;
KW tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW lymphoblastic tumour; ss.
XX
OS Synthetic.

PH Key modified_base Location/Qualifiers
FT 1. .34
FT /*tag= a
FT /note= "phosphodiester oligonucleotide"
XX WO9720924-A1.
XX 12-JUN-1997.
XX 04-DEC-1996; 96WO-EP005388.
XX 04-DEC-1995; 95IT-MI002539.
PA (SAIC-) SAICOM SRL.
XX Scaggiante B, Quadrifoglio F;
PI WPI; 1997-319771/29.
XX
PT New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT selective cytotoxic effect on tumour cells, for treating both solid and
PT liquid tumours.
XX
PS Claim 10; Page 6; 38pp; English.
XX
CC Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-
CC (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''-(GgTg')g''-N', where: N and
CC N' = T or G, equal or different from each other; x = 0-8, equal or
CC different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC 16, equal or different from each other; a''', b''', c''', d''', e''', f''', and g''' = 1-
CC to selectively bind and sequester some proteins which are believed
CC the viability and growth of tumoural cell line. They have specific and
CC selective cytotoxic activity against tumour cells, and can be used for
CC treating tumours of the liquid type, in particular of lymphoblastic
CC origin, and of solid type, in particular lymphomas. The present
CC phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC reduced growth of CCRF-CEM tumoural cells by 71%, which is detectable 48
CC hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 34 BP; 0 A; 0 C; 2 G; 32 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 34;
Best Local Similarity 84.6%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2779 AGAATTGAAAAA 2804
Db 34 ACAAAAAA 9

RESULT 656
AAL07488
ID AAL07488 standard; DNA; 38 BP.
XX AAL07488;
AC
XX 21-NOV-2001 (first entry)
DT
XX Human reproductive system related antigen DNA SEQ ID NO: 10176.
DE Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
KW Homo sapiens.
OS
XX WO200155320-A2.
PN
XX 02-AUG-2001.
PD
XX 17-JAN-2001; 2001WO-US001339.
PF

XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.

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PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.

XX Disclosure; SEQ ID NO 10176; 1297pp + Sequence Listing; English.
PS
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX
SQ Sequence 38 BP; 35 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 38;
Best Local Similarity 84.6%; Pred. No. 2.1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 657
AAZ57404/c
ID AAZ57404 standard; DNA; 38 BP.
XX
AC AAZ57404;
XX
DT 07-APR-2000 (first entry)
XX
DE Hepatitis C virus PCR primer CAC-T35 SEQ ID NO:19.
XX
KW Hepatitis C virus; RNA virus; replication; viral infection; PCR primer;
KW ss.
XX
OS Hepatitis C virus.
XX
PN WO9967394-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003380.
XX
PR 24-JUN-1998; 98JP-00177820.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Kohara M, Kohara K, Taira K, Matsuzaki J, Ohmori H;
XX
DR WPI; 2000-106296/09.
XX
PT Vectors expressing full-length gene of RNA viruses, useful in clarifying
PT mechanisms of RNA viral replication, infection, and developing remedies
PT and therapeutics.
XX
PS Example 2; Page 20; 46pp; Japanese.
XX
CC The present invention describes a vector comprising a cDNA encoding an
CC RNA virus gene, constructed to ensure the exact and homogeneous
CC transcription of both terminals of the RNA virus gene. Also described is
CC a method for screening drugs for inhibiting the replication of RNA virus
CC by using the RNA viral infection model animal, particularly one with
CC hepatitis C viral infection. The vector is useful in clarifying the
CC mechanism of RNA viral replication, onset of RNA viral infection, and
CC developing remedies and therapeutics for RNA viral infections,
CC particularly of a hepatitis C virus. The present sequence represents a
CC PCR primer which is used in the exemplification of the present invention
XX
SQ Sequence 38 BP; 1 A; 2 C; 0 G; 35 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 38;
Best Local Similarity 84.6%; Pred. No. 2.1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804


```
Db      38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 13
RESULT 658
AAL07487
ID      AAL07487 standard; DNA; 38 BP.
XX      AAL07487;
AC      21-NOV-2001 (first entry)
XX      Human reproductive system related antigen DNA SEQ ID NO: 10175.
DT      Human; reproductive system related antigen; reproductive system disorder;
DE      cancer; gene therapy; ds.
XX      Homo sapiens.
KW      WO200155320-A2.
KW      02-AUG-2001.
XX      17-JAN-2001; 2001WO-US001339.
XX      31-JAN-2000; 2000US-0179065P.
PF      04-FEB-2000; 2000US-0180628P.
XX      24-FEB-2000; 2000US-0184664P.
XX      02-MAR-2000; 2000US-0186350P.
XX      16-MAR-2000; 2000US-0189874P.
XX      17-MAR-2000; 2000US-0190076P.
XX      18-APR-2000; 2000US-0198123P.
XX      19-MAY-2000; 2000US-0205515P.
XX      07-JUN-2000; 2000US-0209467P.
XX      28-JUN-2000; 2000US-0214886P.
XX      30-JUN-2000; 2000US-0215135P.
XX      07-JUL-2000; 2000US-0216647P.
XX      07-JUL-2000; 2000US-0216880P.
XX      11-JUL-2000; 2000US-0217487P.
XX      11-JUL-2000; 2000US-0217496P.
XX      14-JUL-2000; 2000US-0218290P.
XX      26-JUL-2000; 2000US-0220963P.
XX      26-JUL-2000; 2000US-0220964P.
XX      14-AUG-2000; 2000US-0224518P.
XX      14-AUG-2000; 2000US-0224519P.
XX      14-AUG-2000; 2000US-0225213P.
XX      14-AUG-2000; 2000US-0225214P.
XX      14-AUG-2000; 2000US-0225266P.
XX      14-AUG-2000; 2000US-0225267P.
XX      14-AUG-2000; 2000US-0225268P.
XX      14-AUG-2000; 2000US-0225270P.
XX      14-AUG-2000; 2000US-0225447P.
XX      14-AUG-2000; 2000US-0225757P.
XX      14-AUG-2000; 2000US-0225758P.
XX      14-AUG-2000; 2000US-0225759P.
XX      18-AUG-2000; 2000US-0226279P.
XX      22-AUG-2000; 2000US-0226681P.
XX      22-AUG-2000; 2000US-0226868P.
XX      22-AUG-2000; 2000US-0227182P.
XX      23-AUG-2000; 2000US-0227009P.
XX      30-AUG-2000; 2000US-0228924P.
XX      01-SEP-2000; 2000US-0229287P.
XX      01-SEP-2000; 2000US-0229343P.
XX      01-SEP-2000; 2000US-0229344P.
XX      01-SEP-2000; 2000US-0229345P.
XX      05-SEP-2000; 2000US-0229509P.
XX      06-SEP-2000; 2000US-0229513P.
XX      06-SEP-2000; 2000US-0230437P.
XX      06-SEP-2000; 2000US-0230438P.
XX      08-SEP-2000; 2000US-0231242P.
XX      08-SEP-2000; 2000US-0231243P.
XX      08-SEP-2000; 2000US-0231244P.
XX      08-SEP-2000; 2000US-0231413P.
PR      08-SEP-2000; 2000US-0231414P.
PR      08-SEP-2000; 2000US-0232080P.
PR      08-SEP-2000; 2000US-0232081P.
PR      12-SEP-2000; 2000US-0231968P.
PR      14-SEP-2000; 2000US-0232397P.
PR      14-SEP-2000; 2000US-0232398P.
PR      14-SEP-2000; 2000US-0232399P.
PR      14-SEP-2000; 2000US-0232400P.
PR      14-SEP-2000; 2000US-0232401P.
PR      14-SEP-2000; 2000US-0233063P.
PR      14-SEP-2000; 2000US-0233064P.
PR      14-SEP-2000; 2000US-0233065P.
PR      21-SEP-2000; 2000US-0234223P.
PR      21-SEP-2000; 2000US-0234274P.
PR      25-SEP-2000; 2000US-0234997P.
PR      25-SEP-2000; 2000US-0234998P.
PR      26-SEP-2000; 2000US-0235484P.
PR      27-SEP-2000; 2000US-0235834P.
PR      27-SEP-2000; 2000US-0235836P.
PR      29-SEP-2000; 2000US-0236327P.
PR      29-SEP-2000; 2000US-0236367P.
PR      29-SEP-2000; 2000US-0236368P.
PR      29-SEP-2000; 2000US-0236369P.
PR      29-SEP-2000; 2000US-0236370P.
PR      02-OCT-2000; 2000US-0236802P.
PR      02-OCT-2000; 2000US-0237037P.
PR      02-OCT-2000; 2000US-0237038P.
PR      02-OCT-2000; 2000US-0237039P.
PR      02-OCT-2000; 2000US-0237040P.
PR      13-OCT-2000; 2000US-0239935P.
PR      13-OCT-2000; 2000US-0239937P.
PR      20-OCT-2000; 2000US-0240960P.
PR      20-OCT-2000; 2000US-0241221P.
PR      20-OCT-2000; 2000US-0241785P.
PR      20-OCT-2000; 2000US-0241786P.
PR      20-OCT-2000; 2000US-0241787P.
PR      20-OCT-2000; 2000US-0241808P.
PR      20-OCT-2000; 2000US-0241809P.
PR      20-OCT-2000; 2000US-0241826P.
PR      01-NOV-2000; 2000US-0244617P.
PR      08-NOV-2000; 2000US-0246474P.
PR      08-NOV-2000; 2000US-0246475P.
PR      08-NOV-2000; 2000US-0246476P.
PR      08-NOV-2000; 2000US-0246477P.
PR      08-NOV-2000; 2000US-0246478P.
PR      08-NOV-2000; 2000US-0246523P.
PR      08-NOV-2000; 2000US-0246524P.
PR      08-NOV-2000; 2000US-0246525P.
PR      08-NOV-2000; 2000US-0246526P.
PR      08-NOV-2000; 2000US-0246527P.
PR      08-NOV-2000; 2000US-0246528P.
PR      08-NOV-2000; 2000US-0246532P.
PR      08-NOV-2000; 2000US-0246609P.
PR      08-NOV-2000; 2000US-0246610P.
PR      08-NOV-2000; 2000US-0246611P.
PR      08-NOV-2000; 2000US-0246613P.
PR      17-NOV-2000; 2000US-0249207P.
PR      17-NOV-2000; 2000US-0249208P.
PR      17-NOV-2000; 2000US-0249209P.
PR      17-NOV-2000; 2000US-0249210P.
PR      17-NOV-2000; 2000US-0249211P.
PR      17-NOV-2000; 2000US-0249212P.
PR      17-NOV-2000; 2000US-0249213P.
PR      17-NOV-2000; 2000US-0249214P.
PR      17-NOV-2000; 2000US-0249215P.
PR      17-NOV-2000; 2000US-0249216P.
PR      17-NOV-2000; 2000US-0249217P.
PR      17-NOV-2000; 2000US-0249218P.
PR      17-NOV-2000; 2000US-0249244P.
PR      17-NOV-2000; 2000US-0249245P.
PR      17-NOV-2000; 2000US-0249264P.
PR      17-NOV-2000; 2000US-0249265P.
PR      17-NOV-2000; 2000US-0249297P.
```

PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; SEQ ID NO 10175; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX
SQ Sequence 38 BP; 34 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 38;
Best Local Similarity 84.6%; Pred. No. 2.1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 1 AAAAAA 26
RESULT 659
AAQ25031/c
ID AAQ25031 standard; DNA; 40 BP.
XX
AC AAQ25031;
XX
DT 13-JUL-1992 (first entry)
XX
DE Oligonucleotide specific for HIV proviral DNA.
XX
KW HIV; thiolation; reverse transcriptase; primer; inhibition; homooligomer;
KW ss.
XX
OS Synthetic.
XX
PN WO9203127-A.
XX
PD 05-MAR-1992.
XX
PF 15-AUG-1991; 91WO-US005919.
XX
PR 16-AUG-1990; 90US-00568131.
XX
XX (UYNY-) RES FOUND UNIV NEW.
PA
XX Bardos TJ, Ho YK, Aradi J, Schinazi RF;
PI
XX WPI; 1992-096567/12.
XX

PT Compsn. contg. 5-thiolated (oligo-poly-)nucleotide(s) - for treating HIV
PT infection, AIDS and for preventing HIV-1 infection.
XX
PS Disclosure; Page 11; 42pp; English.
XX
CC The oligomer comprises a non-thiolated (binding) homooligonucleotide
CC region (d(T)12) to promote the binding of the remaining portion of the
CC 5-thiolated oligonucleotide (MdU 28) to a homopurine site of the viral
CC genome via triple-helix formations. The oligo is used to in the treatment
CC of HIV. See also AAQ22624-27 and AAQ25017-Q25032
XX
SQ Sequence 40 BP; 0 A; 0 C; 0 G; 12 T; 28 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 40;
Best Local Similarity 84.6%; Pred. No. 2.2e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAA 2804
Db 40 AAAAAA 15
RESULT 660
AAA39649/c
ID AAA39649 standard; DNA; 40 BP.
XX
AC AAA39649;
XX
DT 11-SEP-2000 (first entry)
XX
DE Primer used in construction of hybrid CAT RNA.
XX
KW Control element; translation enhancer; pestivirus homology box IV;
KW immune response; viral infection; primer; ss.
XX
OS Unidentified.
XX
PN US6057093-A.
XX
PD 02-MAY-2000.
XX
PF 12-MAY-1995; 95US-00439996.
XX
PR 28-SEP-1992; 92US-00952799.
PR 28-SEP-1993; 93US-00128583.
XX
PA (CHIR) CHIRON CORP.
XX
PI Han JH, Spaete RR, Suh BS, Selby MJ, Houghton M, Yoo BJ;
XX
XX WPI; 2000-338599/29.
DR
XX Enhancing translation of coding region of hepatitis C virus involves
PT making RNA molecule comprising the coding region and 5' untranslated
PT region comprising a sequence fully homologous to pestivirus homology box
PT IV.
XX
PS Disclosure; Col 19-20; 16pp; English.
XX
CC This invention describes a novel method for enhancing translation of a
CC coding region which involves making an RNA molecule, comprising the
CC coding region operably linked to a 5' untranslated region (UTR)
CC comprising a sequence fully homologous to pestivirus homology box IV, and
CC then translating it so that the translation of the coding region is
CC enhanced. The method is useful for enhancing or controlling the
CC translation of HCV nucleic acid, which allows stronger immune responses,
CC where blocking or decreasing translation of viral nucleic acid may
CC decrease the pathology of viral infection. This sequence represents a
CC primer which is used in the construction of hybrid CAT RNA's described in
CC the method of the invention
XX
SQ Sequence 40 BP; 0 A; 0 C; 0 G; 40 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 40;
Best Local Similarity 84.6%; Pred. No. 2.2e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 40 AAAAAAAAAA 15

RESULT 661
AAZ98722/c
ID AAZ98722 standard; cDNA; 40 BP.
XX
AC AAZ98722;
XX
DT 20-JUN-2000 (first entry)
XX
DE PCR primer used for swine vesicular disease virus gene synthesis.
XX
KW Swine vesicular disease virus; SVDV; swine vesicular disease;
KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
KW differentiation; vaccine; prevent; PCR primer; ss.
XX
OS Swine vesicular disease virus.
XX
FN EP982403-A1.
XX
PD 01-MAR-2000.
XX
PF 14-AUG-1998; 98EP-00306486.
XX
PR 14-AUG-1998; 98EP-00306486.
XX
PA (BIOT-) DEV CENT BIOTECHNOLOGY.
XX
PI Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;
XX
DR WPI; 2000-258616/23.
XX
XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
PT to prevent swine vesicular disease.
XX
PS Example 2; Page 6; 66pp; English.
XX

This sequence represents a PCR primer used to determine the full length
cDNA sequence of the swine vesicular disease virus (SVDV) gene sequence
of Taiwan Yu-Li strain (see AAZ98717). SVDV is the causative agent of
swine vesicular disease, which is very similar to foot and mouth disease.
The invention relates to the wild-type Taiwan Yu-Li strain cDNA sequence,
and the gene sequences of the mutant SVDV strains N3, H21 and SP7. The
mutant SVDV nucleotide sequence can be used in a vaccine for the
prophylaxis of swine vesicular disease. The invention also includes a
method for differentiating the mutant SVDV nucleotide sequences from the
wild type strain of SVDV, coxsackievirus and foot-and-mouth disease virus
through the use of polymerase chain reaction

Sequence 40 BP; 1 A; 3 C; 3 G; 33 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 40;
Best Local Similarity 84.6%; Pred. No. 2.2e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 40 AAAAAAAAAA 15

RESULT 662
AAQ55168/c
ID AAQ55168 standard; DNA; 40 BP.
XX
AC AAQ55168;
XX

DT 25-MAR-2003 (revised)
DT 21-JUL-1994 (first entry)
XX
DE Sequence of primer for PCR amplification of HIV-LP Pt.1 isolate.
XX
KW Human immunodeficiency virus; HIV-LP; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9400562-A1.
XX
PD 06-JAN-1994.
XX
PF 23-JUN-1993; 93WO-US0006162.
XX
PR 24-JUN-1992; 92US-00903421.
XX
PA (UYNV) UNIV NEW YORK MT SINAI SCHOOL MEDICINE.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Gelman IH, Laurence JC;
XX
DR WPI; 1994-026200/03.
XX
PT HIV-LP useful in vaccine formulations - is novel HIV virus distinct from
PT HIV-1 and or HIV-2 viruses.
XX
PS Example; Page 7; 75pp; English.
XX

CC HIV-LP is a new variant of the HIV family. A cDNA first strand was
CC synthesised from Pt. 1 pellet using MLV RT. The product was converted
CC into dsDNA and this cDNA was amplified by PCR using primers AAQ55167 and
CC AAQ55168. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 40 BP; 3 A; 2 C; 3 G; 32 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 40;
Best Local Similarity 84.6%; Pred. No. 2.2e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2804
Db 40 AAAAAAAAAA 15

RESULT 663
AAV03013/c
ID AAV03013 standard; DNA; 41 BP.
XX
AC AAV03013;
XX
DT 17-AUG-1998 (first entry)
XX
DE Aspergillus oryzae alpha-amylase transcription factor PCR primer.
XX
KW alpha-amylase; promoter; filamentous fungi; transcription factor;
KW expression; control; production; heterologous polypeptide; medicinal;
KW industrial enzyme; PCR primer; amyR; ss.
XX
OS Synthetic.
OS Aspergillus oryzae.
XX
PN WO9801470-A1.
XX
PD 15-JAN-1998.
XX
PF 07-JUL-1997; 97WO-DK000305.
XX
PR 05-JUL-1996; 96DK-00000740.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Christensen T;

XX WPI; 1998-100998/09.
XX Transcription factor from Aspergillus oryzae which regulates alpha-
PT amylase promoter - useful for producing heterologous proteins, especially
PT medicinal proteins or enzymes, in filamentous fungi.
XX
PS Example 1; Page 25; 64pp; English.
XX
XX The sequence is that of PCR primer oligodT which was used in the analysis
CC of a transcription factor (amyR) which regulates the expression of an
CC alpha-amylase promoter
XX
SQ Sequence 41 BP; 2 A; 1 C; 2 G; 36 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 41;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAAAGAAAAA 2804
Db 41 AAAAAAAAAAAAAAAAAA 16
RESULT 664
AAA37946/C
ID AAA37946 standard; DNA; 42 BP.
XX
AC AAA37946;
XX
DT 18-AUG-2000 (first entry)
XX
DE DNA synthesis primer used in PTAN gene isolation.
XX
XX PTAN; testis specific; prostate cancer; overexpress; chromosome 1q22;
KW diagnose; cancer; breast; vaccine; primer; ss.
KW
XX Synthetic.
OS
XX WO200020589-A2.
PN
XX 13-APR-2000.
PD
XX 30-SEP-1999; 99WO-US022985.
PF
XX 30-SEP-1998; 98US-0102556P.
PR 02-OCT-1998; 98US-0102910P.
PR 21-DEC-1998; 98US-0113229P.
PR 14-APR-1999; 99US-0129518P.
XX
XX (UROG-) UROGENESYS INC.
PA (AFAR/) AFAR D E.
PA (HUBE/) HUBERT R S.
PA (RAIT/) RAITANO A B.
PA (MITC/) MITCHELL S C.
XX
PI Afar DE, Hubert RS, Raitano AB, Mitchell SC;
XX
XX WPI; 2000-317715/27.
DR
XX PTAN proteins, and sequences encoding them, used for diagnosing and
PT treating cancers, especially breast and prostate cancers.
PT
XX Example 1; Page 31; 71pp; English.
PS
XX This sequence represents a primer used in the isolation of cDNA fragments
CC of the PTAN (testis specific protein expressed in prostate cancer) gene.
CC PTAN is expressed in 3 isoforms PTAN-1, 2, and 3. The PTAN gene is
CC located on chromosome 1q22. PTAN is overexpressed in prostate cancer, and
CC has a testis specific expression pattern in adult tissues. PTAN shows no
CC homology to any known gene. PTAN can be used in methods for the diagnosis
CC of cancer, especially prostate or breast cancer, where the normal tissue
CC samples are prostate tissue, or breast tissue, bone tissue, lymphatic

CC tissue, serum, blood, or urine. A vector containing the PTAN nucleotide
CC sequence, a vaccine composition targeting PTAN, PTAN, ribozymes specific
CC for PTAN mRNA and antisense sequences, can be used to treat cancer,
CC especially breast and prostate cancers. Cancer development can be
CC inhibited by a vaccine composition targeting PTAN
XX
SQ Sequence 42 BP; 3 A; 2 C; 2 G; 35 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.6; DB 1; Length 42;
Best Local Similarity 84.6%; Pred. No. 2.4e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2779 AGAATTGAAAAAAGAAAAA 2804
Db 42 AAAAAAAAAAAAAAAAAA 17
RESULT 665
AAD17216/C
ID AAD17216 standard; DNA; 43 BP.
XX
AC AAD17216;
XX
DT 29-NOV-2001 (first entry)
XX
DE Human mRNA hybridisation selection reaction biotin-dT3 oligonucleotide.
XX
KW Human; multiplex ligation-dependent amplification; amplicon;
KW single nucleotide polymorphism; hybridisation selection reaction; ss.
KW
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "Biotin-labelled Thymidine"
XX
PN WO200161033-A2.
XX
PD 23-AUG-2001.
XX
XX 15-FEB-2001; 2001WO-EP001739.
PF
XX 15-FEB-2000; 2000EP-00200506.
PR
XX (SCHO/) SCHOUTEN J P.
PA
XX Schouten JP;
PI
XX WPI; 2001-550053/61.
DR
XX An improved multiplex ligation-dependent amplification method for
PT detecting specific single stranded target nucleic acids in samples.
PT
XX Example 8; Page 137; 158pp; English.
PS
XX The invention relates to an improved multiplex ligation-dependent
CC amplification method for detecting specific single stranded target
CC nucleic acids in samples using a plurality of probe sets comprising at
CC least 2 probes. Each probe comprises a target specific region and a non-
CC complementary region comprising a primer binding site. The probes in each
CC set are ligated when hybridised to a target nucleic acid and amplified by
CC a primer set. The method is used for detecting a nucleotide polymorphism,
CC especially a single nucleotide polymorphism; detecting multiple single
CC stranded target nucleic acid sequences (through the detection of multiple
CC amplicons); determining the absolute or relative abundance of multiple
CC single stranded nucleic acids in a sample; and detection of a break point
CC region in rearranged nucleic acids. By using a femtomolar amount of the
CC probes, a large number of different probe sets can be used to
CC simultaneously detect and quantify a corresponding large number of target
CC sequences with high specificity. The present DNA sequence is biotin-dT3
CC labelled fluorescent oligonucleotide which is used for the hybridisation

Db 1 TTTTTTTTTTTTTTTTCAAC 21

RESULT 668
AAQ75630
ID AAQ75630 standard; DNA; 21 BP.
XX
AC AAQ75630;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTTAAAC 2189
Db 1 TTTTTTTTTTTTTTTTGAAC 21

RESULT 669
AAQ75648
ID AAQ75648 standard; DNA; 21 BP.
XX
AC AAQ75648;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.
PF
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2167 TTTTTTTTTTTTTTTTGA 2187
Db 1 TTTTTTTTTTTTTTTTGA 21

RESULT 670
AAQ75676
ID AAQ75676 standard; DNA; 21 BP.
XX
AC AAQ75676;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2781 AATTGAAAAA 2801
Db 21 AATTAAAAA 1
RESULT 677
AAQ75773/c
ID AAQ75773 standard; DNA; 21 BP.
XX
AC AAQ75773;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
CC

XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2782 ATTGAAAAA 2802
Db 21 ATAGAAAAA 1
RESULT 678
AAQ75780/c
ID AAQ75780 standard; DNA; 21 BP.
XX
AC AAQ75780;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2784 TGAAAAA 2804
Db 21 TGAGAAAAA 1
RESULT 679
AAQ75660/c
ID AAQ75660 standard; DNA; 21 BP.
XX
AC AAQ75660;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 6; 11pp; Japanese.
PS A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
SQ Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2783 TTGAAAAA 2803
Db 21 TTGCAAAAAA 1
RESULT 680
AAQ75684/c
ID AAQ75684 standard; DNA; 21 BP.
XX AAQ75684;
AC 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX

PS Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
SQ Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2784 TGA 2804
Db 21 TGATAAAAAA 1
RESULT 681
AAQ75741/c
ID AAQ75741 standard; DNA; 21 BP.
XX AAQ75741;
AC 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
SQ Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2782 ATTCAAAAAA 2802
Db 21 ATCGAAAAAA 1

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RESULT 682
AAQ75652/c
ID   AAQ75652 standard; DNA; 21 BP.
XX
AC   AAQ75652;
XX
DT   04-AUG-1995 (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993; 93JP-00112515.
XX
PR   16-APR-1993; 93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   2784 TGAAAAAAAAAAAAAAAAAAAA 2804
Db   21 TGACAAAAAAAAAAAAAAAAAAAA 1

RESULT 683
AAQ75753/c
ID   AAQ75753 standard; DNA; 21 BP.
XX
AC   AAQ75753;
XX
DT   04-AUG-1995 (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993; 93JP-00112515.
XX
PR   16-APR-1993; 93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   2784 TGAIAAAAAAAAAAAAAAAAAA 2804
Db   21 TGACAAAAAAAAAAAAAAAAAAAA 1
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XX
PR   16-APR-1993; 93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   2782 ATTGAAAAAAAAAAAAAAAAAAAA 2802
Db   21 ACTGAAAAAAAAAAAAAAAAAAAA 1

RESULT 684
AAQ75788/c
ID   AAQ75788 standard; DNA; 21 BP.
XX
AC   AAQ75788;
XX
DT   04-AUG-1995 (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993; 93JP-00112515.
XX
PR   16-APR-1993; 93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
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